

```

g156      FAPFAAAVLTAHATGNAGQATVNTLAGLFILFRLAFIWCYIADKAALRSLMWAGGFACTV
              70          80          90          100          110          120

m156.pep  GLFVAAAX
            |||||
g156      GLFVAAAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 647>:

```

a156.seq
1  ATGACTTTCG CCTATTGGTG TATTCTGATT GCCTACCTAT TGCCGCTTTT
51 TTGTGCGGCG TATGCCAAAA AAGCGGGCGG ATTCCGGTTT AAAGACAACC
101 ACAATCCGCG CGATTTTCTG GCGCGCACGC AAGGCACAGC CGCCCGTGCC
151 CACGCCGCGC AGCAAAACGG TTTTGAAGCC TTTGCACCGT TTGCAGCCGC
201 CGTTTTGACG GCACACGCAA CCGGCAATGC CGGACAAGCA ACCGTCAACA
251 CGCTTGCCGG CCTGTTTCATC CTGTTCCGCC TCGCCTTTAT CTGGTGCTAC
301 ATCGCAGACA AAGCAGCATT ACGCTCGCTG ATGTGGGTGG GCGGATTTGT
351 CTGCACCGTC GGGCTGTTTG TCGTGGCTGC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 648; ORF 156.a>:

```

a156.pep
1  MTFAYWCILI AYLLPLFCAA YAKKAGGFRE KDNHNPRDFL ARTQGTAAARA
51  HAAQONGFEA FAPFAAAVLTAHATGNAGQA TVNTLAGLFI LFRFAFIWCY
101 IADKAALRSL MWVGGFVCTV GLFVAA*

```

m156/a156 90.6% identity in 127 aa overlap

```

              10          20          30          40          50          60
m156.pep      MTFAYWCILIACLLPLFCAAYAKKAGGFREFKDNHNPRGFLAHTOGAAARAHAAQONGFEA
              |||||
a156          MTFAYWCILIAYLLPLFCAAYAKKAGGFREFKDNHNPRDFLARTQGTAAARAHAAQONGFEA
              10          20          30          40          50          60

              70          80          90          100          110          120
m156.pep      FAPFAAAVLTAHATGNAAQSTINTLACLFI LFRFAFIWCYIADKAAMRSLMWAGGFACTV
              |||||
a156          FAPFAAAVLTAHATGNAGQATVNTLAGLFILFRLAFIWCYIADKAALRSLMWVGGFVCTV
              70          80          90          100          110          120

m156.pep      GLFVAAAX
              |||||
a156          GLFVAAAX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 649>:

```

g157.seq
1  atgaggaacg aggAAAAACg cgcctgcgc cgcaattgC gCgGgcggcg
51  ttgcgAAATg GGgcgagacg tGCGggCGGC GGCGgCgatA Aaaatcaacc
101 gcctgctcaa aCGTtatatc AAGCGCggtc gGaAaatcgG CGTGATTg
151 cCGATGGGCA AGGAATTGcg TTTGGGCGgc tTgtcCGCG CGGCGCAAAA
201 ACGCGGCGCA AAactctatc tgccttATAT CGAACCGCAC ACGCGGCGGA
251 TGTGGTTTAC GCCGTATCCT GAACGCGGAA TGAACGGGA ACGCAAGCGC
301 GGTAGGGCGA AGCTGCATGT CCCTCAGTTT GCAGGGCGCA AAATCCGCGT
351 GCACGGTTTG TCGGTATTGC TCGTCCCGCT TGTCGGCATA GACCGCGAAG
401 GCTACCGTTT GGGGAGGCA GCGGCTATT ACGATGCGAC GCTTTCGGCG
451 ATGAAATACC GTTTCAGGC GAAAACCGTG GCGGTGGGCT TTGCCTGCCA
501 GTTGGTGGAC AGGCTCCAC GCGAGGCGCA CGACCTGCCG CTGGACGGTT
551 TTGTATCGGA AGCGGGGATA TTGTGTTTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 650; ORF 157.ng>:

```
g157.pep
  1 MRNEEKRALR RELRGRRSQM GRDVRAAAAI KINRLKRYI KRGRKIGVYW
  51 PMGKELRLGG FVRAAQKRG A KLYLPYIEPH TRRMWFTYP ERGMRERKR
 101 GRAKLHVPQF AGRKIRVHGL SVLLVPLVGI DREGYRLGQA GGYDATLSA
 151 MKYRLQAKTV GVGAFACQLVD RLPREAHDL LDGFVSEAGI LCF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 651>:

```
m157.seq
  1 ATGAGGAACG AGGAAAACG CGCCTGCGC CGCAATTGC GCGGCGGCG
  51 TTCGCAAATG GGGCGGGACG TCGGGGCGG GCAACGGTA AAAATCAACC
 101 ACCTGCTCAA ACGTTATATT AAAAAAGGC GGAAATCGG CGTGATTGG
 151 CCGATGGGCA AGGAATTGCG TTTGGACGGC TTTGTCCGCG CGGCGCAAAA
 201 ACGCGGTGCG GAACTCTACC TGCCTTATAT CGAACCGCGT TCGGCGGCGA
 251 TGTGGTTTAC GCCGTATCCT GCCGATGGAG TAAAACAAGA ACGCAAGCGC
 301 GGTAGGGCGA AGCTGCATGT CCCTCAGTTT GCAGGTCGGA AAAAGCGTGT
 351 GCATGATTG AACCTCCTGC TTGTGCCAGT GGTGGGTATG GACAGGCTGG
 401 GCTACCGCTT GGGACAGGCA GCGGCTATT ACGATGCGAC GCTTTCAGCG
 451 ATGAAATACC GTTTCAGGC AAAAACCCTG GCGGTGGGCT TTGCCTGCCA
 501 GTTGGTGGAC AGGCTGCCCG TCGAGGCGCA CGACCGGTCT TTGGACGGTT
 551 TTGTGTCGGA GCGGGGATA TTGTGTTTTT AG
```

This corresponds to the amino acid sequence <SEQ ID 652; ORF 157>:

```
m157.pep
  1 MRNEEKRALR RELRGRRSQM GRDVRAAATV KINHLLKRYI KKGRKIGVYW
  51 PMGKELRLDG FVRAAQKRG A ELYLPYIEPR SRRMWFTYP ADGVKQERKR
 101 GRAKLHVPQF AGRKKRVHDL NLLVLPVVG DRLGYRLGQA GGYDATLSA
 151 MKYRLQAKTV GVGAFACQLVD RLPVEAHDRS LDGFVSEAGI LCF*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m157 / g157 88.1% identity in 193 aa overlap

	10	20	30	40	50	60
m157.pep	MRNEEKRALRRELGRRSQMGRDVRAAATVKINHLLKRYIKKGRKIGVYWPMGKELRLDG					
	: : : : :					
g157	MRNEEKRALRRELGRRSQMGRDVRAAAIKINRLKRYIKRGRKIGVYWPMGKELRLGG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m157.pep	FVRAAQKRGAEKLYLPYIEPRSRMWFTYPADGVKQERKRGRAKLHVPQFAGRKRVHDL					
	: : : : :					
g157	FVRAAQKRGAKLYLPYIEPHTRMWFTYPERGMERERKRGRAKLHVPQFAGRKIRVHGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m157.pep	NLLVLPVVGMDRLGYRLGQAGGYDATLSAMKYRLQAKTVGVGFACQLVDRLPVEAHDRS					
	: : : : : :					
g157	SVLLVPLVGIDREGYRLGQAGGYDATLSAMKYRLQAKTVGVGFACQLVDRLPREAHDLP					
	130	140	150	160	170	180
	190					
m157.pep	LDGFVSEAGILCFX					
g157	LDGFVSEAGILCFX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 653>:

```
a157.seq
  1 ATGAGGAACG AGGAAAACA CGCCTTGC GCAGAGTTGC GCCGCGCCCG
  51 CGCGCAGATG GGGCATCAAG GCGGTTGGC GCGGGGCAA ACGATTAACC
```

```

101 GCCTGCTCAA ACGTTATATC AAGCGTGGTC GGAAAATCGG CGTGTATTGG
151 CCGATGGGCA AGGAATTGCG TTTGGACGGC TTTGTCCGCG CGGCGCAAAA
201 ACGCGGTGCA AAACCTTATC TGCCTTATAT CGAACC GCGT TCGCGGCGGA
251 TGTGGTTTAC GCCGTATCCT GAAAGCGGAA TGGAACGGGA GCGCATACGG
301 GGCAGGGCGA AGTTGAACGT GCCGCAGTTT GCAGGGGCGA AAATCCGCGT
351 GCACGGTTTG TCGGTATTGC TCGTCCCGCT TGTCGGCATA GACCGCGAGG
401 GCTACCGCTT AGGACAGGCA GGCGGCTATT ACGATGCGAC GCTTGCGGCG
451 ATGAAATACC GTTTGCAGGC AAAAACCCTG GCGGTGGGCT TTGCTGCCA
501 GTTTGTGGAC AGGCTGCCGC GCGAACC GCA CGATCTGCTG CTGGACGGTT
551 TTGTGTCGGA GCGGGGATA TTGTGCTTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 654; ORF 157.a>:

```

a157.pep
  1 MRNEEKHALR RELRRARAQM GHQGRLAAGQ TINRLLKRYI KRGRKIGVYW
 51 PMGKELRLDG FVRAAQKRGK KLYLPYIEPR SRRMWFTYPY ESGMERERIR
101 GRAKLNVPQF AGRKIRVHGL SVLLVPLVGI DREGYRLGQA GGYDATLAA
151 MKYRLQAKTV GVGFAQCFVD RLPREPHDLL LDGFVSEAGI LCF*

```

m157/a157 82.4% identity in 193 aa overlap

```

              10      20      30      40      50      60
m157.pep    MRNEEKRALRRELGRRRSQMGRDVRAAATVKINHLLKRYIKKGRKIGVYWPMGKELRLDG
              |||||:||||| |:||:| | | ||:|||||:|||||
a157        MRNEEKHALRRELRRARAQMGHQGRLAAGQTINRLLKRYIKRGRKIGVYWPMGKELRLDG
              10      20      30      40      50      60

              70      80      90      100     110     120
m157.pep    FVRAAQKRGAE LYPYIEPRSRMWFTYPYPADGVKQERKGRAKLHVPQFAGRKIRVHDL
              |||||:|||||:|||||:|||||:|:|:| | ||||:||||| ||| |
a157        FVRAAQKRGAKLYLPYIEPRSRMWFTYPYPESGMERERIRGRAKLNVPQFAGRKIRVHGL
              70      80      90      100     110     120

              130     140     150     160     170     180
m157.pep    NLLLVFVGM DRLGYRLGQAGGYDATLSAMKYRLQAKTVGVGFACQLVDRLPVEAHDRS
              ::|||:|:| | |||||:|||||:|||||:|||||:|||||
a157        SVLLVPLVGIDREGYRLGQAGGYDATLAAMKYRLQAKTVGVGFACQFVDRLPREPHDLL
              130     140     150     160     170     180

              190
m157.pep    LDGFVSEAGILCFX
              |||||
a157        LDGFVSEAGILCFX
              190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 655>:

```

g158.seq
  1 ATGAAAACCA ATTCAGAAGA ACTGACCGTA TTTGTTCAAG TGGTGGAAAG
 51 CCGCAGCTTC AGCCGTGCGG CGgagcAGTT GGAGAtggCA AATTCTGCCG
101 TAAGCCGCAT CGTCAAACGG CTGGAGGAAA AGTTGGGCGT GAAcCTGctc
151 aACCGACCA CGCGGCAACT CAATCTGACG GAAGAAGGCG CGCAATATTT
201 CCGCCGCGCG CAGAGAATCC TGCAAGAAAT GGCAGCGGCG GAAACCGAAA
251 TGCTGGCAGT GCACGAAGTA CCGCAAGGCG TGTTGCGCGT GGATTCCGCG
301 ATGCcgatgg TGCTGCATCT GCTGGCGCCG CTGGCAGCAA AATTCAACGA
351 ACGCTATCCG CATATCcgac TTTCGCTCGT TTCTTCCGAa ggctatatca
401 atctGattGA Acgcaaagtc gAtatTGCCT TACGGGCCCG AGAATTGGAC
451 GATTCCGGGC TGCGTGACG CCATCTGTTT GACAGCCACT TCCGCGtagt
501 cgCCAGTCCT GAATATTTAG CAAAACACGG CACGCCACAA TCTGCAGAAG
551 atcTTGCCAA CCATCAATGT TTAGGCTTCA CAGAACCCGG TTCTCTAAAT
601 ACATGGGCGG TTTTAGAtgC GCAGGGAAT CCCTATAAAA TTTCACCGCA
651 CTTTACCGCC AGCAGCGGTG AAATCTTACG CTCGTTGTGC CTTTCAAGtt
701 gCGGTATTGC TTGCTTATCA GATTTTTTGG TTGACAACGA CATCACTGAA
751 GGAAAGTTAA TTCCcctatt cgCCGAACAA ACCTCCAATA AAACACACCC

```

801 CTTTAATGCT GTTTATTACA GCGATAAAGC CGTCAACCTC CGCTTACGCG
 851 TATTTTGGGA TTTTGTAGTG AAGGAACTGG GAAAAAATAT GAATAGAACG
 901 AATACCAAT AA

This corresponds to the amino acid sequence <SEQ ID 656; ORF 158.ng>:

g158.pep
 1 MKTNSEELTV FVQVVESGSF SRAAEQLEMA NSAVSRIVKR LEEKLGVNLL
 51 NRTTRQLNLT EEGAQYFRR AQRILQEMAAA ETEMLAVHEV PQGVLRVDSA
 101 MPMVLHLLAP LAAKFNERYP HIRLSLVSS EYINLIERKV DIALRAGELD
 151 DSGLRARHLF DSHFRVVASP EYLAKHGTPQ SAEDLANHQC LGFTEPGSLN
 201 TWAVLDAQGN PYKISPHFTA SSGEILRSLC LSSCGIACLS DFLVDNDITE
 251 GKLIPLFAEQ TSNKTHPFNA VYYSKAVNL RLRVFLDFLV KELGKNMNR
 301 NTK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 657>:

m158.seq
 1 ATGAAACCA ATTCAGAAGA ACTGACCGTA TTTGTTCAAG TGGTGGAAAG
 51 CGGCAGCTTC AGCCGTGCGG CGGAGCAGTT GGCGATGGCA AATTCTGCCG
 101 TAAGCCGCAT CGTCAAACGG CTGGAGGAAA AGTTGGGTGT GAACCTGCTC
 151 AACCACCA CGCGGCAACT CAGTCTGACG GAAGAAGGCG CGCAATATTT
 201 CCGCCGCGCG CAGAGAATCC TGCAAGAAAT GGCAGCGCGG GAAACCGAAA
 251 TGCTGGCAGT GCACGAAATA CCGCAAGGCG GTTTGAGCGT GGATTCGCGG
 301 ATGCCGATGG TGCTGCATCT GCTGGCGCGG CTGGCAGCAA AATTCAACGA
 351 ACGCTATCCG CATATCCGAC TTTGCTCGT TTCTTCCGAA GGCTATATCA
 401 ATCTGATTGA ACGCAAAGTC GATATTGCCT TACGGGCGCG AGAATTGGAC
 451 GATTCGGGCG TGCGTGACAG CCATCTGTTT GACAGCCGCT TCCGCGTAAT
 501 CGCCAGTCCT GAATACCTGG CAAAACACGG CACGCCGCAA TCTACAGAAG
 551 AGCTTGCCGG CCACCAATGT TTAGGCTTCA CCGAACCCGG TTCTCTAAAT
 601 ACATGGGCGG TTTTAGATGC GCAGGGAAAT CCCTATAAGA TTTACCCGCA
 651 CTTTACCGCC AGCAGCGGTG AAATCTTACG CTCGTTGTGC CTTTCAGGTT
 701 GCGGTATTGT TTGCTTATCA GATTTTGGG TTGACAACGA CATCGCTGAA
 751 GGAAAGTTAA TTCCCTGCT CGCCGAACAA ACCTCCGATA AAACACACCC
 801 CTTTAATGCT GTTTATTACA GCGATAAAGC CGTCAATCTC CGCTTACGCG
 851 TATTTTGGGA TTTTGTAGTG GAGGAACTGG GAAACAATCT CTGTGGATAA

This corresponds to the amino acid sequence <SEQ ID 658; ORF 158>:

m158.pep
 1 MKTNSEELTV FVQVVESGSF SRAAEQLAMA NSAVSRIVKR LEEKLGVNLL
 51 NRTTRQLSLT EEGAQYFRR AQRILQEMAAA ETEMLAVHEI PQGVLSVDSA
 101 MPMVLHLLAP LAAKFNERYP HIRLSLVSS EYINLIERKV DIALRAGELD
 151 DSGLRARHLF DSRFRVIASP EYLAKHGTPQ STEELAGHQC LGFTEPGSLN
 201 TWAVLDAQGN PYKISPHFTA SSGEILRSLC LSGCGIVCLS DFLVDNDIAE
 251 GKLIPLLAEQ TSDKTHPFNA VYYSKAVNL RLRVFLDFLV EELGNNLCG*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m158 / g158 94.3% identity in 297 aa overlap

	10	20	30	40	50	60
m158.pep	MKTNSEELTVFVQVVESGSFSRAAEQLAMANSVSRIVKRLEEKLGVNLLNRTTRQLSLT					
g158	MKTNSEELTVFVQVVESGSFSRAAEQLEMANSAVSRIVKRLEEKLGVNLLNRTTRQLNLT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m158.pep	EEGAQYFRR AQRILQEMAAAE ETEMLAVHEI PQGVLSVDSAMP MVLHLLAP LAAKFNERYP					
g158	EEGAQYFRR AQRILQEMAAAE ETEMLAVHEV PQGVLRVDSAMP MVLHLLAP LAAKFNERYP					
	70	80	90	100	110	120

	130	140	150	160	170	180
m158.pep	HIRLSLVSSSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
g158	HIRLSLVSSSEGYINLIERKVDIALRAGELDDSGLRARHLFDSHFRVVASPEYLAKHGTPQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m158.pep	STEELAGHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGEILRSLCLSGCGIVCLS					
g158	SAEDLANHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGEILRSLCLSSCGIACLS					
	190	200	210	220	230	240
	250	260	270	280	290	300
m158.pep	DFLVDNDIAEGKLIPLLAEQTSKTHPFNAVYYSDKAVNLRRLRVFLDFLVEELGNNLCGX					
g158	DFLVDNDITEGKLIPLFAEQTSNKTHPFNAVYYSDKAVNLRRLRVFLDFLVKELGKNMNR					
	250	260	270	280	290	300
g158	NTKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 659>:

a158.seq

1	ATGAAAACCA	ATTCAGAAGA	ACTGACCGTA	TTTGTTC AAG	TGGTGGAAAG
51	CGGCAGCTTC	AGCCGTGCGG	CGGAGCAGTT	GGCGATGGCA	AATTCTGCCG
101	TAAGCCGCAT	CGTCAAACGG	CTGGAGGAAA	AGTTGGGTGT	GAACCTGCTC
151	AACCGCACCA	CGCGGCAACT	CAGTCTGACG	GAAGAAGGCG	CGCAATATTT
201	CCGCCGCGCG	CAGAGAATCC	TGCAAGAAAT	GGCAGCGGCG	GAAACCGAAA
251	TGCTGGCAGT	GCACGAAATA	CCGCAAGGCG	TGTTGCGCGT	GGATTCCGCG
301	ATGCCGATGG	TGCTGCATCT	GCTGGCGCCG	CTGGCAGCAA	AATTCAACGA
351	ACGCTATCCG	CATATCCGAC	TTTCGCTCGT	TTCTTCCGAA	GGCTATATCA
401	ATCTGATTGA	ACGCAAAGTC	GATATTGCCT	TACGGGCCGG	AGAATTGGAC
451	GATTCCGGGC	TGCGTGCACG	CCATCTGTTT	GACAGCCGCT	TCCGCGTAAT
501	CGCCAGTCCT	GAATACCTGG	CAAAACACGG	CACGCCGCAA	TCTACAGAAG
551	AGCTTGCCGG	CCACCAATGT	TTAGGCTTCA	CCGAACCCGG	TTCTCTAAAT
601	ACATGGGCGG	TTTATAGATG	GCAGGGAAAT	CCCTATAAGA	TTTCACCGCA
651	CTTTACCGCC	AGCAGCGGTG	AAATCTTACG	CTCGTTGTGC	CTTTCAGGTT
701	GCGGTATTGC	TTGCTTATCA	GATTTTTTGG	TTGACAACGA	CATCGCTGAA
751	GGAAAGTTAA	TTCCCCTGCT	CGCCGAACAA	ACCTCCAATA	AAACGCACCC
801	CTTTAATGCT	GTTTATTACA	GCGATAAAGC	CGTCAACCTC	CGCTTACGCG
851	TATTTTTTGA	TTTTTTAGTG	GAGGAACTGG	GAAACAATCT	CTGTGGATAA

This corresponds to the amino acid sequence <SEQ ID 660; ORF 158.a>:

a158.pep

1	MKTNSEELTV	FVQVVESGSF	SRAAEQLAMA	NSAVSRIVKR	LEEKLGVNLL
51	NRTTRQLSLT	EEGAQYFRRR	QRILQEMAAA	ETEMPLAVHEI	PQGVLRVDSA
101	MPMVLHLLAP	LAAKFNERYP	HIRLSLVSSE	GYINLIERKV	DIALRAGELD
151	DSGLRARHLF	DSRFRVIASP	EYLAKHGTPQ	STEELAGHQC	LGFTTEPGSLN
201	TWAVLDAQGN	PYKISPHFTA	SSGEILRSLC	LSGCGIACLS	DFLVDNDIAE
251	GKLIPLLAEQ	TSNKTHPFNA	VYYSKAVNLR	RLRVFLDFLV	EELGNNLCG*

m158/a158 99.0% identity in 299 aa overlap

	10	20	30	40	50	60
m158.pep	MKTNSEELTVFVQVVESGSFSRAAEQLAMANSVSRIVKRLEEKLGVNLLNRTTRQLSLT					
a158	MKTNSEELTVFVQVVESGSFSRAAEQLAMANSVSRIVKRLEEKLGVNLLNRTTRQLSLT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m158.pep	EEGAQYFRRRQRILQEMAAAEETEMPLAVHEIPQGVLSVDSAMPMLVHLLAPLAAKFNERYP					
a158	EEGAQYFRRRQRILQEMAAAEETEMPLAVHEIPQGVLRVDSAMPMLVHLLAPLAAKFNERYP					
	70	80	90	100	110	120

	130	140	150	160	170	180
m158.pep	HIRLSLVSSSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
a158	HIRLSLVSSSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m158.pep	STEELAGHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGEILRSLCLSGCGIVCLS					
a158	STEELAGHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGEILRSLCLSGCGIACLS					
	190	200	210	220	230	240
	250	260	270	280	290	300
m158.pep	DFLVDNDIAEGKLIPLLAEQTSKTHPFNAVYYSDKAVNLRRLRVFLDFLVEELGNNLCGX					
a158	DFLVDNDIAEGKLIPLLAEQTSNKTTHPFNAVYYSDKAVNLRRLRVFLDFLVEELGNNLCGX					
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 661>:

```

g160.seq
1  ATGGAcattc  tgGACAAact  ggtcgatCTC  GCccaATTGA  CGGGCAGTGC
51  GGATGTGCAG  TgcctTTTGG  GCGGACAATG  gcATGaaacc  TTGCAACGCG
101 AAGGGCTGGT  ACACATTGTT  ACGGCGGGCA  GCGGTTATCT  CTGCATCGAC
151 GCGGAAACTT  CCCC CGCTCC  GGTGCGGCAC  GGCATATTG  TATTTTCC
201 GCGCGGCTTG  GGT CATGTGT  TGAGCCACGA  CGGAAAATAC  GGAGAAAGTT
251 TACAACCGGA  CATACGACAA  AACGGCACAT  TTATGGTCAA  ACAGTGCGGC
301 AACGGGCTGG  ATATGAGCCT  GTTTTGCGCC  CGTTTCCGCT  ACGACACCCA
351 CGCCGATTG  ATGAACGGGC  TGCCGGAAAC  CGTTTTCTG  AACATTGCCC
401 ATCCAAGTTT  GCAGTATGTG  GTTTC AATGC  TGCAACTGGA  AAGCGAAAAA
451 CCTTTGACGG  GGACGGTTTC  CGTGGTCAAC  GCATTACCGT  CCGTCTGCT
501 GGTGCTTATC  CTGCGCGCCT  ATCTCGAACA  GGATAAGGAT  GTCGAACTCT
551 CGGGCGTATT  GAAAGGTTGG  CAGGACAAAC  GTTTGGGACA  TTTGATCCAA
601 AAGGTGATAG  ACAACCGGA  AGACGAATGG  AATATTGACA  AAATGGTTGC
651 CGCCGCCAAT  ATGTCGCGCG  CGCAACTGAT  GCGCCGCTTC  AAAAGCCAAG
701 TCGGACTCAG  CCCGACGCGC  TTTGTGAACC  ATATCCGCT  GCAAAAAGGC
751 GCATTGCTGC  TGAAGAAAAC  CCCGATTTCG  GTTTTGGAGG  TCGCGCTGTC
801 GGTGGGCTTT  CAGTCGGAAA  CGCATTTTCG  CAAGGCGTTC  AAACGGCAAT
851 ATCACGTTTC  GCCGGGGCAA  TACCGGAAAG  AAGGCGGGCA  AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 662; ORF 160.ng>:

```

g160.pep
1  MDILDKLVDL  AQLTGSADVQ  CLLGGQWHET  LQREGLVHIV  TAGSGYLCID
51  GETSPRPVGT  GDIVFFPRGL  GHVLSHDGKY  GESLPDIRQ  NGTFMVKQCG
101 NGLDMSLFCA  RFRYDTHADL  MNGLPETVFL  NIAHPSLQYV  VSMLESEK
151 PLTGTVSUVN  ALPSVLLVLI  LRAYLEQDKD  VELSGVLKGW  QDKRLGHLIQ
201 KVIDKPEDEW  NIDKMVAAN  MSRAQLMRRF  KSQVGLSPHA  FVNHIRLQKG
251 ALLLKTPDS  VLEVALSVGF  QSETHFGKAF  KRQYHVSPGQ  YRKEGGQK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 663>:

```

m160.seq
1  ATGGACATTC  TGGACAAACT  GGTGATTTC  GCCCAATTGA  CGGGCAGTGT
51  GGATGTGCAG  TGCCTTTTGG  GCGGACAATG  GTCGGTACGG  CATGAAACCT
101 TGCAACGCGA  AGGATTGGTA  CACATTGTTA  CATCGGGCAG  CGGCTATCTC
151 TGCATCGACG  GCGAAACTTC  CCCGCGTCCG  GTCAGTACAG  GGGATATTGT
201 ATTTTCCCG  CGCGGCTTGG  GTCATGTGTT  GAGCCACGAC  GGAAAATGCG
251 GAGAAAGTTT  ACAACCGGAT  ATGCGGCAGC  ACGGTGCGTT  TACGGTCAAG
301 CAGTGCAGCA  ACGGACAGGA  TATGAGCCTG  TTTTGCGCCC  GTTCCGCTA
351 CGACACCCAC  GCCGATTGTA  TGAACGGGCT  GCCTGAAACC  GTTTTCTGA
401 ACATTGCCCA  TCCGAGTTTA  CAGTATGTGG  TTTCAATGCT  GCAACTGGAA
451 AGCAAAAAAC  CTTTGACGGG  GACGGTTTCC  ATGGTCAACG  CATTGTCGTC

```

```

501 CGTCCTGCTG GTGCTTATCC TGC GCGCCTA TCTCGAACAG GATAAGGATG
551 TCGAACTCTC GGGCGTATTG AAAGGTTGGC AGGACAAACG TTTGGGACAT
601 TTAATCCAAA AGGTGATAGA CAAACCGGAA GACGAATGGA ATGTCGACAA
651 AATGGTGGCG GCTGCCAATA TGTCGCGCGC GCAACTGATG CGCCGTTTCA
701 AAAGCCGGGT CGGACTCAGC CCGCACGCCT TTGTGAACCA TATCCGCTG
751 CAAAAGGCG CGTTGCTGCT GAAAAAAAAC CCGGATTCGG TTTGTGCGGT
801 CGCACTGTCT GTAGGCTTTC AGTCGGAAAC GCACTTCGGC AAGGCGTTCA
851 AACGGCAATA TCACGTTTCG CCGGGTCAAT ACCGGAAAGA AggCGGGCAA
901 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 664; ORF 160>:

```

m160.pep
1 MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL
51 CIDGETSPRP VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK
101 QCGNGQDMSL FCARFRYDTH ADLMNGLPET VFLNIAHPSL QYVVSMLQLE
151 SKKPLTGTVS MVNALSSVLL VLILRAYLEQ DKDVELSGVL KGWQDKRLGH
201 LIQKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS PHAFVNHIRL
251 QKGALLLKN PDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
301 K*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m160 / g160 93.4% identity in 301 aa overlap

```

          10      20      30      40      50      60
m160.pep MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g160      MDILDKLVDL AQLTGSADVQ CLLGGQW--- HETLQREGLV HIVTAGSGYL CIDGETSPRP
          10      20      30      40      50

          70      80      90     100     110     120
m160.pep VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK QCGNGQDMSL FCARFRYDTH
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g160      VGTGDIVFFP RGLGHVLSHD GKYGESLQPD IRQNGTFMVKQCGNGLDMSL FCARFRYDTH
          60      70      80      90     100     110

          130     140     150     160     170     180
m160.pep ADLMNGLPET VFLNIAHPSL QYVVSMLQLE SKKPLTGTVS MVNALSSVLL VLILRAYLEQ
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g160      ADLMNGLPET VFLNIAHPSL QYVVSMLQLE SEKPLTGTVS VVNALPSVLL VLILRAYLEQ
          120     130     140     150     160     170

          190     200     210     220     230     240
m160.pep DKDVELSGVL KGWQDKRLGH LIQKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g160      DKDVELSGVL KGWQDKRLGH LIQKVIDKPE DEWNIDKMVA AANMSRAQLM RRFKSQVGLS
          180     190     200     210     220     230

          250     260     270     280     290     300
m160.pep PHAFVNHIRL QKGALLLKNP DSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g160      PHAFVNHIRL QKGALLLKKTP DSVLEVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
          240     250     260     270     280     290

m160.pep KX
          ||
g160      KX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 665>:

```

a160.seq
1 ATGGACATTC TGGACAAACT GGTGATTTTC GCCCAATTGA CGGGCAGTGT
51 GGATGTGCAG TGCCTTTTGG GCGGACAATG GTCGGTACGG CATGAAACCT

```

```

101 TGCAACGCGA AGGATTGGTA CACATTGTTA CATCGGGCAG CGGCTATCTC
151 TGCATCGACG GCGAAACTTC CCCGCGTCCG GTCAGTACAG GGGATATTGT
201 ATTTTTCCTG CGCGGCTTGG GTCATGTGTT GAGCCACGAC GGAAATGCG
251 GAGAAAGTTT ACAACCGGAT ATGCGGCAGC ACGGTGCGTT TACGGTCAAG
301 CAGTGC GGCA ACGGACAGGA TATGAGCCTG TTTTGC GCCC GTTTCGCTA
351 CGACACCCAC GCCGATTTGA TGAACGGGCT GCCTGAAACC GTTTTCTGA
401 ACATTGCCCA TCCGAGTTTA CAGTATGTGG TTTCAATGCT GCAACTGGAA
451 AGCAAAAAAC CTTTGACGGG GACGGTTTCC ATGGTCAACG CATTGTCGTC
501 CGTCCTGCTG GTGCTTATCC TCGCGCCTA TCTCGAACAG GATAAGGATG
551 TCGAACTCTC GGGCGTATTG AAAGGTTGGC AGGACAAACG TTTGGGACAT
601 TTAATCCAAA AGGTGATAGA CAAACCGGAA GACGAATGGA ATGTCGACAA
651 AATGGTGGCG GCTGCCAATA TGTGCGCGCG GCAACTGATG CGCCGTTTCA
701 AAAGCCGGGT CGGACTCAGC CCGCACGCCT TTGTGAACCA TATCCGCTG
751 CAAAAAGGCG CGTTGCTGCT GAAAAAAAC CCGGATTCGG TTTGTGCGT
801 CGCACTGTCG GTAGGCTTTC AGTCGGAAAC GCACTTCGGC AAGGCGTTCA
851 AACGGCAATA TCACGTTTCG CCGGGTCAAT ACCGGAAAGA AGCGGGCAA
901 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 666; ORF 160.a>:

```

a160.pep
  1 MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL
 51 CIDGETSPRP VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK
101 QCGNGQDMSL FCARFRYDTH ADLMNGLPET VFLNIAHPSL QYVVSMLQLE
151 SKKPLTGTVS MVNALSSVLL VLILRAYLEQ DKDVELSGVL KGWQDKRLGH
201 LIQKVIDKPE DEWNVDMVA AANMSRAQLM RRFKSRVGLS PHAFVNHIRL
251 QKGALLLKN PDSVLSVALS VGFQSETHFG KAFKROYHVS PGQYRKEGGQ
301 K*

```

m160/a160 100.0% identity in 301 aa overlap

```

          10      20      30      40      50      60
m160.pep MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP
          |||
a160      MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP
          10      20      30      40      50      60

          70      80      90     100     110     120
m160.pep VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK QCGNGQDMSL FCARFRYDTH
          |||
a160      VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK QCGNGQDMSL FCARFRYDTH
          70      80      90     100     110     120

          130     140     150     160     170     180
m160.pep ADLMNGLPET VFLNIAHPSL QYVVSMLQLES KKPLTGTV SMVNALSSVLL VLILRAYLEQ
          |||
a160      ADLMNGLPET VFLNIAHPSL QYVVSMLQLES KKPLTGTV SMVNALSSVLL VLILRAYLEQ
          130     140     150     160     170     180

          190     200     210     220     230     240
m160.pep DKDVELSGVL KGWQDKRLGHLI QKVIDKPE DEWNVDMV AAANMSRAQLM RRFKSRVGLS
          |||
a160      DKDVELSGVL KGWQDKRLGHLI QKVIDKPE DEWNVDMV AAANMSRAQLM RRFKSRVGLS
          190     200     210     220     230     240

          250     260     270     280     290     300
m160.pep PHAFVNHIRL QKGALLLKN PDSVLSVALS VGFQSETHFG KAFKROYHVS PGQYRKEGGQ
          |||
a160      PHAFVNHIRL QKGALLLKN PDSVLSVALS VGFQSETHFG KAFKROYHVS PGQYRKEGGQ
          250     260     270     280     290     300

m160.pep KX
          ||
a160      KX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 667>:

```

g161.seq
1   ATGGATACCG CAAAAAAGA CATTTTAGGA TCGGGCTGGA TGCTGGTGGC
51  GGCGGCCTGC TTCACCGTTA TGAACGTATT GATTAAAGAG GCATCGGCAA
101 AATTGGCCCT CGGCAGCGGC GAATTGGTCT TTTGGCGCAT GCTGTTTTCA
151 ACCGTTACGC TCGGTGCTGC CGCCGTATTG CGGCGCGACA CCTTCCGCAC
201 GCCCCATTGG AAAAACCAC TAAACCGCAG TATGGTCGGG ACGGGGGCGA
251 TGCTGCTGCT GTTTTACGCG GTAACGCATC TGCCTTTGAC AACCGGCGTT
301 ACCCTGAGTT ACACCTCGTC GATTTTTttg GCGGTATTTT CCTTCCTGAT
351 TTTGAAAGAA CGGATTTCCG TTTACACGCA GCGCGTGCTG CTCCTTGGTT
401 TTGCCGGCGT GGTATTGCTG CTTAATCCCT CGTTCCGCAG CGGTCAGGAA
451 CCGGCGGCAC TCGCCGGGCT GGCGGGCGGC GCGATGTCCG GCTGGGCGTA
501 TTTGAAAGTG CGCGAACTGT CTTTGGCGGG CGAACCCGGC TGGCGCGTCG
551 TGTTTTACCT TTCCGCAACC GCGGTGGCGA TGTCTGTCggt ttggcgacg
601 Ctgaccggct ggCACAcccT GTCCTTTcca tcggcagttt ATCtgtCGGG
651 CATCGGCGTG tccgcgCtgA TTGCCCAaCT GtcgatgAcg cGCGcctaca
701 aaGTCGGCGA CAAATTCACG GTTGCTCGC tttcctaTat gaccgtcGTC
751 TTTTCCGCCC TGTCTGCCGC ATTTTTTCTg ggcgaagagc ttttctggCA
801 GGAAATACTC GGTATGTGCA TCATTATcct CAGCGGCATT TTGAGCAGCA
851 TCCGCCCCAT TGCCTTCAA CAGCGGCTGC AAGCCCTCTT CCGCCAAAGA
901 TAA

```

This corresponds to the amino acid sequence <SEQ ID 668; ORF 161.ng>:

```

g161.pep
1   MDTAKKDILG SGWMLVAAAC FTVMNVLIKE ASAKFALGSG ELVFWRMLFS
51  TVTLGAAAVL RRDTRFTRPHV KNHLNRSMVG TGAMLLLFYA VTHLPLTTGV
101 TLSYTSIFL AVFSFLILKE RISVYTQAVL LLGFAGVVLL LNPSFRSGQE
151 PAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSAT GVAMSSVWAT
201 LTGWHTLSFP SAVYLSGIGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV
251 FSALSAAFFL GEELFWQEIL GMCIIILSGI LSSIRPIAFK QRLQALFRQR
301 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 669>:

```

m161.seq
1   ATGGATACCG CAAAAAAGA CATTTTAGGA TCGGGCTGGA TGCTGGTGGC
51  GGCGGCCTGC TTTACCATT A TGAACGTATT GATTAAAGAG GCATCGGCAA
101 AATTGGCCCT CGGCAGCGGC GAATTGGTCT TTTGGCGCAT GCTGTTTTCA
151 ACCGTTGCGC TCGGGGCTGC CGCCGTATTG CGTCGGGACA mCTTCCGCAC
201 GCCCCATTGG AAAAACCAC TAAACCGCAG TATGGTCGGG ACGGGGGCGA
251 TGCTGCTGCT GTTTTACGCG GTAACGCATC TGCCTTTGGC CACTGGCGTT
301 ACCCTGAGTT ACACCTCGTC GATTTTTTTT GCGGTATTTT CCTTCCTGAT
351 TTTGAAAGAA CGGATTTCCG TTTACACGCA GCGCGTGCTG CTCCTTGGTT
401 TTGCCGGCGT GGTATTGCTG CTTAATCCCT CGTTCCGCAG CGGTCAGGAA
451 ACGGCGGCAC TCGCCGGGCT GGCGGGCGGC GCGATGTCCG GCTGGGCGTA
501 TTTGAAAGTG CGCGAACTGT CTTTGGCGGG CGAACCCGGC TGGCGCGTCG
551 TGTTTTACCT TTCCGTGACA GGTGTGGCGA TGTCTGTCGT TTGGGCGACG
601 CTGACCGGCT GGCACACCCT GTCCTTTCCA TCGGCAGTTT ATCTGTCTGT
651 CATCGGCGTG TCCGCGCTGA TTGCCCAACT GTCGATGACG CGCGCCTACA
701 AAGTCGCGCA CAAATTCACG GTTGCTCGC TTTCTATAT GACCGCTGTT
751 TTTTCCGCTC TGTCTGCCGC ATTTTTTCTG GGCGAAGAGC TTTTCTGGCA
801 GGAAATACTC GGTATGTGCA TCATCATCCT CAGCGGTATT TTGAGCAGCA
851 TCCGCCCCAC TGCCTTCAA CAGCGGCTGC AATCCCTGTT CCGCCAAAGA
901 TAA

```

This corresponds to the amino acid sequence <SEQ ID 670; ORF 161>:

```

m161.pep
1   MDTAKKDILG SGWMLVAAAC FTIMNVLIKE ASAKFALGSG ELVFWRMLFS
51  TVALGAAAVL RDXFTRPHV KNHLNRSMVG TGAMLLLFYA VTHLPLATGV
101 TLSYTSIFL AVFSFLILKE RISVYTQAVL LLGFAGVVLL LNPSFRSGQE

```

151 TAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSVT GVAMSSVWAT
 201 LTGWHTLSFP SAVYLSGIGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV
 251 FSALSAAFFL GEELFWQEIL GMCIIILSGI LSSIRPTAFK QRLQSLFRQR
 301 *

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m161 / g161 97.0% identity in 300 aa overlap

	10	20	30	40	50	60
m161.pep	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMFLFSTVALGAAAVL					
	: : : : :					
g161	MDTAKKDILGSGWMLVAAACFTVMNVLIKEASAKFALGSGELVFWRMFLFSTVTLGAAAVL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m161.pep	RRDXFRTPHWKNHLNRSVMVGTGAMLLLFYAVTHLPLATGVTLSTSSIFLAVFSFLILKE					
	: : : : :					
g161	RRDTFRTPHWKNHLNRSVMVGTGAMLLLFYAVTHLPLTTGVTLSTSSIFLAVFSFLILKE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m161.pep	RISVYTQAVLLLGFGVLLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
	: : : : :					
g161	RISVYTQAVLLLGFGVLLLNPSFRSGQEPALAGLAGGAMSGWAYLKVRELSLAGEPG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m161.pep	WRVVFYLSVTGVAMSSVWATLTGWHTLSFPSAVYLSGIGVSALIAQLSMTRAYKVGDKFT					
	: : : : :					
g161	WRVVFYLSATGVAMSSVWATLTGWHTLSFPSAVYLSGIGVSALIAQLSMTRAYKVGDKFT					
	190	200	210	220	230	240
	250	260	270	280	290	300
m161.pep	VASLSYMTVVFSALSAAFFLGEELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
	: : : : :					
g161	VASLSYMTVVFSALSAAFFLGEELFWQEILGMCIIILSGILSSIRPIAFKQRLQALFRQR					
	250	260	270	280	290	300
m161.pep	X					
g161	X					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 671>:

a161.seq

1	ATGGATACCG	CAAAAAAGA	CATTTTAGGA	TCGGGCTGGA	TGCTGGTGCC
51	GGCGGCCTGC	TTTACCATTA	TGAACGTATT	GATTAAAGAG	GCATCGGCAA
101	AATTGCCCCT	CGGCAGCGGC	GAATTGGTCT	TTTGGCGCAT	GCTGTTTTCA
151	ACCGTTGCGC	TCGGGGCTGC	CGCCGTATTG	CGTCGGGACA	CCTTCCGCAC
201	GCCCCATTGG	AAAAACCACT	TAAACCGCAG	TATGGTCGGG	ACGGGGGCGA
251	TGCTGCTGCT	GTTTTACGCG	GTAACGCATC	TGCCTTTGGC	CACCGGCGTT
301	ACCCTGAGTT	ACACCTCGTC	GATTTTTTTG	GCGGTATTTT	CCTTCCTGAT
351	TTTGAAAGAA	CGGATTTCGG	TTTACACGCA	GGCGGTGCTG	CTCCTTGCTT
401	TTGCCGGCGT	GGTATTGCTG	CTTAATCCCT	CGTTCCGCAG	CGGTCAGGAA
451	ACGGCGGCAC	TCGCCGGGCT	GGCGGGCGGC	GCGATGTCCG	GCTGGGCGTA
501	TTTGAAAGTG	CGCGAACTGT	CTTTGGCGGG	CGAACCCGGC	TGGCGCGTCC
551	TGTTTTACCT	TTCCGTGACA	GGTGTGCGCA	TGTCATCGGT	TTGGGCGACG
601	CTGACCGGCT	GGCACACCCT	GTCCCTTTCCA	TCGGCAGTTT	ATCTGTCTGT
651	CATCGGCGTG	TCCGCGCTGA	TTGCCCAACT	GTGATGACG	CGCGCCTACA
701	AAGTCGGCGA	CAAATTCACG	GTTGCCTCGC	TTTCTATAT	GACCGTCGTT
751	TTTTCCGCTC	TGTCTGCCGC	ATTTTTTCTG	GCCGAAGAGC	TTTTCTGCA
801	GGAAATACTC	GGTATGTGCA	TCATCATCCT	CAGCGGTATT	TTGAGCAGCA

851 TCCGCCCCAC TGCCTTCAAA CAGCGGCTGC AATCCCTGTT CCGCCAAAGA
901 TAA

This corresponds to the amino acid sequence <SEQ ID 672; ORF 161.a>:

a161.pep
1 MDTAKKDILG SGWMLVAAAC FTIMNVLIKE ASAKFALGSG ELVFWRMLES
51 TVALGAAAVL RRDTRTPHW KNHLNRSVMG TGAMLLLFYA VTHLPLATGV
101 TLSYTSSIFL AVFSFLILKE RISVYTQAVL LLGFAGVLL LNPSFRSGQE
151 TAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSVT GVAMSSVWAT
201 LTGWHTLSFP SAVYLSICIGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV
251 FSALSAAFFL AEELFWQEIL GMCIIILSGI LSSIRPTAFK QRLQSLFRQR
301 *

m161/a161 99.3% identity in 300 aa overlap

	10	20	30	40	50	60
m161.pep	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMLES	TVALGAAAVL				
a161	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMLES	TVALGAAAVL				
	10	20	30	40	50	60
	70	80	90	100	110	120
m161.pep	RRDXFRTPHWKNHLNRSVMGTGAMLLLFYAVTHLPLATGVTLSYTSSIFLAVFSFLILKE					
a161	RRDTRTPHWKNHLNRSVMGTGAMLLLFYAVTHLPLATGVTLSYTSSIFLAVFSFLILKE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m161.pep	RISVYTQAVLLLGAGVLLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
a161	RISVYTQAVLLLGAGVLLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m161.pep	WRVVFYLSVTGVAMSSVWATLTGWHTLSFSAVYLSICIGVSALIAQLSMTTRAYKVGDKFT					
a161	WRVVFYLSVTGVAMSSVWATLTGWHTLSFSAVYLSICIGVSALIAQLSMTTRAYKVGDKFT					
	190	200	210	220	230	240
	250	260	270	280	290	300
m161.pep	VASLSYMTVVFSALSAAFFLGEELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
a161	VASLSYMTVVFSALSAAFFLAEELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
	250	260	270	280	290	300
m161.pep	X					
a161	X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 673>:

g163.seq
1 ATGGTTATTT TGACGACTTT GTTTTTTGTG TGTGTTTTGG TGGTATTGGT
51 TTTAACCGTG CCGGATCAGG TGCAGATGTG gctCGACCGG GCAAAGAAG
101 TCATTTTTAC CGAGTTCAGC TGGTTTTATG TTTTAACGTT TTCCATTTTt
151 ctgGGTTTTc tgctGATACT CTCGGTCAGC GGGTTGGGAA ACATcagGCT
201 AGGACGGGAT GAAGATGTGC CGGAATTCGG CTTCTGTGCG TGGCTGGCGA
251 TGCTGTTTGC GGCCGGGATG GGCGTGGGCC TGATGTTTTT CGGCGTGGCA
301 GAGCCGTTGA TGCATTATTT TTCGGACATT ACGGTCGGCG CGCCGGAACA
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GGCGTTACAG
401 CCTGGTCGGT GTACGGTACG ATTGCATTGG CTTTGGCTTA TTTCGGTTTC

```

451 CGCTACAAAC TGCCGCTTGC CCTGCGTTCT TGTTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTTCGGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATGGGCTGG ATTGCCGAAA ACAGCTTCGG
651 CGTGCAGGTC TTGATTATCG CCGCCGTAAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GGCCTGAAGG TGTGTAGCGA GTTGAACCTG
751 GGCCTTGCGT TTTTGTGCT GTTTTTTGT TTTGGCGCGG ACCCCACTGT
801 TTACCTGTTG TCGGCATTCT GCGACAACAT AGGGAACATC CTCGGAATC
851 TGGTGCGCCT CAGTTTGAAA ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTGAAT CTTGGACGGT GCTTTATTGG GCGTGGTGGT GTTCTTGGgc
951 gcCGTTTGTG GGTtTGTTTA TCGCGCGCAT TTCAAAGGGg cgcaccatCc
1001 gcgagtttgt CTTTCGGGGT TTGCTCATCC CCGGCCTGTT CGGCGTTTTG
1051 TGGTTTACCG TCTTCGGCAA TACGGCGATT TGGCTGAATG ACGGGGTTGC
1101 GGGGGGAATG CTCGAAAAGA TGACCTCCTC TCCGGAACG CTGCTTTTTA
1151 AATTCTTTAA TTACCTCCCC CTGCCCAGAC TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATTT CCCTGTTTTT TGTAACCTCT GCCGACTCCG GGATTTATGT
1251 CCTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGGTGGC
1301 AGGCGGTAT GTGGGGCGTG CTGatgtcTG CCGTTGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CCTGCAGTCT ATGACCCTGA TTGTTTCCCT
1401 GCCGTTTGCC CTGCTGATGC TGATAATGTG TTTCAGCCTG TGGAAAGGCT
1451 TGAGTGCGGA TAAGAAATAT TTTGAGACCC GGGTCAACCC TACCAGTGTA
1501 TTTTGGACGG GCGGCAAGTG GAAAGAACGG CTGGTGCGGA TAATGAGCCA
1551 GACGCAGGAG CAGGATATTT TAAAATTCCT CAAACATACC GCATCGCCCC
1601 CTATGCACGA GTTGCAACGG GAGCTTTCGG AAGAATACGG CTTGAGCGTC
1651 CGGGTCGATA AGATGTTTCA TCAGGACGAG CCCGCAATCG AGTTCGTCAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAG TCTGTGCGGC
1751 AGGATGTATC CGACCAGTTG ATTAACGACG GCAAGCTGCC GCATATCCCG
1801 CACCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GCGCGTCCG
1851 GTACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTTG ATGTTGTTGG ATGATGTCGG TCAGGAACTG
1951 ATGGCGCACG AGCAGGTGGA ATGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 674; ORF 163.ng>:

g163.pep

```

1 MVILTLFFV CVLVVLVLTV PDQVQWLDL AKEVIFTEFS WFYVLTFSEF
51 LGFLLILSVS GLGNIRLGRD EDVPEFGFLS WLAMLF AAGM GVGLMFFGVA
101 EPLMHYFSDI TVGAPEHRQQ QALLHTVFHW GVHAWSVYGT IALALAYFGF
151 RYKLPLALRS CFYPLLKEKI SGRFGDAIDI MALLATFFGI ITTLGFASQ
201 LGAGLOEMGW IAENSFGVQV LIIAAVMSLA VVSAISGVGK GVKVLSEINL
251 GLAFLLLFFV LAADPTVYLL SAFGDNIGNY LGNLVRLSLK TYAYEREHKP
301 WFSWTVLYW AWWCSWAPFV GLFIARISK RTIREFVFGV LLIPGLFGLV
351 WFTVFGNTAI WLNDGVAGGM LEKMTSSPET LLFKFNYLP LPELTSIVSL
401 LVISLFFVTS ADSGIYVLNN ITS RDKGLSA PRWQAVMWGV LMSAVAVLLM
451 RSGGLGNLQS MTLIVSLPFA LLMLIMCFSL WKGLSADKKY FETRVNPTSV
501 FWTGGKWKER LVRIMSQTQE QDILKFLKHT ASPAMHELQR ELSEYGLSV
551 RVDKMFHQDE PAIEFVIRKE TMRDFMYGIK SVGQDVSDQL INDGKLPHIR
601 HQTTYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLDDVQGQEL
651 MAHEQVELAE *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 675>:

m163.seq

```

1 ATGGTTATTT TGACGACTTT GTTTTTGTG TGTGTTTGG TGGTATTGGT
51 TTTAACCGTG CCGGATCAGG TGCAGATGTG GCTCGATCGG GCAAAGAAG
101 TCATTTTAC CGAGTTCAGC TGGTTTTATG TTTTAACGTT TTCCATTTTT
151 CTGGGTTTCC TGCTGATACT CTCGGTCAGC AGTTTGGGAA ACATCAGGCT
201 CGGACGGGAT GAAGATGTGC CGGAATTCGG CTCCTGTCTG TGGCTGGCGA
251 TGCTGTTTGC GGCCGGGATG GCGGTGGGTC TGATGTTTTT CGGCGTGGCA
301 GAGCCGTTGA TGCATTATTT TTCGGACATT ACGGCCGGCA CGCCGGAACA
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GCGGTTACG
401 CTTGGTTCGT GTACGGTACG ATTGCATTGG CTTTGGCTTA TTTCCGTTTC
451 CGCTACAAGC TGCCGCTTGC CCTGCGTTCT TGTTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTTCGGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATGGGCTGG ATTGCCGAAA ACAGCTTCAG

```



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651 CGTGCAGGTT TTGATTATCG CCGCCGTCAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GCGGTGAAGG TGTGAGCGA GTTGAACCTG
751 GGCCTTGCGT TTTTGCTGCT GTTTTGTGTT TTGGCGGCGG GACCCACTGT
801 TTACCTGTTG TCGGCATTCT GCGACAACAT AGGGAACTAC CTCGGAATC
851 TGGTGCGCCT CAGTTTTTAA ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTGAAT CTTGGACGGT GCTTTATTGG GCGTGGTGGT GTTCTGGGGC
951 GCCGTTTGTG GGTTTGTGTT TCGCGCGCAT TTCAAAGGGG CGCACCATCC
1001 GCGAGTTTGT CTTGCGGGTT TTGCTCATCC CCGGCTGTT CGGCGTTTGT
1051 TGGTTTACCG TCTTCGGCAA TACGGCGATT TGGCTGAATG ACGGGTTTGC
1101 GGGGGGAATG CTCGAAAAGA TGACCTCCTC TCCGGAACG CTGCTTTTAA
1151 AATTCTTTAA TTACCTCCCC CTGCCCGAAT TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATTT CTCTGTTTTT TGTAACCTCT GCCGATTCCG GGATTTATGT
1251 CCTGAACAAT ATTACCTCTC GGGACAAGG CTTGAGCGCG CCACGGTGGC
1301 AGGCGGTTAT GTGGGGCGTG CTGATGTCTG CCGTTGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CCTGCAGTCT ATGACCCTGA TTGTTTCCCT
1401 GCCGTTTGCC CTGCTGATGC TGATAATGTG TTTGAGCCTG TGGAAAGGCT
1451 TGAGTGCGGA TAAGAAATAT TTTGAGACCC GGGTTAACC TACCAGTGTA
1501 TTTTGGACGG GCGGCAAGTG GAAAGAACGG CTGGTGCAGA TAATGAGCCA
1551 GACGCAGGAG CAGGATATTT TAAATTCCT CAAACAGACT GCATCGCCCG
1601 CTATGCACGA GTTGCAACGG GAGCTTTCGG AAGAATACGG CTTGAGCGTC
1651 CGGGTCGATA AAATGTTTCA TCGGGACGAG CCCGCAATCG AGTTCGTCAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAAG TCTGTCGGGC
1751 AGGATGTATC CGACCAAGTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CATCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GCGCGCTCGG
1851 GTACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTTG ATGTTGTTGG ATGATGTCGG TCAGGAAGTG
1951 ATGGCGCAGC AGCAGGTGGA ATTGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 676; ORF 163>:

```

m163.pep
1  MVILTTLFFV CVLVVLVLTVPDQVQMWLDR AKEVIFTEFS WFYVLTFSIF
51  LGFLLILSVS SLGNIRLGRD EDVPEFGFLS WLAMLFAGM GVGLMFFGV
101 EPLMHYFS DI TAGTPEHRQQ QALLHTVFWH GVHAWSVYGT IALALAYFGF
151 RYKPLALRS CFYPLLKEKI SGRFGDAIDI MALLATFFGI ITTLGFGASQ
201 LGAGLQEMGW IAENSFSVQV LIIAAVMSLA VVSAISGVGK GVKVLSELNL
251 GLAFLLLFFV LAAGPTVYLL SAFGDNIGNY LGNLVRLSFK TYAYEREHKP
301 WFESWTVLYW AWWCSWAPFV GLFIARISK RTIREFVFGV LLIPGLFGVL
351 WFTVFGNTAI WLNDGVAGGM LEKMTSSPET LLFKFFNYLP LPELTSIVSL
401 LVISLFFVTS ADSGIYVLNN ITS RDKGLSA PRWQAVMWGV LMSAVAVLLM
451 RSGGLGNLQS MTLIVSLPFA LLMILMCFSL WKGLSADKKY FETRVNPTSV
501 FWTGGKWKER LVQIMSQTQE QDILKFLKQT ASPAMHELQR ELSEEYGLSV
551 RVDKMFHRDE PAIEFVIRKE TMRDFMYGIK SVGQDVSDQL INDGKLPHIR
601 HQTTYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVGOEL
651 MAHEQVELAE *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m163 / g163 98.6% identity in 660 aa overlap

```

              10      20      30      40      50      60
m163.pep  MVILTTLFFVCVLVVLVLTVPDQVQMWLDR AKEVIFTEFSW FYVLTFSIFLG FLLILSVS
          |||
g163      MVILTTLFFVCVLVVLVLTVPDQVQMWLDR AKEVIFTEFSW FYVLTFSIFLG FLLILSVS
              10      20      30      40      50      60

              70      80      90      100     110     120
m163.pep  SLGNIRLGRDEDVPEFGFLSWLAMLFAAGMGVGLMFFGV AEPLMHYFS DITAGTPEHRQQ
          :|||
g163      GLGNIRLGRDEDVPEFGFLSWLAMLFAAGMGVGLMFFGV AEPLMHYFS DITVGAPEHRQQ
              70      80      90      100     110     120

              130     140     150     160     170     180

```

m163.pep	QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
g163	QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
	130 140 150 160 170 180
m163.pep	190 200 210 220 230 240
	MALLATFFGIITTLGFGASQLGAGLOEMGWIAENSFSVQVLLIAAVMSLAVVSAISGVGK
g163	MALLATFFGIITTLGFGASQLGAGLOEMGWIAENSFSVQVLLIAAVMSLAVVSAISGVGK
	190 200 210 220 230 240
m163.pep	250 260 270 280 290 300
	GVKVLSELNLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP
g163	GVKVLSELNLGLAFLLLFFVLAADPTVYLLSAFGDNIGNYLGNLVRLSLKTYAYEREHKP
	250 260 270 280 290 300
m163.pep	310 320 330 340 350 360
	WFESWTVLYWAWWCSWAPFVGLFIARISKGRTIREFVFGVLLIPGLFGVLWFTVFGNTAI
g163	WFESWTVLYWAWWCSWAPFVGLFIARISKGRTIREFVFGVLLIPGLFGVLWFTVFGNTAI
	310 320 330 340 350 360
m163.pep	370 380 390 400 410 420
	WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
g163	WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
	370 380 390 400 410 420
m163.pep	430 440 450 460 470 480
	ITSRDKGLSAPRWQAVMWGVLMSAVAVLLMRSGGLGNLQSMTLIVSLPFALLMLIMCFSL
g163	ITSRDKGLSAPRWQAVMWGVLMSAVAVLLMRSGGLGNLQSMTLIVSLPFALLMLIMCFSL
	430 440 450 460 470 480
m163.pep	490 500 510 520 530 540
	WKGLSADKKYFETRVNPTSVFWTGGKWKERLVQIMSQTQEODILKFLKQTASPMHELQR
g163	WKGLSADKKYFETRVNPTSVFWTGGKWKERLVRIMSQTQEODILKFLKHTASPMHELQR
	490 500 510 520 530 540
m163.pep	550 560 570 580 590 600
	ELSEEYGLSVRVDKMFHRDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
g163	ELSEEYGLSVRVDKMFHQDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
	550 560 570 580 590 600
m163.pep	610 620 630 640 650 660
	HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE
g163	HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE
	610 620 630 640 650 660
m163.pep	X
g163	X

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 677>:

```

a163.seq
  1  ATGGTTATTT TGACGACTTT GTTTTTGTG TGTGTTTGG TGGTATTGGT
 51  TTTAACCGTG CCGGATCAGG TGCAGATGTG GCTCGATCGG GCAAAGAAG
101  TCATTTTAC  CGAGTTCAGC TGGTTTTATG TTTAACGTT TTCCATTTT
151  CTGGGTTTCC TGCTGATACT CTCGGTCAGC AGTTTGGGAA ACATCAGGCT

```

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201 CGGACGGGAT GAAGATGTGC CGGAATTCGG CTTCCTGTCTG TGGCTGGCGA
251 TGCTGTTTTGC GGCCGGGATG GCGGTGGGTC TGATGTTTTT CGGCGTGGCA
301 GAGCCGTTGA TGCATTATTT TTCGGACATT ACGGCCGGCA CGCCGGAACA
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GGCGTTCACG
401 CTTGGTTCGGT GTACGGTACG ATTGCATTGG CTTGGGCTTA TTTCGGTTTC
451 CGCTACAAGC TGCCGCTTGC CCTGCGTTCT TGTTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTCCGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATAGGCTGG ATTGCCGAAA ACAGCTTCAG
651 CGTGCCAGGT TTAGATTATCG CCGCCGTCAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GGTGTGAAGG TGTGAGCGA GTTGAACCTG
751 GGTCTTGCGT TTTTGCTGCT GTTTTTTGT TGGCGGCGG GTCCCACTGT
801 TTACCTGTTG TCGGCATTTC GCGACAACAT AGGGAACATC CTCGGAATC
851 TGGTGCGCCT CAGTTTTAAA ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTTGAAT CTTGGACGGT GCTTTATTGG GCGTGGTGGT GTTCTTGGGC
951 GCCGTTTGTG GGTGTTGTTA TCGCGCGCAT TTCAAAGGGG CGCACCATCC
1001 CGGAGTTTGT CTTCCGGGTT TTGCTCATCC CCGGCCTGTT CGGCGTTTTG
1051 TGGTTTACCG TCTTCGGCAA TACGGCGATT TGGCTGAATG ACGGGGTTGC
1101 GGGGGGAGTG CTCGAAAAGA TGACCTCCTC TCCGGAACG CTGCTTTTTA
1151 AATTCCTTAA TTACCTCCCC CTGCCCGAAT TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATTT CTCTGTTTTT TGTAACCTCT GCCGATTCCG GGATTTATGT
1251 CCTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGGTGGC
1301 AGGCGGTTAT GTGGGGCGTG CTGATGTCTG CCGTTGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CCTGCAGTCT ATGACCCTGA TTGTTTCCCT
1401 GCCGTTTGCC CTGCTGATGC TGATAATGTG TTTCAGCCTG TGGAAAGGAT
1451 TGAGTGCGGA TAAGAAATAT TTTGAGACCC GGGTTAACCC TACCAGTGTA
1501 TTTTGGACGG GCGGCAAGTG GAAAGAACGG CTGGTGCAGA TAATGAGCCA
1551 GACGCGAGGAG CAGGATATTT TAAATTCCT CAAACATACC GCATCGCCCG
1601 CTATGCACGA GTTACAACGG GAGCTTTCGG AAGAATACGG CTTGAGCGTC
1651 CGGTCGATA AGATGTTTCA TCAGGACGAG CCCGCAATCG AGTTCGTCAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAAG TCTGTCGGGC
1751 AGGATGTATC CGACCACTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CATCAGACAA CTTACAACCC CTACGCTTAT TTTTTCGACG GCGCGCTCGG
1851 GTACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTTG ATGTTGTTGG ATGATGTCGG TCAGGAACCTG
1951 ATGGCGCAGC AGCAGGTGGA ATTGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 678; ORF 163.a>:

```

a163.pep
1  MVILTTLFFV CVLVVLVLTVPDQVQMWLDR AKEVIFTEFS WFYVLTFESIF
51  LGFLLILSVS SLGNIRLGRD EDVPEFGFLS WLAMLFAAGM GVGLMFFGV
101 EPLMHYFSDI TAGTPEHRQQ QALLHTVFHW GVHAWSVYGT IALALAYFGF
151 RYKLPLALRS CFYPLLKEKI SGRFGDAIDI MALLATFFGI ITTLGFGASQ
201 LGAGLQEIGW IAENSFSVQV LIIAAVMSLA VVSAISGVGK GVKVLSLNL
251 GLAFLLLFFV LAAGPTVYLL SAFGDNIGNY LGNLVRLSEK TYAYERHKP
301 WFESWTVLYW AWWCSWAPFV GLFIARISKG RTIREFVFGV LLIPGLFGLV
351 WFTVFGNTAI WLNDGVAGGV LEKMTSSPET LLFKFFNYLP LPELTSIVSL
401 LVISLFFVTS ADSGIYVLNN ITS RDKGLSA PRWQAVMWGV LMSAVAVLLM
451 RSGGLGNLQS MTLIVSLPFA LLMLIMCFSL WKGLSADKKY FETRVNPTSV
501 FWTGGKWKER LVQIMSQTQE QDILKFLKHT ASPAMHELQR ELSEEYGLSV
551 RVDKMFHQDE PAIEFVIRKE TMRDFMYGIK SVGQDVSDQL INDGKLPHIR
601 HQTTYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVGQEL
651 MAHEQVELAE *

```

m163/a163 99.4% identity in 660 aa overlap

```

          10      20      30      40      50      60
m163.pep  MVILTTLFFV CVLVVLVLTVPDQVQMWLDR AKEVIFTEFS WFYVLTFESIF LGFLLILSVS
          |||||
a163      MVILTTLFFV CVLVVLVLTVPDQVQMWLDR AKEVIFTEFS WFYVLTFESIF LGFLLILSVS
          10      20      30      40      50      60

          70      80      90     100     110     120
m163.pep  SLGNIRLGRD EDVPEFGFLS WLAMLFAAGM GVGLMFFGV AEPLMHYFSDI TAGTPEHRQQ

```

a163						
	SLGNIRLGRDEDVPEFGFLSWLAMLFAAGMGVGLMFFGVAEPLMHYFSDITAGTPEHRQQ					
	70	80	90	100	110	120
m163.pep	130	140	150	160	170	180
	QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI					
a163						
	QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI					
	130	140	150	160	170	180
m163.pep	190	200	210	220	230	240
	MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFSVQVLI IAAVMSLAVVSAISGVGK					
a163						
	MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFSVQVLI IAAVMSLAVVSAISGVGK					
	190	200	210	220	230	240
m163.pep	250	260	270	280	290	300
	GVKVLSELNLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP					
a163						
	GVKVLSELNLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP					
	250	260	270	280	290	300
m163.pep	310	320	330	340	350	360
	WFESWTVLYWAWWCSWAPFVGLFIARISKGRTIREFVFGVLLIPGLFGVLWFTVFGNTAI					
a163						
	WFESWTVLYWAWWCSWAPFVGLFIARISKGRTIREFVFGVLLIPGLFGVLWFTVFGNTAI					
	310	320	330	340	350	360
m163.pep	370	380	390	400	410	420
	WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN					
a163						
	WLNDGVAGGVLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN					
	370	380	390	400	410	420
m163.pep	430	440	450	460	470	480
	ITSRDKGLSAPRWQAVMWGVLMASAVVLLMRSGGLGNLQSMTLIVSLPFPALLMLIMCFSL					
a163						
	ITSRDKGLSAPRWQAVMWGVLMASAVVLLMRSGGLGNLQSMTLIVSLPFPALLMLIMCFSL					
	430	440	450	460	470	480
m163.pep	490	500	510	520	530	540
	WKGLSADKKYFETRVNPTSVEFTGKKWKERLVQIMSQTQEODILKFLKQTASPAMHELQR					
a163						
	WKGLSADKKYFETRVNPTSVEFTGKKWKERLVQIMSQTQEODILKFLKHTASPAMHELQR					
	490	500	510	520	530	540
m163.pep	550	560	570	580	590	600
	ELSEYGLSVRVDKMFHRDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR					
a163						
	ELSEYGLSVRVDKMFHQDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR					
	550	560	570	580	590	600
m163.pep	610	620	630	640	650	660
	HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE					
a163						
	HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE					
	610	620	630	640	650	660
m163.pep	X					
a163	X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 679>:

```

g164.seq (partial)
1  ..ATGAACACAT TTTTGAAAAA CAGCGAATAC GCGTATATCC TGAACGACTG
51  CAAGGCGCGC TTCCTGTTCC CCTCGGCCGG CCTGTCAAAA GAATTGGCGG
101 GCCTGAAGGC GCAAACGCCC GTCGAAAAAA TCATTGGAC GGACAAAAGC
151 CGGCCGGCCG GCGAAACGGC GGAAGGCGAT GCCTTTTTTG AAAACGTGCG
201 CCGCTTCCCC GAAAAACCCG ACTTGGGCCG CCAACCCCGG ATAAATGATT
251 TGGCACACAT CATCTACACC TCCGGCACGA CGGGGCATCC CAAAGGCGCG
301 CTAATCAGTT ACGCCAACCT GTTCGCCAAC CTGAACGGCA TCGAACGCAT
351 CTTtaaAATT TCCAAACGCG ACCGCTTTAT CGTTTTcctg ccgatgTTCC
401 ACAGCTTCAC GCTGACGGCT ATGGTGCTGC TGCCGATTTA TATGGCGTGT
451 TCGATTATTT TGGTCAAAtc cgttttCCCC ttttccaacg TTTTGAAACA
501 GGCCCTGCTC AAACGCGCAA CCGTGTTTTT GGGCGTACCC GCGATTTACA
551 CCGCGATGAG CAAGGCAAAA ATCCCTTGGT ATTTCAAGAT GTTCAACCGC
601 ATCCGCCTGT TTATCAGCGG CGGCGCGCCT TTGGCGGAAC AAACCATCCT
651 CGATTTTAAA GCCAAGTTCC CCCGCGCCAA ATTGCTGGAA GGCTACGGAC
701 TGAGCGAAGC CTCGCCGCTC GTCGCCGTCA ATACGCCCGA ACGGCAAAAG
751 GCGCGCAGCG TCGGCATCCC CCGGCCGGT TTGGAAGCCA AAGCCGTCAA
801 TGAAGAATTG GTCGAAGTGC CGCGCGGCGA AGTGGGCGAA CTGATCGTCA
851 GGGGCGGTTC GGTGATGCGG GGCTACCTCA ATATGCCTGC CGCCACCGAT
901 GAAACCATCG TCAACGGCTG GTTGAAAACG GGCGATTTTC TTACCATAGA
951 CGAGGACGGC TTTATCTTTA TCGTCGACCG CAAAAAAGAT TTGATTATTT
1001 CCAAAGTCA AAACGTCTAT CCGCGCGAGA TCGAAGAAGA AATCCACAAA
1051 CTCGATGCCG TCGAAGCCGC CGCCGTCATC GGCGTGAAAG ACCGTTATGC
1101 CGACGAGGAA ATCGTCGCCT TCGTCCAATT GAAGGAAGGT ATGGATTGG
1151 GCGAGGACGA aatccgcgcg caccTGCGTA CCGTGCTGGC AAATTTCAAA
1201 ATCCCCAAAC AGATCCACTT TAAAGACGGG CTGCCGCGCA ACGCTACGGG
1251 CAAAGTATTG AAACGGGTGC TGAAGGAGCA GTTTGAAGGA AACAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 680; ORF 164.ng>:

```

g164.pep (partial)
1  ..MNTFLKNSEY AYILNDCKAR FLFASAGLSK ELAGLKAQTP VEKIIWTDKS
51  RPAGETAEGD AFFENVRRFP EKPDLGROPR INDLAHIIYT SGTGHPKGA
101 LISYANLFAN LNGIERIFKI SKRDRFIVFL PMFHSFTLTA MVLLPIYMAC
151 SIILVKSVPF FSNVLKQALL KRATVFLGVP AIYTAMSKAK IPWYFRWFNR
201 IRLFISGGAP LAEQTILDFK AKFPRAKLE GYGLSEASPV VAVNTPERQK
251 ARSVGIPLPG LEAKAVDEEL VEVPRGEVGE LIVRGGSVMR GYLNMPAATD
301 ETIVNGWLKT GDFVTIDEDG FIFIVDRKDD LIISKQNVY PREIEEIIHK
351 LDAVEAAAVI GVKDRYADEE IVAFVQLKEG MDLGEDEIRR HLRTVLANFK
401 IPKQIHFKDG LPRNATGKVL KRVLKEQFEG NK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 681>:

```

m164.seq
1  ATGAACCGGA CTTATGCCAA TTTCTACGAA ATGCTCGCCG CCGCCTGCCG
51  CAAAAACGGA AACGGCACGG CAGTGTTCTGA CGGCAAGGAA AAAACCGCCT
101 ACCGCGCGCT CAAGCAGGAG GCCGAAGCCG TCGCGGCGTA TCTGCAAAAT
151 ATCGGCGTGA AGTTCGGCGA CACGGTCGCG CTGGCGGTTT CCAATTCCAC
201 AGAATTTATT ACCGCCTATT TCGCCATCTC CGCCATCGGC GCGGTCGCCG
251 TACCGATGAA CACATTTTTG AAAAACAGCG AATACGCGTA TATCCTGAAC
301 GACTGCAAGG CGCGCTTCCT GTTCGCCTCG GCCGGCCTGT CAAAAGAATT
351 GGCGGGCTTG AAGGCGCAAA CGCCCGTCTGA AAAAATCATT TGACGGACA
401 AAAGCCGTCC GACCGGCGAA ACGGCGGAAG GCGATGCCTT TTTTGAAGAC
451 GTGCGCCGCT TCCCCGAAAA ACCCGACTTG GGCCGCCAAC CCCGGATAAA
501 TGATTTGGCA CACATCATCT ACACCTCCGG CACGACGGGG CATCCCAAAG
551 GCGCGCTAAT CAGTTACGCC AACCTGTTTC CCAACCTGAA CGGCATCGAA
601 CGCATCTTTA AAATTTCCAA GCGCGACCGC TTTATCGTTT TCCTGCCGAT
651 GTTCCACAGC TTCACGCTGA CGGCTATGGT GCTGCTGCCG ATTTATATGG
701 CGTGTTTCGAT TATTTTGGTC AAATCCGTTT TTCCGTTTTT CAACGTTTTG
751 AAACAGACAC TGCTCAAACG CGCGACCGTG TTTTGGGGCG TACCCGCGAT
801 TTACACCGCG ATGAGCAAGG CGAAATCCC TTGGTATTTT AGATGGTTCA
851 ACCGCATTCG CCTGTTTATC AGCGGCGGCG CGCCTTTGGC GGAACAACCC
901 ATCCTCGATT TCAAAGCCAA GTTCCCCCGC GCCAAATTGC TGGAAGGCTA

```

```

951  CGGACTGAGC GAAGCCTCTC CCGTCGTCGC CGTCAATACG CCCGAGAGGC
1001 AAAAAGCCCG CAGCGTCGGC ATCCCCCTGC CCGGTTTGGG AGCCAAAGCC
1051  GTCGATGAAG AATTGGTCGA AGTGCCGCGC GGCGAAGTGG GCGAACTGAT
1101  CGTCAGGGGC GGTTCGGTGA TGCGGGGCTA CCTCAATATG CCTGCCGCCA
1151  CCGATGAAAC CATCGTCAAC GGCTGGTTGA AAACGGGCGA TTTCGTTACC
1201  ATAGACGAAG ACGGCTTTAT CTTTATCGTC GACCGCAAAA AAGATTTGAT
1251  TATTTCCAAA GGTCAAAATG TCTATCCGCG CGAGATTGAA GAAGAAATCT
1301  ACAAACCTCGA TGCCGTCGAA GCCGCCGCCG TCATCGGCGT GAAAGACCGT
1351  TATGCCGACG AGGAAATCGT CGCCTTCGTC CAATTGAAGG AAGGTATGGA
1401  TTTGGGCGAG AACGAAATCC GCCGCCACCT GCGTACCGTG CTGGCAAATT
1451  TCAAAATCCC CAAACAAATC CACTTTAAAG ACGGGCTGCC GCGCAACGCT
1501  ACGGGCAAGG TATTGAAACG GGTGTTGAAG GAGCAGTTTG ACGGAAACAA
1551  ATGA

```

This corresponds to the amino acid sequence <SEQ ID 682; ORF 164>:

```

m164.pep
1  MNRTYANFYE MLAAACRKNQ NGTAVFDGKE KTAYRALKQE AEVAAYLQN
51  IGVKFGDTVA LAVSNSTEFI TAYFAISAIG AVAVPMNTFL KNSEYAYILN
101 DCKARFLFAS AGLSKELAGL KAQTPVEKII WTDKSRPTGE TAEGDAFFED
151 VRRFPEKPD LGRQPRINDLA HIIYTS GTTG HPKALISYA NLFANLNGIE
201 RIFKISKRD R FIVFLPMFHS FTLTAMVLLP IYMACSIILV KSVFPFSNVL
251 KQTLKLRATV FLGVPAIYTA MSKAKIPWYF RWFNRIRLFI SGGAPLAEQT
301 ILDFKAKFPR AKLLEGYGLS EASPVVAVNT PERQKARSVG IPLPGLEAKA
351 VDEELVEVPR GEVGEIVRG GSVMRGYLMN PAATDETIVN GWLKTGFVFT
401 IDEGDFIFIV DRKKDLIISK QONVYPREIE EEIYKLDAVE AAVIGVKDR
451 YADEEIVAFV QLKEGMDLGE NEIRRHRLTV LANFKIPKQI HFKDGLPRNA
501 TGKVLKRVLK EQFDGNK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae* m164 / g164 98.6% identity in 432 aa overlap

```

          60      70      80      90      100      110
m164.pep  GDTVALAVSNSTEFITAYFAISAIGAVAVPMNTFLKNSEYAYILNDCKARFLFASAGLSK
g164      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
          10      20      30
          120     130     140     150     160     170
m164.pep  ELAGLKAQTPVEKIIWTDKSRPTGETAEGDAFFEDVRRFPEKPD LGRQPRINDLAHIIYT
g164      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
          40      50      60      70      80      90
          180     190     200     210     220     230
m164.pep  SGTTHGHPKGALISYANLNFANLNGIERIFKISKRD R FIVFLPMFHSFTLTAMVLLPIYMAC
g164      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
          100     110     120     130     140     150
          240     250     260     270     280     290
m164.pep  SIILVKSVFPFSNVLKQTLKLRATVFLGVPAIYTAMSKAKIPWYFRWFNRIRLFISGGAP
g164      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
          160     170     180     190     200     210
          300     310     320     330     340     350
m164.pep  LAEQTILDFKAKFPRAKLLEGYGLSEASPVVAVNTPERQKARSGIPLPGLEAKAVDEEL
g164      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
          220     230     240     250     260     270
          360     370     380     390     400     410

```

```

m164.pep  VEVPRGEVGEIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKD
          |||
g164      VEVPRGEVGEIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKD
          280      290      300      310      320      330

          420      430      440      450      460      470
m164.pep  LIISKQNVYPREIEEEIYKLDAVEAAAVIGVKDRYADEEIVAFVQLKEGMDLGENEIRR
          |||
g164      LIISKQNVYPREIEEEIHKLDAVEAAAVIGVKDRYADEEIVAFVQLKEGMDLGEDEIRR
          340      350      360      370      380      390

          480      490      500      510
m164.pep  HLRTVLANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFDGNKX
          |||
g164      HLRTVLANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFEGNKX
          400      410      420      430

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 683>:

```

a164.seq
1  ATGAAACGGA CTTATGCCAA TTTCTACGAA ATGCTGACCG CCGCCTGCCG
51  CAAAAACGGC AACGGCACGG CAGTGTTCGA CGGCAAGGAA AAAACCGCCT
101 ACCGCGCGCT CAAGCAGGAA GCCGAAGCCG TTGCGGCGTA TCTGCAAAAT
151 ATCGGCGTGA AGTTCGGCGA CACGGTCGCG CTGGCGGTTT CCAATTCCAC
201 GGAATTTATT ACCGCCTATT TCGCCGTATC CGCCATCGGC GCGGTTGCCG
251 TACCGATGAA CACATTTTTG AAAAAACAGC AATACGCGTA TATCCTGAAC
301 GACTGCAAGG CGCGCTTCCT GTTCGCCTCG GCCGGCCTGT CAAAAGAATT
351 GGCGGGCTTG AAGGCGCAAA CGCCCGTCGA AAAAATCATT TGGACGGGCC
401 AAAGCCGTCC GGACGGCGAA ATGGCGGAAG GCGATGCCTT TTTTGAAGAC
451 GTGCGCCGCT TCCCCGAAAA ACCCGACTTG GGCCGCCAAC CCCGGATAAA
501 TGATTTGGCA CACATCATCT ACACCTCCGG CACGACGGGG CATCCCAAAG
551 GTGCGCTAAT CAGCTACGCC AACCTGTTCG CCAACCTGAA CGGCATCGAA
601 CGCATCTTTA AAATCTCCAA GCGCGACCGC TTTATCGTTT TCCTGCCGAT
651 GTTCCACAGC TTCACGCTGA CGGCTATGGT GCTGCTGCCG ATTTATATGG
701 CGTGTTCGAT TATTTGGTTC AAATCCGTTT TCCCCTTTTC CAACGTTTTG
751 AAACAGGCAC TGCTCAAACG CGCGACCGTG TTTTGGGCG TGCCCGCGAT
801 TTACACCGCG ATGAGCAAGA CGAAAATCCC TTGGTATTTC AGATGGTTCA
851 ACCGCATCCG CCTGTTTATC AGCGGCGGAG CACCTTTGGC GGAACAAACC
901 ATCCTCGATT TCAAAGCCAA GTTCCCCCGC GCCAAATTGC TGGAAGGCTA
951 CGGAATGAGC GAAGCCTCGC CCGTCGTCGC CGTCAATACG CCCGAGAGGC
1001 AAAAAGCCCG CAGCGTCGGC ATCCCCCTGC CCGGTTTGA AGTCAAAGCC
1051 GTCGATGAAG AATTGGTTCG AGTGCCGCGC GGCGAAGTGG GCGAACTGAT
1101 CGTCAGGGGC GGTTCGGTGA TGCGGGGCTA CCTCAATATG CCTGCCGCCA
1151 CCGATGAAAC CATCGTCAAC GGCTGGTTGA AAACGGGCGA TTTCGTTACC
1201 ATAGACGAAG ACGGCTTTAT CTTTATCGTC GACCGCAAA AAGATTTGAT
1251 TATTTCCAAA GGTCAAATG TCTATCCGCG CGAAATCGAA GAAGAAATCT
1301 ACAAACTCGA TGCCGTCGAA GCCGCCGCG TCATCGGCGT GAAAGACCGT
1351 TATGCCGACG AGGAAATCGT CGCCTTCGTC CAATTGAAGG AAGGTATGGA
1401 TTTGGGCGAG AACGAAATCC GCCGCCACCT GCGTACCGTG CTGGCAAATT
1451 TCAAATCCC CAAACAAATC CACTTTAAAG ACGGGCTGCC GCGCAACGCT
1501 ACGGGCAAGG TATTGAAACG GGTGTTGAAG GAGCAGTTTG ACGGAAACAA
1551 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 684; ORF 164.a>:

```

a164.pep
1  MNRTYANFYE MLTAACRKNG NGTAVFDGKE KTAYRALKQE AEAVAAYLQN
51  IGVKFGDTVA LAVSNSTEFI TAYFAVSAIG AVAVPMNTFL KNSEYAYILN
101 DCKARFLFAS AGLSKELAGL KAQTFVEKII WTGQSRPDGE MAEGDAFFED
151 VRRFPEKPD LGRQPRINDLA HIIYTS GTTG HPGALISYA NLFANLNGIE
201 RIFKISKDR FIVFLPMFHS FTLTAMVLLP IYMACSIILV KSVFPFSNVL
251 KQALLKRATV FLGVPPIYTA MSKT KIPWYF RWFNRIRLFI SGGAPLAEQT
301 ILDFKAKFPR AKLLEGYGLS EASPVVAVNT PERQKARSVG IPLPGLEVKA
351 VDEELVEVPR GEVGEIVRG GSVMRGYLNM PAATDETIVN GWLKTGDFVT
401 IDEDGFIFIV DRKKDLIISK QONVYPREIE EEIYKLDAVE AAVIGVKDR
451 YADEEIVAFV QLKEGMDLGE NEIRRHLRTV LANFKIPKQI HFKDGLPRNA

```

501 TGKVLKRVLK EQFDGNK*

m164/a164 98.3% identity in 517 aa overlap

m164.pep	10	20	30	40	50	60
	MNRTYANFYEMLAACRKNNGTAVFDGKEKTAYRALKQAEAEVAAYLQNIQVKGFGDTVA					
a164	:					
	10	20	30	40	50	60
	MNRTYANFYEMLTAAACRKNNGTAVFDGKEKTAYRALKQAEAEVAAYLQNIQVKGFGDTVA					
m164.pep	70	80	90	100	110	120
	LAVSNSTEFITAYFAISAIGAVAVPMNTFLKNSEYAYILNDCKARFLFASAGLSKELAGL					
a164	:					
	70	80	90	100	110	120
	LAVSNSTEFITAYFAVSAIGAVAVPMNTFLKNSEYAYILNDCKARFLFASAGLSKELAGL					
m164.pep	130	140	150	160	170	180
	KAQTPVEKIIWTDKSRPTGETAEGDAFFEDVRRFPEKPDGLGRQPRINDLAHIIYTSGETTG					
a164	:					
	130	140	150	160	170	180
	KAQTPVEKIIWTDKSRPDGEMAEAGDAFFEDVRRFPEKPDGLGRQPRINDLAHIIYTSGETTG					
m164.pep	190	200	210	220	230	240
	HPKGALISYANLFANLNGIERIFKISKDRDFIVFLPMFHSFTLTAMVLLPIYMACSIILV					
a164	:					
	190	200	210	220	230	240
	HPKGALISYANLFANLNGIERIFKISKDRDFIVFLPMFHSFTLTAMVLLPIYMACSIILV					
m164.pep	250	260	270	280	290	300
	KSVFPFSNVLKQTLKTRATVFLGVPPIYTAMSKAKIPWYFRWFNRIRLFISGGAPLAEQT					
a164	:					
	250	260	270	280	290	300
	KSVFPFSNVLKQALLKTRATVFLGVPPIYTAMSKTKIPWYFRWFNRIRLFISGGAPLAEQT					
m164.pep	310	320	330	340	350	360
	ILDFKAKFPRAKLLEGYGLSEASPVVAVNTPERQKARSVGIPLPGLEAKAVDEELVEVPR					
a164	:					
	310	320	330	340	350	360
	ILDFKAKFPRAKLLEGYGLSEASPVVAVNTPERQKARSVGIPLPGLEVAVDEELVEVPR					
m164.pep	370	380	390	400	410	420
	GEVGELIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKDLISK					
a164	:					
	370	380	390	400	410	420
	GEVGELIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKDLISK					
m164.pep	430	440	450	460	470	480
	GQNVYPREIEEEIYKLDAVEAAVIGVKDRYADEEIVAFVQLKEGMDLGENEIRRHLRTV					
a164	:					
	430	440	450	460	470	480
	GQNVYPREIEEEIYKLDAVEAAVIGVKDRYADEEIVAFVQLKEGMDLGENEIRRHLRTV					
m164.pep	490	500	510			
	LANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFDGNKX					
a164	:					
	490	500	510			
	LANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFDGNKX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 685>:

g165.seq
1 ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC


```

51  GACTTTGGGC  GTTTTGCTCA  AAGAACTCGA  ACCGTCTTGG  GAAATCACCC
101 TGATTGAACG  CTTGGAagat  gTGGCGTTGG  AATCGTCAAA  cGCGTGGAAC
151 AACGcCGGca  CGGGGCATTc  CGcGCTGTGc  GAATTGAACT  AtgcgccGCT
201 GGGtgcgga  ggcgtcatCA  ATCCGGCGCg  cgCCCTGAAT  ATTGCCGAAC
251 AGTTTCATGT  CAGCCGCCAG  TTTTGGGcga  cgctgGTCGC  GGAAGGCAAG
301 TTGGAagaCA  ATTCCTTCAT  CAATGCcgtg  ccgcatatGT  Ctttggtgat
351 gAacgaagac  cactgCCgtt  acCTGCAAAA  ACGCTATGAT  GTGTTTAAAA
401 CGCAGAAACT  TTTTGAAAAT  ATGGAATTTT  CCACCGATCG  GAACAAAATT
451 TCCGATTGGG  CtccgCTGAT  TATGCGCGGC  CGGgacgaaA  ACCAACCCGT
501 CGCCGCCAAC  TATTCCGCCG  Aaggcacgga  tgtcgATTTC  GGACGGCTGA
551 CGCGCCAGAT  GGTGAAATAT  TTGCAGGGCA  AGGGCGTAAA  AACCAGGTTC
601 AACCGCCACG  TCGAAGACAT  CAAACGCGAA  TCCGACGGCG  CGTGGGTGCT
651 CAAAACCGCC  GATACCCGCA  ACCCAGACTG  GCAGCTCACC  CTCGCACCC
701 GCTTCCTCTT  CCTCGGCGCG  GCGGCGGCG  CACTGACCCT  GCTGCAAAAA
751 TCCGGCATCC  CCGAAGGCAA  AGGCTACGGC  GGCTTACCCG  TGTCGGCCT
801 GTTCTTCCGC  AACAGCAACC  CCGAAACCGC  CGAACAAAC  AACGCCAAAG
851 TGTACGGGCA  GGCTTCCGTC  GCGCGCGCG  CGATGTCCGT  CCCGCACCTC
901 GACACACGCA  ACGTAGACGG  CAAACGACAC  CTTATGTTTC  GTCCTTACGC
951 AGGTTTCCGT  TCCAACCTCC  TCAAGCAAGG  CTCGTTTATG  GATTTGCCGC
1001 TGTCCATCCA  TATGGACAAC  CTCTATCCTA  TGCTGCGCG  CGGCTGGGCG
1051 AATATGCCGC  TGACCAAATA  CcTGCTGGgC  gAaTTGCgtt  aa

```

This corresponds to the amino acid sequence <SEQ ID 686; ORF 165.ng>:

```

g165.pep
1  MAEATDVVLV  GGGIMSATLG  VLLKELEPSW  EITLIERLED  VALESSNAWN
51  NAGTGHSALC  ELNYAPLGAD  GVINPARALN  IAEQFHVSRQ  FWATLVAEGK
101 LEDNSFINAV  PHMSLVMNED  HCRYLQKRYD  VFKTQKLFEN  MEFSTDNRKI
151 SDWAPLIMRG  RDENQPVAAN  YSAEGTDVDF  GRLTRQMVKY  LQKGKVKTEF
201 NRHVEDIKRE  SDGAWVLKTA  DTRNPDWQLT  LRTRFLFLGA  GGGALTLLOK
251 SGIPGKGYG  GLPVSGLFFR  NSNPETAEOH  NAKVYGOASV  GAPPMSPVPHL
301 DTRNVDGKRH  LMFGPYAGFR  SNFLKQGSFM  DLPLSIHMDN  LYPMLRAGWA
351 NMPLTKYLLG  ELR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 687>:

```

m165.seq (partial)
1  ATGGCTGAAG  CGACAGACGT  TGTCTTGGTG  GGCGGCGGCA  TTATGAGCGC
51  GACTTTGGGC  GTTTTGCTCA  AAGAACTCGA  ACCGTCTTGG  GAAATCACCC
101 TGATTGAACG  CTTGGAAGAT  GTGGCGTTGG  AATCGTCAAA  CGCGTGGAAC
151 AACGCCGGCA  CGGGGCATTc  CGcGCTGTGc  GAATTGAACT  ATGCGCCGTT
201 GGGTGCAAA  GGGATTATCG  ATCCGGCGCG  CGCCCTCAAT  ATTGCCGAAC
251 AGTTTCATGT  CAGCCGCCAG  TTTTGGGCGA  CGCTGGTTCG  GGAAGGCAAG
301 TTGGAAGACA  ATTCCTTCAT  CAATGCCGTG  CCGCATATGT  CTTTGGTATG
351 GAATGAAGAC  CATTGTTCTT  ATCTTCAAAA  ACGTTATGAC  GCGTTTAAAA
401 CCCAAAACT  TTTTGAAAAT  ATGGAATTTT  CCACCGATCG  GAACAAAATT
451 TCCGATTGGG  CTCCGCTGAT  GATGCGCGGC  CGGGACGAAA  ACCAACCCGT
501 CGCCGCCAAC  TACTCCGCCG  AAGgTACGGA  TGTGATTTTC  GGACGGCTGA
551 CGCGCCAAAT  GGTGAAATAT  TTGCAGGGCA  AGGGCGTAAA  AACCGAGTTC
601 AACCGCCACG  TCGAAGACAT  CAAACGCGAA  TCCGACGGCG  CGTGGGTGCT
651 CAAAACCGCC  GATACCCGCA  ACCCCGACGG  GCAGCTCACC  CTCGTACCC
701 GCTTCCTCTT  CCTCGGCGCG  GCGGCGGCG  CGCTGACCCT  GCTGCAAAAA
751 TCCGGCATCC  CCGAAGGCAA  AGGCTACGGC  GGCTTCCCCG  TGTCGGCCT
801 GTTCTTCCGC  AACAGCAACC  CCGAAACCGC  CGAACAAAC  AACGCCAAAG
851 TGTACGGGCA  GGCTTCCGTC  GCGCGCGCG  CGATGTCCGT  CCCGCACCTC
901 GACACACGCA  ACGTGGACGG  CAAACGCCAC  CTTATGTTTC  GCCCTTACGC
951 AGGCTTCCGT  TCCAACCTCC  TCAAGCAAGG  CTCGTTTATG  GATTTGCCGC
1001 TGTCCATCCA  TATGGACAAC  CTCTATCCTA  TGCTGTGCG  CGGCTGGGCG
1051 AATATGCCGC  TGACCAA...

```

This corresponds to the amino acid sequence <SEQ ID 688; ORF 165>:

```

m165.pep (partial)
1  MAEATDVVLV  GGGIMSATLG  VLLKELEPSW  EITLIERLED  VALESSNAWN
51  NAGTGHSALC  ELNYAPLGAN  GIIDPARALN  IAEQFHVSRQ  FWATLVAEGK
101 LEDNSFINAV  PHMSLVMNED  HCSYLQKRYD  AFKTQKLFEN  MEFSTDNRKI
151 SDWAPLMRG  RDENQPVAAN  YSAEGTDVDF  GRLTRQMVKY  LQKGKVKTEF

```

201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTREFLFLGA GGGALTLLQK
 251 SGIPEGKGYG GFPVSGLFFR NSNPETAEOH NAKVYQASV GAPPMSPVPHL
 301 DTRNVDGKRH LMFGPYAGFR SNFLKQGSML DLPLSIHMDN LYPMLCAGWA
 351 NMPLTK...

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m165 / g165 97.2% identity in 356 aa overlap

m165.pep	10	20	30	40	50	60
	MAEATDVVLVGGGIMSATLGVLLKELEPSWEITLIERLEDVALESSNAWNNAGTGHSALC					
g165	10	20	30	40	50	60
	MAEATDVVLVGGGIMSATLGVLLKELEPSWEITLIERLEDVALESSNAWNNAGTGHSALC					
m165.pep	70	80	90	100	110	120
	ELNYAPLGANGIIDPARALNIAEQFHVSQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
g165	70	80	90	100	110	120
	ELNYAPLGADGVINPARALNIAEQFHVSQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
m165.pep	130	140	150	160	170	180
	HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMRGRDENQPVAANYSAEGTDVDF					
g165	130	140	150	160	170	180
	HCRYLQKRYDVFKTQKLFENMEFSTDRNKISDWAPLMRGRDENQPVAANYSAEGTDVDF					
m165.pep	190	200	210	220	230	240
	GRLTRQMVKYLGKGVKTEFNRHVEDIKRESGAWVLKTADTRNPDGQTLRTRFLFLGA					
g165	190	200	210	220	230	240
	GRLTRQMVKYLGKGVKTEFNRHVEDIKRESGAWVLKTADTRNPDWQTLRTRFLFLGA					
m165.pep	250	260	270	280	290	300
	GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAEOHNAKVYQASVGAPPMSPVPHL					
g165	250	260	270	280	290	300
	GGGALTLLQKSGIPEGKGYGLPVSGLFFRNSNPETAEOHNAKVYQASVGAPPMSPVPHL					
m165.pep	310	320	330	340	350	
	DTRNVDGKRHLMFGPYAGFRSNFLKQGSMDLPLSIHMDNLYPMLCAGWANMPLTK					
g165	310	320	330	340	350	360
	DTRNVDGKRHLMFGPYAGFRSNFLKQGSFMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG					
g165	ELRX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 689>:

a165.seq

1	ATGGCTGAAG	CGACAGACGT	TGTCTTGGTG	GGCGGCGGCA	TTATGAGCGC
51	GACTTTGGGC	GTTTGTCTCA	AAGAACTCGA	ACCGTCTTGG	GAAATCACCC
101	TGATTGAACG	CTTGAAGAT	GTGGCGTTGG	AATCGTCAAA	CGCGTGAAC
151	AACGCCGGCA	CGGGGCATTC	CGCGCTGTGC	GAATTGAAC	ATGCGCCGT
201	GGGTGCAAAT	GGGATTATCG	ATCCGGCGCG	CGCCCTCAAT	ATTGCCGAAC
251	AGTTTCATGT	CAGCCGCCAG	TTTTGGGCGA	CGTTGGTCGC	GGAAGGCAAG
301	TTGGAAGACA	ATTCCTTCAT	CAATGCCGTG	CCGCATATGT	CTTTGGTGAT
351	GAATGAAGAC	CATTGTTCTT	ATCTTCAAAA	ACGTTATGAC	GCGTTTAAAA
401	CCCAAAAAC	TTTTGAAAAT	ATGGAATTTT	CCACCGATCG	GAACAAAATT
451	TCCGATTGGG	CTCCGCTGAT	GATGCGCGGC	CGGGACGAAA	ACCAACCCGT
501	CGCCGCCAAC	TACTCCGCGG	AAGGCACGGA	TGTCGATTTC	GGACGGCTGA
551	CGCGCCAAAT	GGTGAAATAT	TTGCAGGGCA	AGGCGGTAAA	AACCGAGTTC

```
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCCGACGG GCAGCTCACC CTCCGTACCC
701 GCTTCCTCTT CCTCGGCGCG GCGGCGGGCG CGCTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGT GGCTTTCCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCCG CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTTCG GCCCTTACGC
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCACTTATG GATTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAAATA CCTGCTGGGC GAATTGCGTA AAACCAAAGA
1101 AGAACGCTTC GCCTCCCTGC TGAATACTA CCCCAGGGCA AACCCGACG
1151 ACTGGGAACT CATCACCGCA GGGCAACGCG TTCAAATCAT TAAAAAGAC
1201 TCCGAAAAAG GCGGCGTGTG GCAGTTTGGT ACGGAGATTG TCGCACACGC
1251 CGACGGCTCG CTCGCCGCAT TGCTGGGCGC GTCGCCGGGC GCATCGACCG
1301 CCGTGCCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAACGCACC
1351 CCGTCTTGGG AAGGCCGTCT GAAAGAGCTG GTACCGGGTT ACGGCATCAA
1401 GTTGAACGAA AACCCCGAAA GGGCGGATGA AATTATCGCC TATACCGCGA
1451 AAGTGTGGA TATTTAA
```

This corresponds to the amino acid sequence <SEQ ID 690; ORF 165.a>:

```
a165.pep
  1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
 51 NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSRO FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDNRKI
151 SDWAPLMMRG RDENQPVAA N YSAEGTDVDF GRLTRQMVKY LQKGVCATFE
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRFLFLGA GGGALTLLQK
251 SGIPEGKGYG GFPVSGLFRR NSNPETAEOH NAKVYQASV GAPPMSVPHL
301 DTRNVDGKRH LMFGPYAGFR SNFLKQGSML DLPLSIHMDN LYPMRLAGWA
351 NMPLTKYLLG ELRKTKEERF ASLLEYYPEA NPDDWELITA GQRVQIIKID
401 SEKGVVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERT
451 PSWEGRLKEL VPGYGIKLE NPERADEIIA YTAKVLDI*
```

m165/a165 99.7% identity in 356 aa overlap

```

      10      20      30      40      50      60
m165.pep MAEATDVVLVGGGIMSATLG VLLKELEPSWEITLIERLEDVALESSNAWN NAGTGHSALC
          |||
a165      MAEATDVVLVGGGIMSATLG VLLKELEPSWEITLIERLEDVALESSNAWN NAGTGHSALC
          |||
      10      20      30      40      50      60

      70      80      90     100     110     120
m165.pep ELNYAPLGANGI IDPARALNIAEQFHVSROFWATLVAEGKLEDNSFINAVPHMSLVMNED
          |||
a165      ELNYAPLGANGI IDPARALNIAEQFHVSROFWATLVAEGKLEDNSFINAVPHMSLVMNED
          |||
      70      80      90     100     110     120

      130     140     150     160     170     180
m165.pep HCSYLQKRYDAFKTQKLFENMEFSTDNRKISDWAPLMMRGRDENQPVAA NYS AEGTDVDF
          |||
a165      HCSYLQKRYDAFKTQKLFENMEFSTDNRKISDWAPLMMRGRDENQPVAA NYS AEGTDVDF
          |||
      130     140     150     160     170     180

      190     200     210     220     230     240
m165.pep GRLTRQMVKY LQKGVKTEFNHVEDIKRES DGAWVLKTADTRNPDGQLT LRTRFLFLGA
          |||
a165      GRLTRQMVKY LQKGVKTEFNHVEDIKRES DGAWVLKTADTRNPDGQLT LRTRFLFLGA
          |||
      190     200     210     220     230     240

      250     260     270     280     290     300
m165.pep GGGALTLLQKSGIPEGKGYGGFPVSGLFRRNSNPETAEOHNAKVYQASVGAPPMSVPHL
          |||
a165      GGGALTLLQKSGIPEGKGYGGFPVSGLFRRNSNPETAEOHNAKVYQASVGAPPMSVPHL
          |||
      250     260     270     280     290     300
```

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          310      320      330      340      350
m165.pep  DTRNVDGKRHLMFGPYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLCAGWANMPLTK
          |||||
a165      DTRNVDGKRHLMFGPYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG
          310      320      330      340      350      360
a165      ELRKTKEERFASLLEYYPEANPDDWELITAGQVRVQIIKKDSEKGGVLQFGTEIVAHADGS
          370      380      390      400      410      420

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 691>:

g165-1.seq

```

1  ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGGCA TTATGAGCGC
51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAagat gTGGCGTTGG AATCGTCAAA cGCGTGGAAc
151 AACGcCGgca CGGGGCATTC CGcGCTGTGc GAATTGAACT AtgcgccGCT
201 GGGtgccggac ggcgtcatCA ATCCGGCGCg cgCCCTGAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGa cgctggtTCGc GGAAGGCAAG
301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTGGTGAT
351 GAACGAAGAC CACTGCCGTT ACCTGCAAAA ACGCTATGAT GTGTTTAAAA
401 CGCAGAAACT TTTTAAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CtcgcCTGAT TATGCGCGGC CGGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TATTCCGCCG AAGGCACGGA TGTCGATTTC GGACGGCTGA
551 CGCGCCAGAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCGAGTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCAGACTG GCAGCTCACC CTCGCCACCC
701 GCTTCTCTTT CCTCGCGCGC GCGGCGGGCG CACTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTACCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCCG CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTAGACGG CAAACGACAC CTTATGTTTC GTCCCTACGC
951 AGGTTTCCGT TCCAACCTCC TCAAGCAAGG CTCGTTTATG GATTTGCCCG
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCCG TGACCAAATA CCTGTGGGCG GAATTGCGTA AAACCAAAGA
1101 AGAACGCTtt gCCTCCCTGC TGgaatacta cccGaggcag acccGACGAc
1151 tggTactctt cacgcaggnc acGCGTcata tcattanata tgactCgaaa
1201 ctgcgcgtgc tgcagttgta cgagattgtg ccaCGCGacg ctcgctcgcg
1251 cattctggag cgtcgcggcg catcacgctn tgcgctgata tccgctgatg
1301 acactgctcc gaGCGcgccc gtcttgaaaa gtgtctga

```

This corresponds to the amino acid sequence <SEQ ID 692; ORF 165-1.ng>:

g165-1.pep

```

1  MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51  NAGTGHSALC ELNYAPLGAD GVINPARALN IAEQFHVSRQ FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCRYLQKRYD VFKTKQLFEN MEFSTDNRKI
151 SDWAPLIMRG RDNQNPVAAN YSAEGTDVDF GRLTROMVKY LQKGKVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDWQLT LRTREFLFLGA GGGALTLLQK
251 SGIPGEGGYG GLPVSGLFRR NSNPETAEOH NAKVYGOASV GAPPMSPVPHL
301 DTRNVDGKRH LMFGPYAGFR SNFLKQGSFM DLPLSIHMDN LYPMLRAGWA
351 NMPLTKYLLG ELRKTKEERF ASLLEYPRQ TRRLVLITQX TRHIIXYDSK
401 LRVLYEIV PRDARSRIE RRGASRXALI SADDTAPSAP VLESV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 693>:

m165-1.seq

```

1  ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGGCA TTATGAGCGC
51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGGAAc
151 AACGCGCGCA CGGGGCATTC CGCGCTGTGc GAATTGAACT ATGCGCCGTT
201 GGGTGCAAAAT GGGATTATCG ATCCGGCGCG CGCCCTCAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGa CGCTGGTTCGc GGAAGGCAAG
301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTGGTGAT
351 GAATGAAGAC CATTGTTCTT ATCTTCAAAA ACGTTATGAC GCGTTTAAAA
401 CCAAAAAACT TTTTAAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CTCGCTGAT GATGCGCGGC CGGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TACTCCGCCG AAGGTACGGA TGTCGATTTC GGACGGCTGA
551 CGCGCCAAAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCGAGTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCCGACGG GCAGCTCACC CTCCTACCC
701 GCTTCTCTTT CCTCGCGCGC GCGGCGGGCG CGCTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTCCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG

```

```
851 TGTACGGGCA GGCTTCCGTC GGC GCGCCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTATGTTCG GCCCTTACGC
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCGCTTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGTGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAAATA CCTGCTGGGC GAATTGCGTA AAACCAAAGA
1101 AGAACGCTTC GCCTCCCTGC TGAATACTA CCCCAGGCA AACCCGACG
1151 ACTGGGAAC CATCACCGCA GGGCAACGCG TCCAAATCAT TAAAAAGAC
1201 TCCGAAAAAG GCGGCGTGCT CCAGTTTGGT ACGGAGATTG TCGCCACGC
1251 CGACGGCTCA CTCGCCGCAT TGCTGGGCGC GTCGCCGGC GCATCGACCG
1301 CTGTGCCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAGCGCGCC
1351 CCGTCTTGGG AAGACCGTCT GAAAGAGCTG GTACCGGGT ACGGCATCAA
1401 GTTGAACGAA AACCTGAAA GGGCGGATGA AATTATCGCC TATACCGCGA
1451 AAGTATTGGA TATTAA
```

This corresponds to the amino acid sequence <SEQ ID 694; ORF 165-1>:

m165-1.pep

```
1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51 NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSRQ FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDRNKI
151 SDWAPLMRGR DENQPVAAAN YSAEGTDVDF GRLTRQMVKY LQKGKVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LTRFLFLGA GGGALTLLQK
251 SGIPGKGYG GFFVSGLFFR NSNPETAQH NAKVYQASV GAPPMSVPHL
301 DTRNVGKRHL MFPGYAGFR SNFLKQGS LMPLSIHMDN LYPMLCAGWA
351 NMPLTKYLLG ELRKTKEERF ASLLEYYPEA NPDDWELITA GQRVQIIKKD
401 SEKGGVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERA
451 PSWEDRLKEL VPGYGIKLE NPERADEIIA YTAKVLDI*
```

m165-1/g165-1 89.7% identity in 428 aa overlap

	10	20	30	40	50	60
m165-1.pep	MAEATDVVLVGGGIMSATLG	VLLKELEPSWEITLIERLED	VALESSNAWN	NAGTGHSALC		
g165-1	MAEATDVVLVGGGIMSATLG	VLLKELEPSWEITLIERLED	VALESSNAWN	NAGTGHSALC		
	70	80	90	100	110	120
m165-1.pep	ELNYAPLGANGIIDPARALN	IAEQFHVSRQFWATLVAEGK	LEDNSFINAVPHMSLVMNED			
g165-1	ELNYAPLGADGVINPARALN	IAEQFHVSRQFWATLVAEGK	LEDNSFINAVPHMSLVMNED			
	130	140	150	160	170	180
m165-1.pep	HCSYLQKRYDAFKTQKLFEN	MEFSTDRNKISDWAPLMRGR	DENQPVAAANYSAEGTDVDF			
g165-1	HCRYLQKRYDVFKTQKLFEN	MEFSTDRNKISDWAPLMRGR	DENQPVAAANYSAEGTDVDF			
	190	200	210	220	230	240
m165-1.pep	GRLTRQMVKYLQKGKVKTEF	NRHVEDIKRES	DGAWVLKTADTRNPDGQLT	LTRFLFLGA		
g165-1	GRLTRQMVKYLQKGKVKTEF	NRHVEDIKRES	DGAWVLKTADTRNPDWQLT	LTRFLFLGA		
	250	260	270	280	290	300
m165-1.pep	GGGALTLLQKSGIPGKGYGG	FVSGLFFRNSNPETAQH	NAKVYQASVGAPPMSVPHL			
g165-1	GGGALTLLQKSGIPGKGYGG	LPVSGLFFRNSNPETAQH	NAKVYQASVGAPPMSVPHL			
	310	320	330	340	350	360
m165-1.pep	DTRNVGKRHLMFPGYAGFR	SNFLKQGSMDLPLSIHMDN	LYPMLCAGWANMPLTKYLLG			
g165-1	DTRNVGKRHLMFPGYAGFR	SNFLKQGSFMDLPLSIHMDN	LYPMLRAGWANMPLTKYLLG			
	370	380	390	400	410	420
m165-1.pep	ELRKTKEERFASLLEYYPEA	NPDDWELITAGQRVQIIKKD	SEKGGVLQFGTEIVAHADGS			
g165-1	ELRKTKEERFASLLEYYP	QTRRLVLITQXTR-HIIXYDS	-KLRVLQLYEIVPRDARSR			
	430	440	450	460	470	480

m165-1.pep LAALLGASPGASTAVPLMIRLMHQCFPERAPSWEDRLKELVPGYGIKLNNPERADEIIA
:
|||
g165-1 ILERRGASRXALISADDTAPSAPVLESVX
420 430 440

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 695>:

a165-1.seq
1 ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC
51 GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGGAAC
151 AACGCCGGCA CGGGGCATTG CGCGCTGTGC GAATTGAACT ATGCGCCGTT
201 GGGTGCAAAAT GGGATTATCG ATCCGGCGCG CGCCCTCAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGA CGTTGGTTCG GGAAGGCAAG
301 TTGGAAGACA ATTCCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
351 GAATGAAGAC CATTGTTCTT ATCTTCAAAA ACATTATGAC GCGTTTAAAA
401 CCCAAAAACT TTTTGAATAA ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CTCCGCTGAT GATGCGCGGC CGGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TACTCCGCCG AAGGCACGGA TGTCGATTTC GGACGGCTGA
551 CGCGCCAAAT GGTGAAATAT TTGCAGGGCA AGGCGGTAAA AACCGAGTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCCGACGG GCAGCTCACC CTCCGTACCC
701 GCTTCCTCTT CCTCGGCGCG GCGGCGGCGC CGCTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGT GGCTTTCCCG TGTCGGCCTT
801 GTTCTTCCGC AACAGCAACC CCGAAACGCG CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTATGTTCG GCCCTTACGC
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCATTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAATA CCTGCTGGGC GAATTGCGTA AAACCAAAGA
1101 AGAACGCTTC GCCTCCCTGC TGGAACTACTA CCCCAGGGCA AACCCCGACG
1151 ACTGGGAAC CATCACCGCA GGGCAACGCG TCAAAATCAT TAAAAAAGAC
1201 TCCGAAAAAG GCGGCGTGTT GCAGTTTGGT ACGGAGATTG TCGCACACGC
1251 CGACGGCTCG CTCGCCGCAT TGCTGGGCGC GTCGCGGGC GCATCGACCG
1301 CCGTGCCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAACGCACC
1351 CCGTCTTGGG AAGGCCGTCT GAAAGAGCTG GTACCGGGTT ACGGCATCAA
1401 GTTGAACGAA AACCCGAAA GGGCGGATGA AATTATCGCC TATACCGCGA
1451 AAGTGTGGA TATTTAA

This corresponds to the amino acid sequence <SEQ ID 696; ORF 165-1.a>:

a165-1.pep
1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51 NAGTGHSALE ELNYAPLGAN GIIDPARALN IAEQFHVSQ FWTALVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDRNKI
151 SDWAPLMMRG RDENQVPAAN YSAEGTDVDF GRLTRQMVKY LQKGKVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTFLFLGA GGGALTLLQK
251 SGIPEGKGYG GFPVSGLFFR NSNPETAEOH NAKVYQASV GAPPMSVPHL
301 DTRNVDGKRH LMFGPYAGFR SNFLKQGSML DLPLSIHMDN LYPMLRAGWA
351 NMPLTKYLLG ELRKTKEERF ASLLEYYPEA NPDDWELITA QORVQIIKGD
401 SEKGGVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERT
451 PSWEGRLKEL VPGYGIKLNE NPERADEIIA YTAKVLDI*

a165-1/m165-1 99.4% identity in 488 aa overlap

a165-1.pep	10	20	30	40	50	60
m165-1	10	20	30	40	50	60
a165-1.pep	70	80	90	100	110	120
m165-1	70	80	90	100	110	120
a165-1.pep	130	140	150	160	170	180
m165-1	130	140	150	160	170	180
a165-1.pep	190	200	210	220	230	240
m165-1	190	200	210	220	230	240

```
a165-1.pep  GRLTRQMVKYLGKGKTEFNRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA
|||||
m165-1      GRLTRQMVKYLGKGKTEFNRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA
              190      200      210      220      230      240

              250      260      270      280      290      300
a165-1.pep  GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAEOHNAKVYQASVGAPPMSVPHL
|||||
m165-1      GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAEOHNAKVYQASVGAPPMSVPHL
              250      260      270      280      290      300

              310      320      330      340      350      360
a165-1.pep  DTRNVDGKRHLMFPGPYAGFRSNFLKQGSMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG
|||||
m165-1      DTRNVDGKRHLMFPGPYAGFRSNFLKQGSMDLPLSIHMDNLYPMLCAGWANMPLTKYLLG
              310      320      330      340      350      360

              370      380      390      400      410      420
a165-1.pep  ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVAHADGS
|||||
m165-1      ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVAHADGS
              370      380      390      400      410      420

              430      440      450      460      470      480
a165-1.pep  LAALLGASPGASTAVPLMIRLMHQCFPERTPSWEGRLKELVPGYGIKLNENPERADEIIA
|||||
m165-1      LAALLGASPGASTAVPLMIRLMHQCFPERAPSWEDRLKELVPGYGIKLNENPERADEIIA
              430      440      450      460      470      480

              489
a165-1.pep  YTAKVLDIX
|||||
m165-1      YTAKVLDIX
```

a165-1/p33940

sp|P33940|YOJH_ECOLI HYPOTHETICAL 60.2 KD PROTEIN IN ECO-ALKB INTERGENIC REGION
>gi|1736851|gnl|PID|d1016718 (D90850) ORF_ID:o372#5; similar to [SwissProt Accession Number P33940] [Escherichia coli] >gi|1788539 (AE000310) f548; This 548 aa ORF is 100 pct identical to 490 residues of YOJH_ECOLI SW: P33940 (492 aa) but contains 56 additional N-ter aa; 100 pct identical to GB: ECOHU49_33
ACCESSION: U00008 (490 aa) but contains 58 additional N-term resi... Length = 548
Score = 458 bits (1167), Expect = e-128
Identities = 233/490 (47%), Positives = 303/490 (61%), Gaps = 5/490 (1%)

```
Query: 3  EATDVVLVGGGIMSATLGVLKLELPSWEITLIERLEDVALESSNAWNNAGTGHSALCEL 62
+ TDV+L+GGGIMSATLG L+ELEP W +T++ERLE VA ESSN WNNAGTGHSAL EL
Sbjct: 30  QETDVLLIGGGIMSATLGTYLRELEPEWSMTMVERLEGVAQESSNGWNNAGTGHSALMEL 89

Query: 63  NYAPLGGANGIIDPARALNIAEQFHVSQFWATLVAEGKLED-NSFINAVPHMSLVMNEDH 121
NY P A+G I +A+ I E F +SRQFWA V G L SFIN VPHMS V ED+
Sbjct: 90  NYTPQNADGSISIEKAVINEAFQISRQFWAHQVERGVLRTPRSFINTVPHMSFVWGEDN 149

Query: 122 CSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGRDENQPVAANYSAEGTDVDFG 181
++L+ RY A + LF M +S D +I +WAPL+M GRD Q VAA + GTDV++G
Sbjct: 150 VNFLRARYAALQQSSLFRGMRYSEDHAQIKEWAPLVMEGRDPQKVAATRTEIGTDVNYG 209

Query: 182 RLTRQMVKYLGKG-VKTEFNRHVEDIKRESDGAWVLKTADTRNPDGQLTXXXXXXXXXX 240
+TRQ++ LQ K + + V +KR D W + AD +N Q
Sbjct: 210 EITRQLIASLQKKSNFSLQLSSEVRALKRNDNTWTVTVDLKNGTAG-NIRAKFVFIGA 268

Query: 241 XXXXXXXXQKSGIPEGKGYGGFPVSGLFFRNSNPETAEOHNAKVYQASVGAPPMSVPHL 300
Q+SGIPE K Y GFPV G F + NP+ H AKVYG+ASVGAPPMSVPH+
Sbjct: 269 GGAALKLLQESGIPEAKDYAGFPVGGQFLVSENPDVNVHHLAKVYGKASVGAPPMSVPHI 328

Query: 301 DTRNVDGKRHLMFPGPYAGFRSNFLKQGSMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG 360
DTR +DGKR ++FGP+A F + FLK GSL DL S N+ PM+ G N L KYL+
Sbjct: 329 DTRVLDGKRVVLFPGFATFSTKFLKNGSLWDLMSSTTTSNVMPMMHVGLDNFDLVKYLVS 388

Query: 361 ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVXXXXXX 420
++ ++E+RF +L EYYP+A +DW L AGQRVQIIK+D+EKGGVL+ GTE+V
Sbjct: 389 QVMLSEEDRFEALKEYYPQAKKEDWRLWQAGQRVQIIKRDAEKGGVLRGLTEVVSQQGT 448

Query: 421 XXXXXXXXXXXXXXXXVPLMIRLMHQCFPER--TPSWEGRLKELVPGYGIKLNENPERADEI 478
```

P+M+ L+ + F +R +P W+ LK +VP YG KLN + +
 Sbjct: 449 IAALLGASPGASTAAPIMLNLLKVFVGDVSSPQWQATLKAIVPSYGRKLNQDVAAATERE 508

Query: 479 IAYTAKVLDI 488

+ YT++VL +

Sbjct: 509 LQYTSEVLGL 518

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 697>:

g204.seq

```

1 atggcgggcgg cggaaataaa acgccccctc gctgtcgatt tccagcacat
51 agcgtccggt ctgcacggcg gcatagccgc ttttgctgc ctgatagggt
101 tgcagggcgg aatgcgaaat caggtaatca gtcagtttgc cgccgtcttc
151 ggcgatattg cccaccagtt tggcaaacaa ggtatggcac acgccgtttt
201 ccgcccagcc cgaaggcgcg tcctttccgt cggtttccat acatttgccg
251 acgacggcct ccaagtcggt gggatgcttt ccggtcagcc ggacggcggt
301 ttgttccggc aagcctttaa tccgataact gatttgtttt ttgccgtcgt
351 tggttttgcc ttcgctactt tgtcccaaag ccaaaccggc aatcgccgta
401 ttgtcgatgt atttgacttt gaaaaccggt ttcggcgcg cttgtgcccgc
451 attttgccgc tgttccgcgc tattttcggg tttgccgcag gcggcaagca
501 gcaggcagcc gcccaacacg gcaaaaggta ttttcagcat tccgcactcc
551 tgatggtttc aaaatgccgt ctgaaatgcc gtctgaaacg tggcaggcgg
601 aggttcggac ggcattgggt ttatttcaac gggcggatgc cgaccgcac
651 gcgtacttta tccaacaatt cgcgcgcttc tttgcgcgc ttttgcgcgc
701 ctgcctgcaa aatctcttcg atttgcaag gattagaggt caatgcgttg
751 tag
  
```

This corresponds to the amino acid sequence <SEQ ID 698; ORF 204.ng>:

g204.pep

```

1 MAAAEIKRPL AVDFQHIASV LHGGIAAFAC LIGLQGGMRN QVISQFAAVF
51 GDIAHQFGKQ GMAHAVFRPA RRRVLSVGFH TFADDGFQV GMLSGQPDGV
101 LFRQAFNRIT DLFFAVVGFA FATLSQSQTG NRRIVDVDF ENRFRALCR
151 ILRLFRIRIFG FAAGGKQQA AOHGKRYFOH SALLMVSOCR LKRLKRGRR
201 RFGRHWVYFN GRMPTASRTL SNNSRASLRA FCAPACKISS ICEGLEVNAL
251 *
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 699>:

m204.seq

```

1 ATGGCGGCGG CGGAAATAAA ACGCCCCTTC GCTGTGCGATT TCCAGCACAT
51 AGCGTCCGTT CTGCACGGCG GCATAGCCGC TTTTGCTGCTGC CTGATAGGGT
101 TGCAGGCGCG CATGCGAAAC TAGGTAATCC GTCAGTTTGC CGCCGTCTTC
151 GGCGATATTG CCCACCAGTT TGGCAAACAA GGTATGGCAC ACGCCGTTTT
201 CTGCCCAACC TGCCGACTG TCCTTATCAT CGGTTTCCAT ACATTTGCCG
251 CTGACGGCTT CCAAGTCGCC GGGATGCTTG CCGATCAGTC GGATAACATT
301 TTGTTCCGGC AAGCCTTTAA TCGGATAACT GATTGTGTTT TTGCCGTCGT
351 TGGTTTTGCC TTCGCTGCTT TGTCCCAAAT CCAAACCGGC AATCGCCGTA
401 TTGTCGATAT ATATGACTTT GAAAACCGGT TTCGGCGCGC TTTGTACCGC
451 GTTTTGCGGC TGTACCGCCG TATTTwCGGA TTTGCCGCaC GGCaArgCAG
501 CAGGCAGCCG CCAATACGG CAAAaAwGT wTTCAGCATT CCACaYTCCT
551 GATGGTTTCA AAATGCCGTC TGAAACGCGG CAGGCGGAGG TTCGGACGGC
601 ATCGGGTTCA TTTCAACGGG CGGATGcCGA CCGCATCgGT ACTTTGTCCA
651 ATAATTGCGG TGCTTCTTTA CGCGCTTTCG CCGCGCCTGC CTGCAAAATC
701 TCTTCGATTT GCGAAGGGTC GCGGTCAGC TCGTTGTAG
  
```

This corresponds to the amino acid sequence <SEQ ID 700; ORF 204>:

m204.pep

```

1 MAAAEIKRPF AVDFQHIASV LHGGIAAFAC LIGLQGGMRN *VIRQFAAVF
51 GDIAHQFGKQ GMAHAVFCPT CRTVLIIGFH TFAADGFQVA GMLADQSDNI
101 LFRQAFNRIT DLFFAVVGFA FAALSQIQTG NRRIVDIYDF ENRFRALYR
151 VLRLYRRIXG FAATAXQQA AQYKXXXQH STXLMVSKCR LKRGRRRFRGR
201 HRVHFNRRMP TASGTLNNS RASLRAFAAP ACKISSICEG SAVSSL*
  
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 204 shows 82.0% identity over a 250 aa overlap with a predicted ORF (ORF 204.ng) from *N. gonorrhoeae*:

m204/g204

	10	20	30	40	50	60
m204 . pep	MAAAEIKRPFVDFQHIASVLHGIIAFAACLIQLGGMRNXVIRQFAAVFGDIAHQFGKQ					
g204	MAAAEIKRPLAVDFQHIASVLHGIIAFAACLIQLGGMRNQVISQFAAVFGDIAHQFGKQ					
	10	20	30	40	50	60
m204 . pep	GMAHAVFCPTCRTVLIIGFHTFAADGFQVAGMLADQSDNILFRQAFNRITDLFFAVVGFA					
g204	GMAHAVFRPARRRVLSVGFHTFADDGFQVVGMLSGQPDGVLFRQAFNRITDLFFAVVGFA					
	70	80	90	100	110	120
m204 . pep	FAALSQIQTNRRIVDIYDFENRFRRLALYRVLRLYRRIXGFAATAQQAAAQYKXXXQH					
g204	FATLSQSQTGNRRIVDVDFENRFRRLALCRILRLFRIFGFAAGGKQAAAQHGKRYFQH					
	130	140	150	160	170	180
m204 . pep	STXLMVSKCRLK---RGRRRFGRHVRHFNGRMPTASGTLNNRSLRAFAAPACKISS					
g204	SALLMVSKCRLKRLKRGRRRFGRHWVYFNGRMPTASRTLSNNRSLRAFCAPACKISS					
	190	200	210	220	230	240
m204 . pep	ICEGSAVSSLX					
g204	ICEGLEVNAL					
	240					
		250				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 701>:

a204 . seq

1	ATGGCGGCGG	CGGAAATAAA	ACGCCCCCTC	GCTGTCGATT	TCCAGCACAT
51	AGCGTCCGTT	CTGCACGGCG	GCATAGCCGC	TTTGCCTGC	CTGATAGGGT
101	TGCAGGGCGG	AATGCGAAAT	CAGGTAATCC	GTCAGTTTGC	CGCCGTCTTC
151	GGCGATATTG	CCCACCAATT	TGGCAAACAA	GGTATGGCAC	ACGCCGTTTG
201	CCGCCCAGCC	CGAAGGCGCG	CCCTTTCCGT	CGGTTTCCAT	ACATTTGCCG
251	ACGACGGCTT	CCAAGTCGTT	GGGATGCTTG	CCGGTCAGCC	GGACGACGTT
301	TTGTTCCGGC	AAGCCTTT..
351
401
451
501
551AAGAG	GTTCGGACGG
601	CATTGGGTTT	ATTTCACGG	GCGGATACCG	ACCGCATCAC	GTACTTTGCC
651	CAATAATTCG	CGTGCTTCTT	TACGCGCTTT	TTGCGCGCCT	GCCTGCAAAA
701	TCTCTTCGAT	TTGCGAAGGG	TCGGCGGTCA	GCTCGTTGTA	G

This corresponds to the amino acid sequence <SEQ ID 702; ORF 204.a>:

a204 . pep

1	MAAAEIKRPL	AVDFQHIASV	LHGIIAFAAC	LIGLQGGMRN	QVIRQFAAVF
51	GDIAHQFGKQ	GMAHAVCRPA	RRRALSVEFH	TFADDGFQVV	GMLAGQPDDV
101	LFRQAF....
151KREGR
201	HWVYFNGRIP	TASRTLPNNS	RASLRAFCAP	ACKISSICEG	SAVSSL*

m204/a204 54.5% identity in 246 aa overlap

```

      10      20      30      40      50      60
m204.pep  MAAAEIKRPFVDFQHIASVLHGGIAAFACLIQLGGMRNXVIRQFAAVFGDIAHQFGKQ
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a204      MAAAEIKRPLAVDFQHIASVLHGGIAAFACLIQLGGMRNQVIRQFAAVFGDIAHQFGKQ
          10      20      30      40      50      60

      70      80      90      100     110     120
m204.pep  GMAHAVFCPTCRTVLIIGFHTFAADGFQVAGMLADQSDNILFRQAFNRITDLFFFAVVGFA
          ||||| |: |: |: ||||| |||||:||||| |||||:|||||
a204      GMAHAVCRPARRRALSFGFHTFADDGFQVVGMLAGQPDVLFROAF-----
          70      80      90      100

      130     140     150     160     170     180
m204.pep  FAALSQIQTNRRIVDIYDFENRFRRLYRVLRLYRRIXGFAATAXQAAAQYKXXXQH
a204      -----

      190     200     210     220     230     240
m204.pep  STXLMVSKCRLKRGRRRFRGRHVRHFNGRMPTASGTLNNSRASLRFAAPACKISSICEG
          :||||| :|||||:||||| |||||:|||||
a204      -----KRFGRHWVYFNGRIPTASRTLPNNSRASLRFCAPACKISSICEG
          110     120     130     140     150

m204.pep  SAVSSLX
          |||||
a204      SAVSSLX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 703>:

```

g205.seq
1  atgctgaaaa taccttttgc cgtgttgggc ggctgcctgc tgcttgccgc
51  ctgcggaata tccgaaaata cggcggaaca gccgcaaat gcggcacaaa
101 gcgcgccgaa accggttttc aaagtcaaat acatcgacaa tacggcgatt
151 gccggtttgg ctttgggaca aagtagcgaa ggcaaaacca acgacggcaa
201 aaaacaaatc agttatccga ttaaaggctt gccggaacaa aacgccgtcc
251 ggctgaccgg aaagcatccc aacgacttgg aagccgtcgt cggcaaatgt
301 atggaaaccg acggaaagga cgcgccttcg ggctgggagg aaaacggcgt
351 gtgccatacc ttgtttgcca aactgggtgg caatatcgcc gaagacggcg
401 gcaaaactgac tgattacctg atttcgcatt ccgccctgca accctatcag
451 gcaggcaaaa gcggctatgc cgcggtgcag aacggacgct atgtgtgga
501 aatcgacagc gagggggcgt tttatttccg ccgccgccat tattga

```

This corresponds to the amino acid sequence <SEQ ID 704; ORF 205.ng>:

```

g205.pep
1  MLKIPFAVLG GCLLLAACGK SENTAEQPQN AAQSAPKPVF KVKYIDNTAI
51  AGLALQSSE GKTNDGKKQI SYPIKGLPEQ NAVRLTGKHP NDLEAVVGKC
101 METDGKDAPS GWAENGVCHT LFAKLVGNI A EDGGKLT DYL ISHSALQPYQ
151 AGKSGYAAVQ NGRYVLEIDS EGAFYFRRRH Y

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 705>:

```

m205.seq
1  ATGCTGAAwA CwTyTTTTGC CGTATTGGGC GGCTGCCTGC TGCyTtGCCG
51  tGCGGCAAAT CCGwAAATAC GGCGGTACAG CCGCAAAACG CCGTACAAAG
101 CGCGCCGAAA CCGGTTTTCA AAGTCATATA TATCGACAAT ACGGCGATTG
151 CCGGTTTGA TTTGGGACAA AGCAGCGAAG GCAAAACCAA CGACGGCAAA
201 AAACAAATCA GTTATCCGAT TAAAGGCTTG CCGGAACAAA ATGTTATCCG
251 ACTGATCGGC AAGCATCCCG GCGACTTGA AGCCGTCAGC GGCAAATGTA
301 TGGAACCGA TGATAAGGAC AGTCCGGCAG GTTGGGCAGA AAACGGCGTG
351 TGCCATACCT TGTTTGCCAA ACTGGTGGC AATATCGCG AAGACGGCGG
401 CAACTGACG GATTACCTAG TTTCGCATGC CGCCCTGCAA CCCTATCAGG
451 CAGGCAAAAG CGGCTATGCC GCCGTGCAGA ACGGACGCTA TGTGCTGGAA
501 ATCGACAGCG AAGGGGCGTT TTATTTCCGC CGCCGCCATT ATTGA

```

This corresponds to the amino acid sequence <SEQ ID 706; ORF 205>:

```
m205.pep
1  MLXTXFAVLG GCLLXCRCGK SXNTAVQPQN AVQSAPKPVF KVIYIDNTAI
51 AGLDLGQSSE GKTNDGKKQI SYPIKGLPEQ NVIRLIGKHP GDLEAVSGKC
101 METDDKDSA GWAENGVCHT LFAKLVGNIA EDGGKLTDL VSHAALQPYQ
151 AGKSGYAAVQ NGRYVLEIDS EGAFYFRRRH Y*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 205 shows 88.4% identity over a 181 aa overlap with a predicted ORF (ORF 205.ng) from *N. gonorrhoeae*:

```
m205/g205

      10      20      30      40      50      60
m205.pep MLXTXFAVLGGCLLXCRCGKSXNTAVQPQNAVQSAPKPVFKVIYIDNTAIAGLDLGQSSE
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g205      MLKIPFAVLGGCLLLAACGKSENTAEQPQNAAQSAKPKPVFKVKYIDNTAIAGLALGQSSE
          10      20      30      40      50      60

      70      80      90      100     110     120
m205.pep GKTNDGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKCMETDDKDSAPAGWAENGVCHT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g205      GKTNDGKKQISYPIKGLPEQNAVRLTGKHPNDLEAVVGKCMETDGKDAPSGWAENGVCHT
          70      80      90      100     110     120

      130     140     150     160     170     180
m205.pep LFAKLVGNIAEDGGKLTDLVSHAALQPYQAGKSGYAAVQNGRYVLEIDSEGAFYFRRRH
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g205      LFAKLVGNIAEDGGKLTDLISHSALQPYQAGKSGYAAVQNGRYVLEIDSEGAFYFRRRH
          130     140     150     160     170     180

m205.pep YX
          |
g205      Y
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 707>:

```
a205.seq (partial)
1  TCCGAACCTC TTAAAGGCTT GCCGGAACAA AACGTCGTCC GGCTGACCGG
51 CAAGCATCCC AACGACTTGG AAGCCGTCGT CGGCAAATGT ATGGAAACCG
101 ACGGAAAGGG CGCGCCTTCG GGCTGGGCGG CAAACGGCGT GTGCCATACC
151 TTGTTTGCCA AACTGGTGGG CAATATCGCC GAAGACGGCG GCAAACCTGAC
201 GGATTACCTG ATTTGCGATT CCGCCCTGCA ACCCTATCAG GCAGGCAAAA
251 GCGGCTATGC CGCCGTGCAG AACGGACGCT ATGTGCTGGA AATCGACAGC
301 GAGGGGGCGT TTTATTTCCG CCGCCGCCAT TATTGA
```

This corresponds to the amino acid sequence <SEQ ID 708; ORF 205.a>:

```
a205.pep (partial)
1  SEPLKGLPEQ NVVRLTGKHP NDLEAVVGKC METDGKGAPS GWAANGVCHT
51 LFAKLVGNIA EDGGKLTDL ISHSALQPYQ AGKSGYAAVQ NGRYVLEIDS
101 EGAFYFRRRH Y*
```

m205/a205 88.3% identity in 111 aa overlap

```
      50      60      70      80      90      100
m205.pep KVIYIDNTAIAGLDLGQSSEGKTNDGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKC
          | : |||||: || ||||: |||| |||
a205      SEPLKGLPEQNVVRLTGKHPNDLEAVVGKC
          10      20      30

      110     120     130     140     150     160
m205.pep METDDKDSAPAGWAENGVCHTLFAKLVGNIAEDGGKLTDLVSHAALQPYQAGKSGYAAVQ
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 709>:

1	ATGCTGAAAA	TACCTTTTGC	CGTGTGGGC	GGCTGCCTGC	TGCTTGCCGC
51	CTGCGGCAAA	TCCGAAATA	CGGCGGAACA	GCCGCAAAAT	GCGGCACAAA
101	GCGCGCCGAA	ACCGGTTTTC	AAAGTCAAAT	ACATCGACAA	TACGGCGATT
151	GCGGGTTTGG	CTTTGGGACA	AAGTAGCGAA	GGCAAAACCA	ACACGGCAAT
201	AAAACAAATC	AGTTATCCGA	TTAAAGGCTT	GCCGGAACAA	AACCGCGTCC
251	GGCTGACCGC	AAAGCATCCC	AACGACTTCG	AAGCGCTCGT	CGGCAATGTG
301	ATGGAACAACG	ACGGAAGGGA	CGCGCTTCG	GGCTGGGCGG	AAAACGGCGT
351	GTGCCATACC	TTGTTTGCCA	AACTGGTGGG	CAATATCGCC	GAAAGACGGC
401	GCAAACTGAC	TGATTACCTG	ATTTGCGATT	CCGCCCTGCA	ACCCTATCAG
451	GCAAGCAAAA	GCGGCTATGC	CCCGCTGCAG	AACGGACGCT	ATGTGCTGGA
501	AATCGACGAG	GAGGCGGCGT	TTTA		

```

1  MLKIPFAVLG GCLLLAACGK SENTAEQPQN AAQSAPKPVF KVKYIDNTAI
51  AGLALGQSSE GKTNDGKKQI SYPTKGLPEQ NAVRLTGKHP NDLEAVVGKC
101 METDGKDAPS GWAENGVCHT LFAKLVGNIA EDGGKLTDL ISHSALQPYQ
151 AGKSGYAAVQ NGRYVLEIDS EGAF

```

1	ATGCTGAAAA	CATCTTTTGC	CGTATTGGGC	GGCTGCCTGC	TGCTTGCCGC
51	CTGCGGCAAA	TCCGAAAATA	CGGCGGAACA	GCCGCAAAAC	GCGGTACAAA
101	GCGCGCCGAA	ACCGGTTTTT	AAAGTCAAAT	ATATCGACAA	TACGGCGATT
151	CGCGGTTTGG	ATTTGGGACA	AAGCAGCGTA	GGCAAAACCA	ACGACGGCAA
201	AAAACAAATC	AGTTATCCGA	TTAAAGGCTT	CCCGGAACAA	AATGTTATCC
251	GACTGATCGG	CAAGCATCCC	GGCGACTTGG	AAGCCGTCAG	CGGCAAAATG
301	ATGGAACCGG	ATGATAAGGA	CAGTCCGGCA	GGTTGGGCGA	AAAACGGCGT
351	GTGCCATGAC	TTGTTTGCCA	AACCTGGTGG	CAATATCGCC	GAAGACGGCG
401	GCAAACTAGC	GGATTACCTA	GTTTCGCATC	CCGCCCTGCA	ACCTGATCAG
451	GCAAGCAAAA	CGCGCTATGC	CGCGCTGCAG	AACGACGCCT	ATTGTGCTGGA
501	AATCGACAGC	GAAGGGGCGT	TTTATTTCCG	CGCGCCGCAT	TATTGA

1 MLKTSFAVLG GCLLLAACGK SENTAEQPQN AVQSAPKPVF KVKYIDNTAI
51 AGLDLGQSSE GKTNDGKKQI SYPIKGLPEQ NVIRLIGKHP GDLEAVSGKC
101 METDDKDSPA GWAENGVCHT LFAKLVGNTA EDGGKLTIDL VSHAALQPYQ
151 AGKSGYAAVQ NGRYVLEIDS EGAFYFRRRH Y*

	10	20	30	40	50	60
g205-1.pep	MLKIPFAVLGGCLLLAACGKSENTAEQPQNAAQSA	PKPVFKVKYIDNTAIAGLALGQSSE				
m205-1	MLKTSFAVLGGCLLLAACGKSENTAEQPQNAVQSA	PKPVFKVKYIDNTAIAGLDLGQSSE				
	10	20	30	40	50	60
	70	80	90	100	110	120
g205-1.pep	GKTNDGKKQISYPIKGLPEQNAVRLTGKHPNDLEAVVGKCMETDGKDAPSGWAENGVC	HT				
m205-1	GKTNDGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKCMETDDKDS	PAGWAENGVC				

70 80 90 100 110 120
 130 140 150 160 170
g205-1.pep **LF**AKLVGN**IAEDGGK**LT**DY**LISH**SALQ**PY**QAGKSGYA**A**VQ**NGRY**VL**EID**SEGA**F
 |||||
m205-1 **LF**AKLVGN**IAEDGGK**LT**DY**LV**SHAALQ**PY**QAGKSGYA**A**VQ**NGRY**VL**EID**SEGA**F**YFR**RRH
 |||||
 130 140 150 160 170 180
m205-1 YX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 713>:

a205-1.seq (partial)

1	CCTCTTAAAG	GCTTGCCGGA	ACAAAACGTC	GTCCGGCTGA	CCGGAAGCA
51	TCCCAACGAC	TGGAAGCCG	TCGTCCGGCA	ATGTGTGGAA	ACCCACGGAA
101	AGGCGCGCC	TTCCGGCTGG	CGGCCAAACG	CGGTGTGCCA	TACCTTGTTT
151	GCCAACTGG	TGGGCAATAT	CGCCGAAGAC	GGCGGCAAA	TGACGGATTA
201	CCTGATTCG	CATTCCGCCC	TGCAACCTTA	TCAGGCAGGC	AAAAGCGGCT
251	ATGCCGCCGT	GCAAGACGGA	CGCTATGTGC	TGGAAATCGA	CAGCGAGGGG
301	CGCTTTTATT	TCCGCGCCCG	CCATTATTGA		

This corresponds to the amino acid sequence <SEQ ID 714; ORF 205-1.a>:

a205-1.pep (partial)

```
1  PLKGLPEQNV VRLTGKHPND LEAVVGKCM ETDGKGAPSGW AANGVCHTLF
51 AKLVGNIAED GGKLT DY LIS HSALQPYQAG KSGYAAVQNG RYVLEIDSEG
101 AFYFRRRRHY*
```

m205-1/a205-1 89.0% identity in 109 aa overlap

[illegible]

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEO ID 715>:

g206.seq

```
1 atgttttccc cgcacaaaac ccttttcctc tgtctcggcg cactgctcct
51 cgcctcatgc ggcacgacct ccggcaaac aacccaaac
101 agacagtccg gcaaattcaa gccgtccgca tcagccacat cggccgcaca
151 caaggctcgc aggaactcat gctccacagc ctccgactca tcggcacgcg
201 ctacaaatgg ggcggcagca gcaccgcaac cggcttcgac tgcagcggca
251 tgattcaatt ggtttacaaa aacgccctca acgtcaagct gccgcgcacc
301 gccgcgcaca tggcggcggc aagccgcaaa atccccgaca gccgcctcaa
351 ggccggcgac atcgtattct tcaacaccgg cggcgcacac cgctactcac
401 acgtcggact ctacatcggc aacggcgaat tcattccatgc cccggcgagc
451 ggcaaaacca tcaaaaccga aaaactctcc acaccgtttt acgccccaaa
501 ctaccttgga gcgcatacgt tttttacaga atga
```

This corresponds to the amino acid sequence <SEQ ID 716; ORF 206.ng>:

g206.pep
1 MFSPDKTLFL CLGALLLASC GTTSGKHRQP KPKOTVROIO AVRISHIGRT

```

51 QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQLVYK NALNVKLPR
101 ARDMAAASRK IPDSRLKAGD IVFFNTGGAH RYSHVGLYIG NGEFIHAPGS
151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 717>>:

```

m206.seq
1  ATGTTTCCCC CCGACAAAAC CCTTTTCCTC TGTCTCAGCG CACTGCTCCT
51  CGCCTCATCG GGCACGACCT CCGGCAAACA CCGCCAACCG AAACCCAAAC
101 AGACAGTCCG GCAAATCCAA GCCGTCCGCA TCAGCCACAT CGACCGCACA
151 CAAGGCTCGC AGGAACTCAT GCTCCACAGC CTGGACTCA TCGGCACGCC
201 CTACAAATGG GCGGCGCAGC GCACCGCAAC CCGGTTCGAT TGCAGCGGCA
251 TGATTCAATT CGTTTACAAT AACGCCCTCA ACGTCAAGCT GCCGCGCACC
301 GCCCGCGACA TGGCGGCGGC AAGCCGsAAA ATCCCCGACa GCCGcyTCAA
351 GGCCGGCGAC CTCGTATTCT TCAACACCGG CGGCGCACAC CGCTACTCAC
401 ACGTCGGACT CTACATCGGC AACGGCGAAT TCATCCATGC CCCCAGCAGC
451 GGCAAAACCA TCAAAACCGA AAAACTTCTC ACACCGTTTT ACGCCAAAAA
501 CTACCTCGGC GCACATACTT TTTTACAGA ATGA

```

This corresponds to the amino acid sequence <SEQ ID 718; ORF 206>:

m206.pep..

1	<u>MFPPDKTLFL</u>	<u>CLSALLLASC</u>	<u>GTTSGKHRQP</u>	KPKQTVRQIQ	AVRISHIDRT
51	QGSQELMLHS	LGLIGTPYKW	GGSSSTATGFD	CSGMIQFVYK	NALNVKLPRT
101	ARDMAAASRK	IPDSRKXAGD	LVFFNTGGAH	RYSHVGLYIG	NGEFIHAPSS
151	GKTIKTEKLS	TPFYAKNYLG	AHTFFE*		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 206 shows 96.0% identity over a 177 aa overlap with a predicted ORF (ORF 206.ng) from *N. gonorrhoeae*:

m206/g206

		10	20	30	40	50	60
m206.pep		MFPDPKTLFLCL	SALLASCGTTS	SGKHRQPKPKQ	TVRQIQAVRISH	IDRTQGSQELML	HS
g206		MFSPDKTLFLCL	GALLASCGTTS	SGKHRQPKPKQ	TVRQIQAVRISH	IGRTQGSQELML	HS
		10	20	30	40	50	60
		70	80	90	100	110	120
m206.pep		LGLIGTPYKWGGS	STATGFDCSGMI	QFVYKNALNVKL	PRTARDMAAASRK	IPDSRXKAGD	
g206		LGLIGTPYKWGGS	STATGFDCSGMI	QLVYKNALNVKL	PRTARDMAAASRK	IPDSRLKAGD	
		70	80	90	100	110	120
		130	140	150	160	170	
m206.pep		LVFFNTGGAHRYSH	VGLYIGNGEFIH	APSSGKTIKTEKL	STPPFYAKNYLGA	HTFFTEX	
g206		IVFFNTGGAHRYSH	VGLYIGNGEFIH	APGSGKTIKTEKL	STPPFYAKNYLGA	HTFFTE	
		130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 719>:

a206.seq

```
1 ATGTTTCCCC CCGACAAAAC CCTTTTCCTC TGTCTCAGCG CACTGCTCCT
51 CGCCTCATGC GGCACGACCT CCGGCAAACA CCGCCAACCG AAACCCAAAC
101 AGACAGTCCG GCAAATCCAA GCCGTCCGCA TCAGCCACAT CGACCGCACA
151 CAAGGCTCGC AGGAATCAT GCTCCACAGC CTCGGACTCA TCGGCACGCC
201 CTACAAATGG GCGCGCAGCA GCACCGCAAC CGGCTTCGAT TGCAGCGGCA
251 TGATTCAATT CGTTTACAAA AACGCCCTCA ACGTCAAGCT GCCGCGCACC
301 GCCCGCGACA TGGCGGCGGC AAGCCGCAAA ATCCCCGACA GCCGCCTTAA
351 GGCCGCGCAG CTCGTATTCT TCAACACCGG CGGCGCACAC CGCTACTCAC
401 ACGTCGGACT CTATATCGGC AACGGCGAAT TCATCCATGC CCCCAGCAGC
451 GGCAAAACCA TCAAAACCGA AAAACTCTCC ACACCGTTTT ACGCCAAAAA
501 CTACCTCGGC GCACATACTT TCTTTACAGA ATGA
```

This corresponds to the amino acid sequence <SEQ ID 720; ORF 206.a>:

```
a206.pep
  1 MFPPDKTLFL CLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT
 51 QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPRT
101 ARDMAAASRK IPDSRLKAGD LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS
151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*
```

m206/a206 99.4% identity in 177 aa overlap

	10	20	30	40	50	60
m206.pep	MFPPDKTLFLCLSALLLASC	GTTSGKHRQPKPKQTVRQIQ	AVRISHIDRTQGSQELMLHS			
a206	MFPPDKTLFLCLSALLLASC	GTTSGKHRQPKPKQTVRQIQ	AVRISHIDRTQGSQELMLHS			
	10	20	30	40	50	60
	70	80	90	100	110	120
m206.pep	LGLIGTPYKWGGSSTATGFD	CSGMIQFVYK	NALNVKLPRTARDMAAASRK	IPDSRXKAGD		
a206	LGLIGTPYKWGGSSTATGFD	CSGMIQFVYK	NALNVKLPRTARDMAAASRK	IPDSRLKAGD		
	70	80	90	100	110	120
	130	140	150	160	170	
m206.pep	LVFFNTGGAHRYSHVGLYI	GNGEFIHAPSSGKTIKTEKLS	TPFYAKNYLGAHTFFTEX			
a206	LVFFNTGGAHRYSHVGLYI	GNGEFIHAPSSGKTIKTEKLS	TPFYAKNYLGAHTFFTEX			
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 721>:

```
g209.seq
  1 atgctgcggc atttaggaaa cgacttcgcc ttgggcgcgt tgtttttcga
 51 tgctgcggtt gatgtgccac tgctggcgca tggtcaggag gttgttgacc
101 acccagtaga gaaccaaacc ggcagggaag aagaagaaca tgacggagaa
151 aaccaacggc atgattttca tcattttcgc ctgcatcggg tcggtcggcg
201 gcggttccag ataggttttg gcgaacatcg ttgccccat aatgatgggc
251 aggatgtagt aggggtcggc gcggctgagg tcggtaatcc agcccagcca
301 aggtgccttg cgcaattcta cggaggcgaa caatgccag tacaagccga
351 tgaagacggg gatttgcaac agcataggca gacagccgcc cagcgggttg
401 atttcctcgt cttcgaaaag ctgcatcatc gcttgctgtt gcgccatacg
451 gtcgtcgccg tatttttctt tgatggtctg cagttcgggt gcggcggcac
501 gcattttcgc catcgaaagg taggaggcgt tggtaaatgg atacagtacg
551 gctttgacga tgatggtcaa aacgacgatt gccagcccc agttgccgat
601 aatgttgtgc agttggttca ggagccagaa gagcggcgat gcgaaccagt
651 gtactttacc gtagtctttt gccagttgca ggttgctcgg gatgtttgcg
701 ataacggatg tggtttgccg accggcatac aggttgaccg ccattttcgg
751 ttttggtccc cggttggtga tagcgggttaa
```

This corresponds to the amino acid sequence <SEQ ID 722; ORF 209.ng>:

```
g209.pep
  1 MLRHLGNDFA LGALFFDAV DVPLLGDGQE VVDHPVENQT GREEEHEDGE
 51 NQRHDFHHFR LHRVGRRRVQ IGLGEHRCRH NDGQDVVG VG AAEVGNPAQP
101 RCLAQFYGGE QCPVQADEDG DLQQHRQTAA QRVDLFVFEK LHHRLLLRHT
151 VVAVFFFDGL QFGCGGTHFR HRTVGGVGQW IQYGFDDDGQ NDDCPAPVAD
201 NVVQLVQEP EERRCEPVYFT VFVCQLQVVG DVCNCGCLR TGIQVDRHFR
251 FWPPGWDSG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 723>:

```
m209.seq
  1 ATGCTGCGGC ATTTAGGAAA CGACTTCGCC TTGGGCGGTT GTTTTTCGAT
 51 GCTGCGGTTG ATGTGCCATT GCTGGGCGAT GGTCAGGAGG TTGTTGACTA
101 CCCAGTACAA TACCAGACCG GCAGGGAAGA AGAAGAACAT GACGGAGAAA
151 ACCAACGGCA TGATTTTCAT CATTTCGCC TGCATCGGGT CGGTCGGCGG
201 CGGGTTCAGA TAAGTTTGGG CGAACATCGT TGCCGCCATA ATGATGGGCA
251 GGATGTAGTA GGGGTCGGCG CGGCTGAGGT CGGTAATCCA ACCCAGCCAA
```

```

301 GGTGCCTGGC GCAATTCTAC GGAGGCGAAC AATGCCCAAT ACAATCCGAT
351 GAAGACGGGG ATTTGCAACA GCATAGGCAG GCAGCCGCC AGCGGGTTGA
401 TTTTCTCGTC TGTGTAAAGC TGCATCATCG CCTGTTGTTG CGCCATACGG
451 TCGTCGCCGT ATTTCTCTTT GATGGCTTGC AGTTTGGGTG CGCGGCACG
501 CATTTCGCC ATAGAGCGGT AAGAGCGGTT GGTCAATGGA TACAGTACGG
551 CTTTGACGAT GATGGTTAAA ACGATAATCG CCCAGCCCCA GTTGCCGATG
601 ATGTTGTGCA GTTGGTTCAG GAGCCAGAAG AGCGGGGAGG CGAACCAGTG
651 TACTTTGCCG TAGTCTTTGG CCAGTTGCAG GTTGTGCGCG ATGTTTGCGA
701 TGACGGATGT GGTCTGCGGG CCGGCGTAGA GGTGATGGA GGCTTCGgTT
751 TCGCGCCGT TTGGATGGCG GCTAAAGGCA CGCTGACGCT GGTGCTGTAC
801 AGCTTGTCGT TCGGCGGTTT GATGTCGATG TTGCACTCGC CTGCGGCGCA
851 AACGCTTTGT CTGCCTTTAG GTTGGAGAAT CCAGGTGGAC ATGAAGTGGT
901 GTTCAATCAT GCCGAGCCAG CCGGTGCGGG TTTTGCGGAT GTATTGCGCC
951 TCGGATTGTC CGGATTGTC ATCGTCGTCC AAGTCGAAA AGCTGACTTT
1001 TTGGAAGTTG CCTTCAGGGG TATAA

```

This corresponds to the amino acid sequence <SEQ ID 724; ORF 209>:

```

m209.pep
1 MLRHLGNDFA LGALFFDAAV DVPLLGDGQE VVDYPVQYQT GREEEEHDGE
51 NQRHDFHHFR LHRVGRRRVQ ISLGEHRCRH NDGQDVVGVG AAEVGNPTQP
101 RCLAQFYGGE QCPIQSDG DLQQRQAAA QRVDFLVCVK LHHRLLRHT
151 VVAVFLFDGL QFGCGGTHFR HRAVRGVGQW IQYGFDDG* NDNRPAPVAD
201 DVVQLVQEPE ERGGEVPYFA VVFGQLQVVG DVCDDGCGLR AGVEVDGGFG
251 FAPFWMAAKG TLTLVLYSL LRLMSMLHS PAAQTLCLPL GWRIQVDMKW
301 CSIMPSQPVG VLRMYSASDL PDLASSKSE KLTFWKLPSP V*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 209 shows 88.5% identity over a 253 aa overlap with a predicted ORF (ORF 209.ng) from *N. gonorrhoeae*:

```

m209/g209
      10      20      30      40      50      60
m209.pep MLRHLGNDFA LGALFFDAAV DVPLLGDGQE VVDYPVQYQT GREEEEHDG ENQRHDFHHFR
g209      MLRHLGNDFA LGALFFDAAV DVPLLGDGQE VVDHFPVENQT GREEEEHDG ENQRHDFHHFR
      10      20      30      40      50      60
      70      80      90     100     110     120
m209.pep LHRVGRRRVQ ISLGEHRCRH NDGQDVVGVG AAEVGNPTQP RCLAQFYGGE QCPIQSDG
g209      LHRVGRRRVQ ISLGEHRCRH NDGQDVVGVG AAEVGNPAQ PRCLAQFYGGE QCPVQADEG
      70      80      90     100     110     120
      130     140     150     160     170     180
m209.pep DLQQRQAAA QRVDFLVCVK LHHRLLRHT VVAVFLFDGL QFGCGGTHFR HRAVRGVGQW
g209      DLQQRQTAA QRVDFLVFEKLHRLLRHT VVAVFFFDGL QFGCGGTHFR HRTVGGVQW
      130     140     150     160     170     180
      190     200     210     220     230     240
m209.pep IQYGFDDG XNDNRPAPVAD DVVQLVQEPE ERGGEVPYFA VVFGQLQVVG DVCDDGCGLR
g209      IQYGFDDG QNDDCPAPVAD NVVQLVQEPE ERRCPEPVYFT VVFCQLQVVG DVCNDGCGLR
      190     200     210     220     230     240
      250     260     270     280     290     299
m209.pep AGVEVDGGFGF-APFWMAAKG TLTLVLYSL LRLMSMLHS PAAQTLCLPL GWRIQVDMK
g209      :::|| | | | |
      TG IQVDRHFRFWPPGWDSG
      250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 725>:

```

a209.seq
1 ATGCTGCGGC ATTTAGGAAA CCACTTCGCC TTGGGCGCGT TGTTTTTCGA

```



```

51 TGCTGCGGTT GATGTGCCAT TGCTGGGCGA TGGTCAGGAG GTTGTGATC
101 ACCCAGTACA ATACCAGACC GGCAGGGAAG AAGAAGAACA TGACGGAGAA
151 AACCAAAGGC ATGATTTTCA TCATTTTCGC CTGCATCGGG TCGGTCGGCG
201 GCGGGTTCAG ATAGGTTTGG GCGAACATCG TTGCCGCCAT AATGATGGGC
251 AGGATGTAGT AGGGGTCGGC GCGGCTGAGG TCGGTAATCC AACCCAGCCA
301 AGGTGCCTGG CGCAATTCTA CGGAGGCGAA CAATGCCCAA TACAATCCGA
351 TGAAGACGGG GATTTGCAAC AGCATAGGCA GGCAGCCGCC CAGCGGGTTG
401 ATTTTCTCGT CTGTGTAAAG CTGCATCATG GCTTGTGCT GCGCCATACG
451 GTCGTCGCGG TATTTCTCTT TGATGGCTTG CAGTTTGGGC GCGGCGGCAC
501 GCATTTTCGC CATCGAACGG TAAGAGGCGT TGGTCAATGG ATACAGTACG
551 GCTTTGACGA TGATGGTTAA AACGATAATC CCCCAGCCCC AGTTGCCGAT
601 GATGTTGTGC AGTTGGTTCA AAAGCCAAAA GAGGGGGGAG GCGAACCACT
651 GTACTTTGCC GTAGTCTTTG GCCAGTTGCA GGTTGTCGGC GATGTTTGGC
701 ATAACGGATG TGGTCTGTGG GCCGGCGTAG AGGTTGATGG AGGCTTCGGT
751 TTCGCACCGT TTTGGATAGC GGCTAAAGGC ACGCTGACGC TGCTGCTGTA
801 CAGCTTGTCG TTGCGCGCTT TGATGTCGAT ACGGCAGTCG CCAGCGGCGC
851 AAACGCTTTG TCCGCCTTTG GGTGAGGA TCCAGGTGGA CATGAAGTGC
901 TGTTCAATCA TGCCGAGCCA GCCGGTCGGG GTTTTGC GGA TGTATTCCGC
951 CTCGGATTG CCGGATTG CATCGTCGTC CAAGTCGGAG AAGCTGACTT
1001 TTTGGAAGTT GCCTTCAGGG GTATAA

```

This corresponds to the amino acid sequence <SEQ ID 726; ORF 209.a>:

```

a209.pep
1 MLRHLGNDEFA LGALFFDAAV DVPLLGDGQE VVDHPVQYQT GREEEEHDGE
51 NQRHDFHHFR LHRVGRRRVQ IGLGEHRCRH NDGQDVVGVG AAEVGNPTQP
101 RCLAQFYGGE QCPIQSDG DLQQRQAAA QRVDFLVCVK LHHGLLLRHT
151 VVAVFLFDGL QFGRGGTHFR HRTVRGVQW IQYGFDDDG* NDNRPAPVAD
201 DVVQLVQKPK EGGGEPVYFA VVFGQLQVVG DVCDNGCGLW AGVEVDGGFG
251 FAPFWIAAKG TLTLVLYSL LRLMSIRQS PAAQTLCPPL GWRIQVDMKW
301 CSIMPSQPVG VLRMYSASDL PDLASSSKSE KLTFWKLPSPG V*

```

m209/a209 95.6% identity in 341 aa overlap

	10	20	30	40	50	60
m209.pep	MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDYPVQYQTGREEEEHDGENQRHDFHHFR					
a209	MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDHPVQYQTGREEEEHDGENQRHDFHHFR					
	10	20	30	40	50	60
m209.pep	LHRVGRRRVQISLGEHRCRHNDGQDVVGVGAAAEVGNPTQPRCLAQFYGGEQCPIQSDG					
a209	LHRVGRRRVQIGLGEHRCRHNDGQDVVGVGAAAEVGNPTQPRCLAQFYGGEQCPIQSDG					
	70	80	90	100	110	120
m209.pep	DLQQRQAAAQRVDFLVCVKLHHRLLLRHTVVAVFLFDGLQFGCGGTHFRHRAVRGVQW					
a209	DLQQRQAAAQRVDFLVCVKLHHGLLLRHTVVAVFLFDGLQFGRGGTHFRHRTVRGVQW					
	130	140	150	160	170	180
m209.pep	IQYGFDDDGXNDNRPAVADDVVQLVQPEERGGEVYFAVVFGQLQVVGDVCDNGCGLW					
a209	IQYGFDDDGXNDNRPAVADDVVQLVQKPEGGGEVYFAVVFGQLQVVGDVCDNGCGLW					
	190	200	210	220	230	240
m209.pep	AGVEVDGGFGFAPFWMAAKGTLTLVLYSLSLRRLMSMLHSPAAQTLCLPLGWRIQVDMKW					
a209	AGVEVDGGFGFAPFWIAAKGTLTLVLYSLSLRRLMSIRQSPAAQTLCPPLGWRIQVDMKW					
	250	260	270	280	290	300
m209.pep	CSIMPSQPVGVLRMYSASDL PDLASSSKSEKLTFWKLPSPGVX					
a209	CSIMPSQPVGVLRMYSASDL PDLASSSKSEKLTFWKLPSPGVX					
	310	320	330	340		
m209.pep						

a209
CSIMPSQPVGLRMYASDLPDLASSKSEKLTFWKLP SGVX
310 320 330 340

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 727>:

```
g211.seq
1  atgttgcgga  ttgctgctgc  caatcagttg  ggcggtcgaa  atggtgcggc
51  ggtgggaaac  ggggtcgata  agtttgggcg  tggtgctgat  aatcaggttg
101 agtttttgga  aggaaacctg  attgtagtcg  gcgcgtccgg  gcgtgccgct
151 gtaacggtag  ccgtggcgca  attcagagct  gctgttctgt  tccttcacgg
201 agaagttacc  ttctttggcg  aagatgatgt  tgcgcgcgcc  gttttgttcc
251 tgttcgcgca  ggaacaggtt  tttcatgatg  ccggattcgg  ttgcaaaggt
301 ttcgacgaaa  taaacctctg  cgttgcgctt  gcccaagtta  ttgaactcgc
351 cggcttccac  caaagacaat  tcctgcttct  gcttcaaaat  tcgggcatat
401 tcgcgggtgc  gcaagctctg  ccacggtatc  acccaaagct  gcatgacggc
451 aatcaggatg  gcaaaccgca  cggcgaactg  catgacgggg  cgtatccact
501 gtttcaacgc  caatccgcag  gatag
```

This corresponds to the amino acid sequence <SEQ ID 728; ORF 211.ng>:

g211.pep

1	MLRIAAANQL	GGRNGAAVGN	GVDKFGRGAD	NQVEFLEGNL	<u>IVVGASGRAA</u>
51	<u>VTVAVAQFER</u>	AFVVLQREVT	<u>FFGEDDVVAA</u>	VFVLFAQEQV	FHDAGFGVKG
101	FDEINPAVAL	AQVILELGFH	<u>QROFLLLLQN</u>	FGIFAAAQLC	PRYHPKLHDG
151	NQDGKRHGKL	HDGAYPLFQR	QSAG*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 729>:

```
m211.seq
1  ATGTTGCGGG TTGCTGCTGC CAATCAGTTG GCGGGTCGGA ATGGTACGGC
51  GGTGGGAAAC GGGGTCGATG AGTTTGGGCG TGGTGCTGAT AATCAGGTTG
101 AGTTTTTTGGA AGGAAACCTG ATTGTAGTCG GCGCGTCCGG GCGTGCCGCT
151 GTAACGCTAG CCGTGGCGCA ATTCGAGCGT GCGTTTGTTG TCGTTACAGC
201 AGAAGTTACC TTCTTTGGCG AAGATGATGT TGTGCGCGCC GATTTTTGTC
251 TGTTGCGGCA GGAACAGGTT TTTCATGATG CCGGATTCCG TATCGAAGGT
301 TTCGACAAAA TAAACCTGTC CGTTGCGCTT GCCCAAAC TGAACTCGC
351 CTGCCTCCAC CAAAGACAAAT TCCTGCTTCT GCTTCAGGAT TTCAGCGTAT
401 TCGCGGCTGC GTAGCTCTGC CCACGGTATC ACCCAAAGCT GCATGACGGC
451 AACCAAAACG GCAACGCGCA CGGCAAAC TGATCACC GGCGTATCCATT
501 GTTTC AATGC CAATCCGCag GATAG
```

This corresponds to the amino acid sequence <SEQ ID 730; ORF 211>:

m211.pep

1	MLRVAAANQL	GGRNGTAVGN	GVDEFGRGAD	NQVEFLEGNL	<u>IVVGASGRAA</u>
51	<u>VTVAVAQFER</u>	AQVVVQREVT	FFGEDDVVAA	VFVLFAQEQV	FHDAGFGIEG
101	FDKINPAVAL	ACTVELACLH	<u>QRQFLLLLQD</u>	FSVFAAAXLC	PRYHPKLHDG
151	NQNGKRHGKL	HHRAYPLFCQ	QSAG*		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 211 shows 89.1% identity over a 174 aa overlap with a predicted ORF (ORF 211.ng) from *N. gonorrhoeae*:

m211/g211

	10	20	30	40	50	60
m211.pep	MLRVAAANQLGGRNGTAVGNQVDEFGRGADNQVEFLEGNLI VVGASGRAAVTVAVAQFER					
	: : : : : : : : : : : : : : : : : :					
g211	MLRIAANQLGGRNGAAGVGNQVDKFRGADNQVEFLEGNLI VVGASGRAAVTVAVAQFER					
	10	20	30	40	50	60

	70	80	90	100	110	120
m211.pep	AFVVVQREVTFFGEDDVVAAVFLFAQEQQVFHDAGFGIEGFDPINPAVALAQTVELACL					



```
a211.seq
1  ATGTTGCGGG TTGCTGCTGC CAATCAGTTG GCGGTCGGA ATGGTACGGC
51  GGTGGGAAAC GGGGTCGATG AGTTTGGGCG TGGTGCTGAT AATCAGGTTG
101 AGTTTTTTGGA AGGAAACCTG ATTGTAGTCG GCGCGTCCGG GCGTGCCGCT
151 GTAACGGTAG CCGTGGCGCA AATCGAGCTG GCGTTTGTTG TCGTTGACGG
201 AGAAGTTACT TTCTTTGGCG AAGATGATGT TGTCCGCCCC GTTTTGTCC
251 TGTTGCGGCA GGAACAGGTT TTTCATGATG CCGGATTCCG TATCGAAGGT
301 TTCGACAAAA TAAACCCTGC CGTTGCGCTT GCCCAAAC TGGAACCCGC
351 CTGCCTCCAC CAAAGACAAT TCCTGCTTCT GCTTCAGGAT TTCAGCGTAT
401 TCGCGGCTGC GTAGCTCTGC CCACGGTATC ACCCAAAGCT GCATGACGGC
451 AACCAAAACG GCAAAACGGCA CGGCAAAC TG CATACCGGG CGTATCCATT
501 GTTTCAAATGC CAATCCGCGAG GATAG
```

a211.pap

1	MLRVAAANQL	GGRNGTAVGN	GVDEFGRGAD	NQVEFLEGNL	<u>IVVGASGRAA</u>
51	<u>VTVAVAQFER</u>	AFVVVQREVT	FFGEDDVVAA	VFVLFAQEQV	FHDAGFGIEG
101	FDKINPAVAL	AQTVEPACLF	<u>QRQFLLLLQD</u>	<u>FSVFAAA*LC</u>	PRYHPKLHDG
151	NONGKRHGKL	HHRAYPLFOC	OSAG*		

	10	20	30	40	50	60
m211.pep	MLRVAAANQLGGRNGTAVGNGVDEFGRGADNQVEFLEGNLIVVGASGRAAVTVAVAQFER					
a211	MLRVAAANQLGGRNGTAVGNGVDEFGRGADNQVEFLEGNLIVVGASGRAAVTVAVAQFER					
	10	20	30	40	50	60
	70	80	90	100	110	120
m211.pep	AFVVVQREVTFFGEDDVVAAVFVLFAQEQVFHDAGFGIEGFDKINPAVALAQTVELACLH					
a211	AFVVVQREVTFFGEDDVVAAVFVLFAQEQVFHDAGFGIEGFDKINPAVALAQTVEPACLH					
	70	80	90	100	110	120
	130	140	150	160	170	
m211.pep	QRQFLLLLQDFSVFAAAXLCPRYHPKLHDGNQNGKRHGKLGHHRAYPLFQCQSAGX					
a211	QRQFLLLLQDFSVFAAAXLCPRYHPKLHDGNQNGKRHGKLGHHRAYPLFQCQSAGX					
	130	140	150	160	170	

```
g212.seq (partial)
      1  atggacaatc tcgatatggga cggcattccc gacatccgca cactcgacca
     51  aaccatccgc aaacacgcac acccgctcaa cctgattgtc tgccctccccg
    101  ataatcagat tcccgatttt caaacccgac aagatgcttc ggactcggaa
    151  tgccgtctga agcaccgttt ggatcaggca acccagtgcc tccagttcga
    201  cagcatcaac ctcatcgaac acatcctgcc cgatgtccgc ttctggctgg
    251  ttcccccttc acgcaccctc cgctgcagc aacattcca ccacatttcc
    301  tggcgaccgc aagccatccc gcaaacgcaa agcaagtccg acaaacctcg
    351  gtttgcactt ccacaaacat ccgaacggaa aaaaccggaa cagctcctcc
```

```

401 tcatcgggtgc aggcattgcc ggcgcatcga cgcgccacgc cttagcatca
451 cacggcattt ccgttaccgt attggaagcc cgaaaagccg ctcaagccgc
501 cagcggcaac cggcaagggc tgctttacgc caaaatctcg ccgcacgaca
551 ccggacagac cgaactgctg cttgccggct acggctacac caaacgcctg
601 ctcggaacaca tctgccccga ctccgacact tggggcggca acggcatcat
651 ccacctcaat tacagccgca ccgaacaaca acgcaatcac gaattgggtt
701 tgcaaaaaca ccataaccac ctctaccgca gcatcacgtc tgcagaagcc
751 gaaaaaatcg ccggcatccc gctgaacacg ccctacgccg aaccattatg
801 cggactctac tggcaacacg gcgtatggct caatccgccc gcattcgctc
851 gcaccctcct cagccatccg ctgatcgaac tatatgaaaa cacaacgtta
901 accggcattt cccacgacgg agaaaagtgg attgcaagca cgccaaacgg
951 cacatttacc gccacacaca tcatctactg caccggcgcg cacagccctt
1001 gcctgccccga aaccaacctc gccgccctac ccctcaggca aatacgcgga
1051 caaacccggc tcacaccgtc caccctgttt tccgaacaac tgcgttgccg
1101 cgtttcaggc gaaagctaca tcagcccgtc gtggcacgga ctgcactgct
1151 acggcgcgag ttttattccc aacagcagca ataccggatg gaacgaagcc
1201 gaagaagcct caaacgccca agcattggca caccctaacc ccgcccttgc
1251 cgaatcattg ttt...

```

This corresponds to the amino acid sequence <SEQ ID 734; ORF 212.ng>:

g212.pep (partial)

```

1 MDNLVWDGIP DIRTLDQTIR KHAHPLNLIV CLPDNQIPDF QTAQDASDSE
51 CRLKHLRLDQA TQCLQFDSIN LIEHILPDVR FWLVPPSRTR RLHEHFHHIS
101 WQTEAIPQTE SKSDKPWFAL POTSERKKPE HVLVIGAGIA GASTAHALAS
151 HGISVTVLEA RKAAQAASGN RQGLLYAKIS PHDTGQTELL LAGYGYTKRL
201 LGHILPDSDT WGGNGIIHLN YSRTEQQRNH ELGLQKHNNH LYRSITSAEA
251 EKIAGIPLNT PYAEPLCGLY WQHGVLNPP AFVRTLLSHP LIELYENTTL
301 TGISHDGEKW IASTPNGTFT ATHIIYCTGA HSPCLPETNL AALPLRQIRG
351 QTGLTPSTPF SEQLRCAVSG ESYISPSWHG LHCYGASFIP NSSNTGWNEA
401 EEASNRQALA HLNPALAESL F...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 735>:

m212.seq

```

1 ATGGACAATC TCGTATGGGA CGGCATTCCC GACATCCGCA CACTCGACCA
51 AGCCATCCGC AAACACGCAC CCCCCTCAA CCTGATTATC TGCCTCCCCG
101 ATAATCAGAT TCCCGATTTT CAAACCGCAC AAGATGCTTC GGACCGGAA
151 TGCCGTCTGA AGCACCGTTT GGATCAGGCA ATGCAGTGCC TCCAGTTCGA
201 CAGCATCAAC CTCATCGAAC ACATCCTGCC CGATGTCCGC TTCTGGCTGG
251 TTCCCCCTTC ACGCACCCAC CACCTGCACG AACATTCCA CCACATTTCC
301 TGGCAGACCG AAGCCATCCC GCAAACCGAA AGCAAGCCCG ACAAAACCTG
351 GTTTGCACTT CCACAAACAT CCGAACGGCA AAAACCGGAA CACATCCTCG
401 TTATCGGCGC GGGCATATCC GGCGCGGCAA CCGCCACGC CTTAGCATCA
451 CACGGCATT TCGTTACCGT ATTGGAAGCC CGAAAAGCCG CCCAAGCCGC
501 CAGCGGCAAC CGCCAAGGGC TGCTCTACGC CAAAATCTCG CCGCACGACA
551 CCGAACAGAC CGAACTTTTG CTGCGCGGCT ACGGCTACAC CAAACGCCTG
601 CTCGGACACA TCCTGCCCGA ATCCGAAACC TGGGGCGGCA ACGGCATCAT
651 CCACCTCAAT TACAGCCGCA CCGAACAACA ACGCAATCAC GAATTGGGTT
701 TGCAAAAACA CCATAACCAC CTCTACCGCA GCATCACATC TGCAGAAGCC
751 GAAAAAATCG CCGGTATCCC ACTGTCCGTC CCATACGACC ACCCTTCATG
801 CGGACTCTAC TGGCAACACG GCGTATGGCT CAATCCACCC GCATTGCTCC
851 GCACCCTCCT CAACCATCCG CTCATTGGAC TACACGAAGA CACACCCTTG
901 ACCGACATT CCCACGACGG GGAAAAGTGG ATTGCAAGCA CGCCAAACGG
951 CACATTTACC GCCACACACA TCATCTACTG CACCGGTGCG AACAGCCCCT
1001 ACCTACCCGA AACCAACCTC GCCGCCCTGC CTCTCAGGCA AATACGCGGA
1051 CAAACCGGCC TCACACCGTC CACCCCGTTT TCCGAACAAC TGCGTTGCGC
1101 CGTTTCAGGC GAAAGCTACA TCAGCCCGTC GTGGCACGGA CTGCACTGCT
1151 ACGGCGCGAG TTTTATTCCC AACAGCAGCC ATACCGGATG GAACGAAGCC
1201 GAAGAAGCCT CAAACCGCCA AGCATTGGCA CACCTTAACC CCGCCCTTTC
1251 CGAATCATTG TTTGCCGCA ACCCAAACCC CCAAAAACAC CAAGGGCAGC
1301 CCGCCATACG CTGCGACAGC CCCGACCACC TTCCCTAGT CGGCGCACTC
1351 GCGGACATTG CCGCATGCG GCAGACCTAC ACCAAACTCG CGCTGGACAA
1401 AAACCTACCG ATCGACACCC CATGCCATA CCTGCCTAAT GCCTACGTCA
1451 ACACCGCGCA CGGCACCCGC GGAATCGCCA CCGCCCCCAT CTGCGCCGCC

```

1501 GmCAwTGcAG CCCAAATCst AGGCyTGCCC CATCCCTTTT yAcAAcGCCT
 1551 gCGCCACGCC cTAcACCCCA ACCGCACCAT CATCCGCGCC ATCGTCAGAA
 1601 GGAAGGATCT AACCCCTTAA

This corresponds to the amino acid sequence <SEQ ID 736; ORF 212>:

m212.pep
 1 MDNLVWDGIP DIRTLDQAIR KHAPPLNLII CLPDNQIPDF OTAQDASDAE
 51 CRLKHLRDQA MQCLQFDSIN LIEHILPDVR FWLVPPSRTH HLHEHFHHIS
 101 WQTEAIPQTE SKPDKPWFAI POTSERQKPE HILVIGAGIS GAATAHALAS
 151 HGISVTVLEA RKAQAASGN ROGLLYAKIS PHDTEQTELL LAGYGYTKRL
 201 LGHILPESET WGGNGIIHLN YSRTEQQRNH ELGLQKHHNH LYRSITSAEA
 251 EKIAGIPLSV PYDHPSCGLY WQHGVLNPP AFVRTLLNHP LIGLHEDTPL
 301 TDISHDGEKW IASTPNGTFT ATHIIYCTGA NSPYLPETNL AALPLRQIRG
 351 QTGLTPSTPF SEQLRCAVSG ESYISPSWHG LHCYGFASFI NSSHTGWNEA
 401 EEASNRQALA HLNPALESSE FAANPNPQKH QGHAAIRCDP PDHPLVLGAL
 451 GDIAAMRQTY TKLALDKNYR IDTPCPYLPN AYVNTAHGTR GLATAPICAA
 501 XXAAQIXGLP HPFXQRLRHA LHPNRTIIRA IVRRKDLTP*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 212 shows 92.9% identity over a 421 aa overlap with a predicted ORF (ORF 212.ng) from *N. gonorrhoeae*:

m212/g212

m212.pep	MDNLVWDGIPDIRTLDQAIRKHAPPLNLII	CLPDNQIPDFOTAQDASDAECRLKHLRDQA
g212	MDNLVWDGIPDIRTLDQTIRKHAHPLNLIVCLPDNQIPDFOTAQDASDSECRKHLRDQA	
m212.pep	MQCLQFDSINLIEHILPDVRFWLVPPSRTHHLHEHFHHISWQTEAIPQTESKPDKPWFAI	
g212	TQCLQFDSINLIEHILPDVRFWLVPPSRTRLHEHFHHISWQTEAIPQTESKSDKPWFAL	
m212.pep	POTSERQKPEHILVIGAGISGAATAHALASHGISVTVLEARKAAQAASGNROGLLYAKIS	
g212	POTSERKKPEHVLVIGAGIAGASTAHALASHGISVTVLEARKAAQAASGNROGLLYAKIS	
m212.pep	PHDTEQTELLLAGYGYTKRLLGHILPESETWGGNGIIHLNYSRTEQQRNHELGLQKHHNH	
g212	PHDTGQTELLLAGYGYTKRLLGHILPDSDTWGGNGIIHLNYSRTEQQRNHELGLQKHHNH	
m212.pep	LYRSITSAEAEKIAGIPLSVPYDHPSCGLYWQHGVLNPPAFVRTLLNHP LIGLHEDTPL	
g212	LYRSITSAEAEKIAGIPLNTPYAEPLCGLYWQHGVLNPPAFVRTLLSHPLIELYENTTL	
m212.pep	TDISHDGEKWIASTPNGTFTATHIIYCTGANSPLYLPETNL AALPLRQIRGQTGLTPSTPF	
g212	TGISHDGEKWIASTPNGTFTATHIIYCTGAHSPCLPETNL AALPLRQIRGQTGLTPSTPF	
m212.pep	SEQLRCAVSGESYISPSWHGLHCYGFASFI	PNSSHTGWNEAEEASNRQALAHLPALSESSE

	:
g212	SEQLRCAVSGESYISPSWHGLHCYGASFIPNSSNTGWNEAEEASNRQALAHLPALAESL
	370 380 390 400 410 420
	430 440 450 460 470 480
m212.pep	FAANPNPQKHQGHAAIRCDSPDHLPLVGALGDIAAMRQTYTKLALDKNYRIDTPCPYLPN
g212	 F

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 737>>:

a212.seq

1	ATGGACAATC	TCGCATGGAA	CGGCATTCCC	GACATCCGCA	CACTCGACCA
51	AACCATCCGC	AAACACGCAC	ACCCGCTCAA	CCTGATTGTC	TGCTCCCCG
101	ATAATCAGAT	TCCCAATTTT	CAAAACCGCA	AAGATGCTTC	GGACGCGGAA
151	TGCCGTCTGA	AGCACCGTTT	GGATCAGGCA	ACCCGATGCC	TCCAGTTCGA
201	CAGCATCAAC	CTGATTGAAC	ACATCCTGCC	CGATGTCCGC	TTCTGGCTG
251	TTCCCCCTTC	ACGCACCCGC	CGCCTGCACG	AACACTTCCA	CCACATTTCC
301	TGGCAGACCG	AAGCCATCCC	GCAAACCGAA	AGTAAGCCCG	ACAAACCCCTG
351	GTTTGCATT	CAGAACAAT	CCGAACGGCA	AAAACCGGAA	CACATCCTCG
401	TTATCGGAGC	GGGCATATCC	GGCGCGGCAA	CCGCCACGC	CTTAGCATCA
451	TACGGCATT	CCGTTACCGT	ATTGGAAGCC	CGAAAAGCCG	CCCAAGCCGC
501	CAGCGGCAAC	CGCCAAGGGC	TGCTCTAGCC	CAAATCTCG	CCGCACGACA
551	CCGAACAACA	CGAACTCTGT	CTTGCCGGCT	ACGGCTACAC	CAAACGCCTG
601	CTCGGACATA	TCTTGCCCGA	ATCCGAAACC	TGGGCGGGCA	ACGGCATCAT
651	CCACCTCAAT	TACAGCCGCA	CCGAACAACA	ACGCAATCAC	GAATTGGGTT
701	TGCAAAAACA	CCATAACCAC	CTCTACCGCA	GCATCACGCA	GGCAGAAGCC
751	GAAAAAATCG	CCGGCATCCC	TCTGAACACG	CCCTACGCCG	AACCATTATG
801	CGGACTGTTT	TGGCAGTACG	GCGTATGGCT	CAATCCTCCC	ACATTCTGTC
851	GCGCCCTCCT	CAGCATCCG	CTCATTGGAC	TACACGAAGA	CACACCGTTA
901	ACCGACATT	CCCACGACGG	GGAAAAGTGG	ATTGCAAGCA	CGCCAAACGG
951	CACATTTACC	GCCACACACA	TCATCTACTG	CACCGGTGCG	AACAGCCCCCT
1001	ACCTACCCGA	AACCAACCTC	GCCACCCTGC	CCCTCAGGCA	AATACGCGGA
1051	CAAAACCGGCC	TCACACCGTC	CACCCCGTTT	TCCGAACAAC	TGCGTTGCGG
1101	CGTTTTCAGG	GAAAGTACAC	TCAGCCCGTC	GTGGCAGGGA	CTGCACTGCT
1151	ACGGCGCGAG	TTTTATTCCC	AACAGCAGCC	ATACCGGATG	GAACGAAGCC
1201	GAAGAAGCCT	CAAACCGCCA	AGCATTGGCA	CACCTTAACC	CCGCCCTTTC
1251	CGAATCATTG	TTTGCCGCCA	ACCCAAACCC	CCAAAAACAC	CAAGGGCAGC
1301	CGCCATACG	CTGCGACAGC	CCCGACCACC	TTCCCCTAGT	CGGCGCACTC
1351	GGCGACATTG	CCGCTATGCA	ACAAACTTAC	GCCAAACTCG	CGCTGGACAA
1401	AAACTATCGC	ATCGATGCCC	CCTGCCCGTA	CCTGCCCAAT	GCCTACGCCA
1451	ACACCGCCCC	CGGCACACGC	GGGCTTGCCA	CCGCCCCCAT	CTGCGCCGCC
1501	GCCGTTGCAG	CCGAATCCTT	AGGCTTGCCC	CATCCCCTCT	CAAAACGCCT
1551	GCGCCACGCC	CTACACCCCA	ACCGCGCCAT	CATCCGCGCC	ATCGTCAGAA
1601	GGAAGGATCT	AACCCCTTAA			

This corresponds to the amino acid sequence <SEQ ID 738; ORF 212.a>:

```

a212.pap
1 MDNLAWNGIP DIRTLDQITR KHAHPLNLIV CLPDNQIPNF QTAQDASDAE
51 CRLKHLRLDQA TQCLQFDSIN LIEHILPDVR FWLVPPSRTR RLHEHFHHIS
101 WQTEAIPQTE SKPKDKPWFAL POTSERQKPE HILVIGAGIS GAATAHALAS
151 YGISVTVLEA RKAQAAGASN RGQLLYAKIS PHDTEQTELL LAGYGYTKRL
201 LGHILPESET WGGNGIIHLM YSRTEQQRNH ELGLQKHNNH LYRSITQAE
251 EKIAGIPLNT PYAEPLCGLF WQYGVWLNPP TFVRALLSHP LIGLHEDTPL
301 TDISHDGEKW IASTPNGTFT ATHIIYCTGA NSPYLPETNL ATLPLRQIRG
351 QTGLTPSTPF SEQLRCAVSG ESYISPSWHG LHCYGASFIP NSSHTGWNEA
401 EEASNRLQALA HLNPALESF FAANPNPQKH QGHAAIRCDS PDHPLPLVGAL
451 GDIAAMQQTY AKLALDKNYR IDAPCPYLPN AYANTANGTR GLATAPICAA
501 AVAAEILGLP HPLSKRLRHA LHPNRAIIRA IVRRKDLTP*

```

m212/a212 93.7% identity in 539 aa overlap

[illegible]

	10	20	30	40	50	60
	70	80	90	100	110	120
m212.pep	MQCLQFDSINLIEHILPDVRFVLVPPSRTHLHEHFHHISWQTEAIPQTESKPKDPWFAL					
a212	TQCLQFDSINLIEHILPDVRFVLVPPSRTRRLHEHFHHISWQTEAIPQTESKPKDPWFAL					
	130	140	150	160	170	180
m212.pep	PQTSEKQKPEHILVIGAGISGAATAHALASHGISVTVLEARKAAQAASGNRQGLLYAKIS					
a212	PQTSEKQKPEHILVIGAGISGAATAHALASYGISVTVLEARKAAQAASGNRQGLLYAKIS					
	190	200	210	220	230	240
m212.pep	PHDTEQTELLLAGYGYTKRLLGHILPESETWGGNGIIHLNYSRTEQQRNHELGLQKHNNH					
a212	PHDTEQTELLLAGYGYTKRLLGHILPESETWGGNGIIHLNYSRTEQQRNHELGLQKHNNH					
	250	260	270	280	290	300
m212.pep	LYRSITSAEAEKIAGIPLSVPYDHPSCGLYWQHGVLNPPAFVRTLLNHPHPLIGLHEDTPL					
a212	LYRSITQAEAEKIAGIPLNTPYAEPLCGLFWQYGVWLNPPFTFVRALLSHPLIGLHEDTPL					
	310	320	330	340	350	360
m212.pep	TDISHDGEKWIASTPNGTFTATHIIYCTGANSPLYLPETNLAALPLRQIRGQTGLTPSTPF					
a212	TDISHDGEKWIASTPNGTFTATHIIYCTGANSPLYLPETNLATLPLRQIRGQTGLTPSTPF					
	370	380	390	400	410	420
m212.pep	SEQLRCAVSGESYISPSWHGLHCYGFIPNSSHTGWNEAEASNRQALAHLPALSES					
a212	SEQLRCAVSGESYISPSWHGLHCYGFIPNSSHTGWNEAEASNRQALAHLPALSES					
	430	440	450	460	470	480
m212.pep	FAANPNPQKHQGHAAIRCDSPDHLPLVGALGDIAAMRQTYTKLALDKNYRIDTPCPYLPN					
a212	FAANPNPQKHQGHAAIRCDSPDHLPLVGALGDIAAMQQTAKLALDKNYRIDAPCPYLPN					
	490	500	510	520	530	540
m212.pep	AYVNTAHGTRGLATAPICAAAXXAAQIXGLPHFPXQRLRHALHPNRTIIRAIIVRRKDLPX					
a212	AYANTAHGTRGLATAPICAAAVAAEILGLPHPLSKRLRHALHPNRAIRAIIVRRKDLPX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 739>:

```

g214.seq
1   atgatacaaa agatatgtaa gctatttgtt ttaattgtaa tttttgcaac
51  ttctcccgtt ttgccccttc aaagcgacag cagacggccc atccaaatcg
101 aagccgacca aggttcgctc gatcaagcca accaaaggac cacatttagc
151 ggcaatgtca tcatcagaca gggtagcttc aacatttccg cctcgtgtgt
201 caacgtcaca cgcggcaggg aaaggcggcg aatccgtgag ggcggaaggt
251 tcgcccgtcc gcttcagcca aacgttggac gggggcaaaag ggacgggtcg
301 cggtcaggca aacaacgtta cctattcctc cgcaggaagc actgtcgttc
351 tgaccggcaa tgccaaagtg cagcgcggcg gcgacgttgc cgaaggtgag
401 gtcattacct acaacaccaa aaccgaagtc tataccatca acggcagcac
451 gaaatcgggt gcgaaatccg cttccaaaac cggcagggtc agcgtcgtca
501 tccagccttc aagcacacaa aaaaccgaat aaccccgatg ccgtctgaaa
551 cggaaacgca gttcagacgg catttgccga ccgaaatgcc gagaagagat
601 tattga

```

This corresponds to the amino acid sequence <SEQ ID 740; ORF 214.ng>:

g214.pep

```

1  MIQKICKLFV LIVIFATSPA FALQSDSRFP IQIEADQGSF DQANQRTTFS
51  GNVIIROGTL NISASCVNVT RGRQRRRIRE GGRFARPLQP NVGRGQORDGA
101 RSGKQRYLFL RRKHCRSDRQ CQSAARRRRC RRCGHYLQHQ NRSLYHQRQH
151 EIGCEIRFQN RQGQRRHPAF KHTKNRITPM PSETETQFRR HLPTEMPRRD
201 Y

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 741>:

```

m214.seq (partial)
1  ATGATACAAA AGATATGTAA GCTATTGTGTT TTAATAGCAT TTTTTCGGC
51  GTCCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTTGCTC GATCAAGCCA ACCAAAGCAC CACATTCAGC
151 GGAAACGTCG TCATCAGACA GGTACGCTC AATATTTCCG CCGCCCGCGT
201 CAATGTTACA CGCGGCGGCA AAGGCGGCGA ATCCGTGAGG GCGGAAGGTT
251 CGCCAGTCCG CTTGAGCCAG ACATTGGACG GCGGCAAAGG CACGGTGCGC
301 GGACAGGCAA ACAACGTTGC TTATTCATCT GCAGGCAGCA CCGTAGTCTT
351 AACCGGTAAT GCCAAAGTAC AGCGGCGCGG CGATGTCGCC GAAGGTGCGG
401 TGATTACATA CAACACCAAA ACCGAAGTCT ATACCATCAG CGGCAGCACA
451 AAATT...

```

This corresponds to the amino acid sequence <SEQ ID 742; ORF 214>:

```

m214.pep (partial)
1  MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGSF DQANQSTTFS
51  GNVVIRQGTI NISAARVNVT RGRQRRRIRE GGRFASPLQP DIGRRQRHGA
101 RTGKQRCLEI CRQHRSLNR* CQSTARRRRC RRCGDIQHQ NRSLYHQRQH
151 KI...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 214 shows 80.3% identity over a 152 aa overlap with a predicted ORF (ORF 214.ng) from *N. gonorrhoeae*:

```

m214/g214

      10      20      30      40      50      60
m214.pep  MIQKICKLFVLIAFFSASPALQSDSRQPIQIEADQGSFDQANQSTTFSGNVVIRQGTI
          |||||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||
g214      MIQKICKLFVLIVIFATSPAFLQSDSRRIQIEADQGSFDQANQRTTFSGNVIRQGTI
          10      20      30      40      50      60

      70      80      90      100     110     120
m214.pep  NISAARVNVTGRGRRRRIREGGRFASPLQPDIGRRQRHGARTGKQRCLEICRQHRSLNRX
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g214      NISASCVNVTGRGRRRRIREGGRFARPLQPNVGRGQRDGARGKQRYLFLRRKHCRSDRQ
          70      80      90      100     110     120

      130     140     150
m214.pep  CQSTARRRCRRRCGDIQHQNRSLYHQRHKI
          |||:|||||:|||||:|||||:|||||:|||||:
g214      CQSAARRRRCRRRCGHYLQHQNRSLYHQRQHEIGCEIRFQNRQGQRRHPAFKHTKNRITPM
          130     140     150     160     170     180

g214      PSETETQFRRHLPTMPRRDY
          190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 743>:

```

a214.seq
1  ATGATACAAA AGATATGTAA GCTATTGTGTT TTAATAGCAT TTTTTCGGC
51  GTCCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTTGCTC GATCAAGCCA ACCAAAGCAC CACATTCAGC
151 GGAAACGTCG TCATCAGACA GGTACGCTC AATATTTCCG CCGCCCGCGT
201 CAATGTTACA CGCGGC.GGC AAAGCGGCG AATCCGTGAG GCGGAAGGTT
251 TCGCCAGTCC GCTTCAGCCA GACATTGGAC GCGGCAAAG GCACGGTGCG
301 CGGACAGGCA AACAACGTTG CTTATTCATC TGCAGGCAGC ACCGTAGTCT

```


a214.pep

1	<u>MIQKICKLFV</u>	<u>LIAFFSASPA</u>	FALQSDSRQP	IQIEADQGS	L DQANQSTTFS
51	GNVVIROGTL	NISAARVNV	RGXQRRRIE	GGRFASPLQ	P DIGRRQRHGA
101	RTGKQRCLE	F CRQHRS	LNR* CQSTARR	RCR RCGDYIQ	HQ NRSLYHQ
151	KIRRKIRFQ	I RQGQRRY	PAF EYAKIRI	IPM PSET*TW	FGR HLPTEIL
201	L*				KRY

	10	20	30	40	50	60
m214.pep	MIQKICKLFVLIAFFSASP	FALQSDSRQPIQIEADQGS	LDQANQSTTFSGNVVIR	QGT		
a214	MIQKICKLFVLIAFFSASP	FALQSDSRQPIQIEADQGS	LDQANQSTTFSGNVVIR	QGT		
	10	20	30	40	50	60
	70	80	90	100	110	120
m214.pep	NISAARVNVTRGRQRRRI	REGGRFASPLQPDIGRR	QRHGARTGKQRC	LFICRQHRSLNR		
a214	NISAARVNVTRGXQRRRI	REGGRFASPLQPDIGRR	QRHGARTGKQRC	LFICRQHRSLNR		
	70	80	90	100	110	120
	130	140	150			
m214.pep	CQSTARRRRCRRRCGDI	QHQNRS	SLYHQ	RQHKI		
a214	CQSTARRRRCRRRCGDI	QHQNRS	SLYHQ	RQHKIRRKIRFQIR	QGORRYPAFEYAKIR	IIPM
	130	140	150	160	170	180
a214	PSETXTWFG	RHLPT	EILKRYLX			
	190	200				

```
g214-1.seq
1  ATGATACAAA  AGATATGTAA  GCTATTTGTT  TTAATTGTAA  TTTTTCGAAC
51  TTCTCCCGCT  TTTGCCCTTC  AAAGCGGACG  CAGACGGGCC  ATCCAAATCG
101  AAGCCGACCA  AGGTTGCTCT  GATCAACGTA  ACCAAAGTAC  CACATTTAGC
151  GGCAATGTCA  TCATCAGACA  GGGTACGCTC  ACCAATTCGG  CCTCGCGCGT
201  CAACGTCACA  CGCGCGGGCA  AAGCGGGCGA  ATCGGTGAGG  GCGGAAGGTT
251  CGCCCGTCCG  CTTCAGCCAA  ACGTTGGACG  GGGGCAAAGG  GACGGTGCGC
301  GGTCAAGGCA  ACAAAGTTAC  CTATTCTCTC  CGAGGAAGCA  CGCTCGTTCT
351  GACCGGCAAT  GCCAAAGTGC  AGCGCGGGCG  CGACGTTGCC  GAAGGTGCGG
401  TCATTACCTA  CAAACACAAA  ACCGAAAGCT  ATACCATCAA  CGGCAGCAGC
451  AAATCGGGTG  CGAAATCCGC  TTCCAAAAAC  GGCAGGGTCA  GCGTCGTCAT
501  CCAGCGCTTC  AGCACACAAA  ATCCCGAATA  A
```

g214-1.pap

1	MIQKICKLFV	LIVIFATSPA	FALQSDSRRP	IQIEADQGS	LQANQSTTF
51	GNVIRQGT	NISASRVNT	RGGKGGESV	AEGPSVRF	SLDGGKGTV
101	QGANVTYSS	AGSTVVL	TGN AKVQR	GGDVA EGA	VITYNTK TE
151	KSGAKSASK	GRVSVVIQ	PS STOKTE	*	

m214-1.seq

```
1  ATGATACAAA  AGATATGTAA  GCTATTTGTT  TTAATAGCAT  TTTTTTCGGC
51  GTCCCCCGCT  TTTGCCCTTC  AAAGCGACAG  CAGGCAGCCT  ATTCAGATTG
101 AGGCGGACCA  AGGTCGCTC  GATCAAGCCA  ACCAAAGCAC  CACATTCAGC
151 GGAACGTCG  TCATCAGACA  GGGTACGCTC  AATATTTCCG  CGCGCCCGCT
```

```

201 CAATGTTACA CGCGGCGGCA AAGGCGGCGA ATCCGTGAGG GCGGAAGGTT
251 CGCCAGTCCG CTTACGCCAG ACATTGGACG GCGGCAAAGG CACGGTGCGC
301 GGACAGGCAA ACAACGTTGC TTATTCATCT GCAGGCAGCA CCGTAGTCTT
351 AACCGGTAAT GCCAAAGTAC AGCGCGGCGG CGATGTCGCC GAAGGTGCGG
401 TGATTACATA CAACACCAA ACCGAAGTCT ATACCATCAG CGGCAGCACA
451 AAATCCGGCG CAAATCCGC TTCCAAATCC GGCAGGGTCA GCGTCGTTAT
501 CCAGCCTTCG AGTACGCAA AATCCGAATA A

```

This corresponds to the amino acid sequence <SEQ ID 748; ORF 214-1>:

m214-1.pep

```

1  MIQICKLFLV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS
51  GNVVIRQGT L NISAARVNV T RGGKGGESV R AEGSPVRF S Q TLDGGKGTVR
101 GQANNVAY S S AGSTVVLT G N AKVQRGGDVA E GAVITYNT K TEVYTISG S T
151 KSGAKSASK S GRVSVVIQ P S STQKSE*

```

m214-1/g214-1 93.8% identity in 176 aa overlap

```

          10      20      30      40      50      60
m214-1.pep MIQICKLFLV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS GNVVIRQGT L
          10      20      30      40      50      60
g214-1      MIQICKLFLV LIVIFATSPAFALQSDSRRP IQIEADQGS L DQANQSTTFS GNVVIRQGT L
          10      20      30      40      50      60
          70      80      90     100     110     120
m214-1.pep NISAARVNV TRGGKGGESV R AEGSPVRF S Q TLDGGKGT VR GQANNVAY S S AGSTVVLT G N
          70      80      90     100     110     120
g214-1      NISASRVNV TRGGKGGESV R AEGSPVRF S Q TLDGGKGT VR GQANNVY S S AGSTVVLT G N
          70      80      90     100     110     120
          130     140     150     160     170
m214-1.pep AKVQRGGDVA E GAVITYNT K TEVYTISG S T KSGAKSASK S GRVSVVIQ P S S TQKSEX
          130     140     150     160     170
g214-1      AKVQRGGDVA E GAVITYNT K TEVYTING S T KSGAKSASK T GRVSVVIQ P S S TQKTEX
          130     140     150     160     170

```

g214-1/p38685

sp|P38685|YHBN ECOLI 17.3 KD PROTEIN IN MURA-RPON INTERGENIC REGION PRECURSOR (ORF185)
>gi|551336 (U12684) orf185 [Escherichia coli] >gi|606139 (U18997) ORF_o185 [Escherichia coli]
>gi|1789592 (AE000399) orf, hypothetical protein [Escherichia coli] Length = 185
Score = 97.1 bits (238), Expect = 6e-20
Identities = 57/126 (45%), Positives = 74/126 (58%), Gaps = 3/126 (2%)

```

Query: 19  PAFALQSDSRQP IQIEADQGS L DQANQSTTFS GNVVIRQGT L NISAARVNV TR--GGKGG 76
          PAF A+ D+ QPI IE+DQ SLD TF+GNV++ QGT+ I+A +V VTR G +G
Sbjct: 24  PAFAVTGD TDQPIHIESDQQSLDMQGNVVTFTGNVIVTQGTIKINADKV VVTRPGGEQ GK 83

Query: 77  ESVRAEGSPVRF S Q TLDGGKGT VR GQANNVAY S S AGSTVVLT G NAKVQRGGDVA E GAVIT 136
          E + G P F Q D GK V G A+ + Y A VVLTGNA +Q+ +G IT
Sbjct: 84  EVIDGYGK PATFYQM QDNGK-PVEGHASQMHYELAKDFV VLTGNAYLQQVDSNIKGDKIT 142

Query: 137 YNTKTE 142
          Y K +
Sbjct: 143 YLVKEQ 148

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 749>:

a214-1.seq

```

1  ATGATACAAA AGATATGTAA GCTATTTGTT TTAATAGCAT TTTTTCGGC
51  GTCCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTTGCTC GATCAAGCCA ACCAAAGCAC CACATT CAGC
151 GGAAACGTCTG TCATCAGACA GGGTACGCTC AATATTTCCG CCGCCCCGCT
201 CAATGTTACA CGCGGCGGCA AAGGCGGCGA ATCCGTGAGG GCGGAAGGTT
251 CGCCAGTCCG CTTACGCCAG ACATTGGACG GCGGCAAAGG CACGGTGCGC
301 GGACAGGCAA ACAACGTTGC TTATTCATCT GCAGGCAGCA CCGTAGTCTT
351 AACCGGTAAT GCCAAAGTAC AGCGCGGCGG CGATGTCGCC GAAGGTGCGG
401 TGATTACATA CAACACCAA ACCGAAGTCT ATACCATCAG CGGCAGCACA
451 AAATCCGGCG CAAATCCGC TTCCAAATCC GGCAGGGTCA GCGTCGTTAT
501 CCAGCCTTCG AGTACGCAA AATCCGAATA A

```

This corresponds to the amino acid sequence <SEQ ID 750; ORF 214-1.a>:

a214-1.pep

```

1  MIQICKLFLV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS

```

51 GNVVIRQGTI NISAARVNVT RGGKGGESVR AEGSPVRFSQ TLDGGKGTVR
 101 QANNVAYSS AGSTVVLGTN AKVQRGGDVA EGAVITYNTK TEVYTISGST
 151 KSGAKSASKS GRVSVVIQPS STQKSE*

a214-1/m214-1 100.0% identity in 176 aa overlap

	10	20	30	40	50	60
a214-1.pep	MIQKICKLFVLIAFFSASP	FALQSDSRQPIQIEADQ	GSLDQANQSTTFSGNV	VIRQGTI		
m214-1	MIQKICKLFVLIAFFSASP	FALQSDSRQPIQIEADQ	GSLDQANQSTTFSGNV	VIRQGTI		
	10	20	30	40	50	60
	70	80	90	100	110	120
a214-1.pep	NISAARVNVT	RGGKGGESVRAEGSP	VRFSTLDGGKGTVR	QANNVAYSSAGST	VVLGTN	
m214-1	NISAARVNVT	RGGKGGESVRAEGSP	VRFSTLDGGKGTVR	QANNVAYSSAGST	VVLGTN	
	70	80	90	100	110	120
	130	140	150	160	170	
a214-1.pep	AKVQRGGDVAEGAVITY	NTKTEVYTISGSTK	SAGKSASKSGRVSV	VIQPSSTQKSEX		
m214-1	AKVQRGGDVAEGAVITY	NTKTEVYTISGSTK	SAGKSASKSGRVSV	VIQPSSTQKSEX		
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 751>:

g215.seq

```

1   atgaaagtaa gatggcggta cgggaattgcg ttccattga tattggcgggt
51  tgccttgggc agcctgtcgg catggttggg ccgtatcagc gaagtcgaaa
101 tcgagggaagt caggctcaat cccgacgaac ctcaatacac aatggacggc
151 ttggacggaa ggcggtttga cgaacagggg tacttgaaag aacatttgag
201 cgcgaaaggt gcgaaacagt ttcccgaaaa cagcgacatc cattttgatt
251 agccgcatct cgtgttcttc caagaaggca ggctgttgta cgaagtcggc
301 agcgatgaag ccgtttacca taccgaaaac aaacaggttc ttttataaaa
351 caacgttgtg ctgacaaaaa ccgccgacgg caggcggcag gcgggttaaag
401 tcgaaaccga aaaactgcac gtcgataccg aatctcaata tgcccaaacc
451 gatacgcttg tcagtttcca atatggcgcg tcgcacggtc aggcgggagg
501 tatgacctac aaccacaaaa caggcatgtt gaacttctca tctaaagtga
551 aagccgcgat ttatgatata aaagatatgt aa

```

This corresponds to the amino acid sequence <SEQ ID 752; ORF 215.ng>:

g215.pep

```

1   MKVRWRYGIA FPLILAVALG SLSAWLGRIS EVEIEEVRLN PDEPQYTMDS
51  LDGRRFDEQG YLKEHLSAKG AKQFPENSDI HFDSPHLVFF QEGRLLYEVG
101 SDEAVYHTEN KQVLFKNVNV LTKTADGRRQ AGKVETEKLN VDTESQYAQT
151 DTPVSFQYGA SHGQAGGMTY NHKTGMLNFS SKVKAIIYDT KDM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 753>:

m215.seq (partial)

```

1   ..AGCCTGTCGG CATGGTTGGG TCGTATCAGC GAAGTCGAGA TTGAAGAAGT
51  CAGGCTCAAT CCCGACGAAC CGCAATACAC AATGGACAGC TTGGACGGCA
101 GGCGGTTTGA CGAACAGGGA TACTTGAAAG AACATTTGAG CGCGAAGGGC
151 GCGAAACAGT TTCCGGAAAG CAGCGACATC CATTTTGATT CGCCGCATCT
201 CGTGTTCCTC CAAGAAGGCA GGTGTGTGTA CGAAGTCGGC AGCGACGAAG
251 CCGTTTACCA TACCGAAAAC AAACAGGTTC TTTTAAAAA CAACGTTGTG
301 CTGACCAAAA CCGCCGACGG CAAACGGCAG GCGGGTAAAG TTGAAGCCGA
351 AAAGCTGCAC GTCGATACCG AATCTCAATA TGCCCAAACC GATACGCCTG
401 CAGTTTCCA ATATGGTGCA TCGCACGGTC AGCGGGCGCG CATGACTTAC
451 GACCACAWWA CAGGCATGTT GAACCTCTCA TCTAAAGTGA AAGCCACGAT
501 TTATGATACA AAAGATATGT AA

```

This corresponds to the amino acid sequence <SEQ ID 754; ORF 215>:

m215.pep (partial)

```

1   ..SLSAWLGRIS EVEIEEVRLN PDEPQYTMDS LDGRRFDEQG YLKEHLSAKG
51  AKQFPENSDI HFDSPHLVFF QEGRLLYEVG SDEAVYHTEN KQVLFKNVNV
101 LTKTADGKRQ AGKVEAEKLN VDTESQYAQT DTPVSFQYGA SHGQAGGMTY

```

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 215 shows 96.0% identity over a 173 aa overlap with a predicted ORF (ORF 215.ng) from *N. gonorrhoeae*:

m215/q215

		10	20	30	40
m215.pep		SLSAWLGRISEVEIEEVR LNPDEPQYTMDSLDGRRFDEQG			
		:			
g215		MKVRWRYGIAFP LILAVALGSLSAWLGRISEVEIEEVR LNPDEPQYTMDGLDGRRFDEQG			
		10	20	30	40
		50	60	70	80
m215.pep		YLKEHLSAKGAKQFPESDIHFDSPHLVFFQEGRLLYEVGSDEAVYHTENKQVLFKNNVV			
		:			
g215		YLKEHLSAKGAKQFPESDIHFDSPHLVFFQEGRLLYEVGSDEAVYHTENKQVLFKNNVV			
		70	80	90	100
		110	120	130	140
m215.pep		LTKTADGKROAGKVEAEKLHVDTESQYAQTDTTPVSFOYGASHGQAGGMTYDHTGMLNFS			
		: :			
g215		LTKTADGRRROAGKVEATEKLHVDTESQYAQTDTTPVSFOYGASHGQAGGMTYNHKTGMLNFS			
		130	140	150	160
		170	180	190	200
m215.pep		SKVKATIIYDTKDMX			
		:			
g215		SKVKAAIYDTKDM			
		190			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 755>:

a215.seq

```
1  ATGAAAGTAA  GATGGCGGTA  CGGAATTGCG  TTCCCATTTGA  TATTGGCGGT
51  TGCCTTGGGC  AGCCTGTCCG  CATGGTTGGG  ACGCATCAGC  GAAGTCGAGA
101 TTGAAGAAAT  CAGGCTCAAT  CCCAGCGAAC  CGCAATACAC  AATGGACGGA
151 TTGGATGGCA  GGCGGTTTGA  CGAACAGGGA  TACTTGAAG  AACATTTGAG
201 TTCGAAGGGC  GCGAAACAGT  TTCCCGAAAG  CAGCGACATT  CATTTCTGACT
251 CACCGCATCT  CGTGTTCCTC  CAAGAAGGCA  GGTGTGTGTA  CGAAGTCGGC
301 AGCGATGAAG  CCGTTTACCA  TACCGAAAA  AAACAGGTTT  TTTTAAAAA
351 CAACGTTGTG  CTGACCAAAA  CCGCCGACGG  CAAACCGCAG  CGGGTAAAG
401 TTGAAGCCGA  AAAGCTGCAC  GTCGATACCG  AATCTCAATA  TGCCCAAACC
451 GATACGCTGT  TCAGTTTCCA  ATATGGTGCA  TCGCACGGTC  AGCGGGCGG
501 CATGACTTAC  GACCACAAA  CAGGCATGTT  GAACTTCTCA  TCTAAAGTGA
551 AAGCCACGAT  TTATGATACA  AAAGATATGT  AA
```

This corresponds to the amino acid sequence <SEQ ID 756; ORF 215.a>:

a215.pap

1	<u>MKVRWRYGIA</u>	<u>FPLILAVALG</u>	<u>SLSAWLGRIS</u>	EVEIEEVRLN	PDEPQYTM DG
51	LDGRRFDEQG	YLKEHLS SSG	AKQFPES SDI	HFDSPHLVFF	QEGRLLYE VG
101	SDEAVYHTEN	KQVLFKNNV V	LTKTADGKR Q	AGKVEAEKL H	VDTESQYAQT
151	DTPVSFQYGA	SHQVAGG MTY	DHKTGM LNFS	SKVKATIIDYT	KDM*

m215/a215 98.3% identity in 173 aa overlap

```

                                     10      20      30      40
m215.pep      SLSAWLGRISEVEIEEVRLNPDEPQYTMDSLDGRRFDEQG
               |||||
a215      MKVRWRYGIAFPPLILAVALGSLSAWLGRISEVEIEEVRLNPDEPQYTMGDLDGRRFDEQG
               10      20      30      40      50      60
               50      60      70      80      90     100
m215.pep      YLKEHLSAKGAKQFPSSDIHFDSPLHVFQEGRLLYEVGSDEAVYHTENKOVLEKNNV

```

```

a215      |||||:|||||
          YLKEHLSSKGAKQFPSSDIHFDSPHLVFFQEGRLLYEVGSDEAVYHTENKQVLFKNNVV
          70      80      90      100     110     120

          110     120     130     140     150     160
m215.pep  LTKTADGKRQAGKVEAEKLHVDTESQYAQTDTPVSFQYGASHGQAGGMTYDHXTGMLNFS
          |||||:|||||
a215      LTKTADGKRQAGKVEAEKLHVDTESQYAQTDTPVSFQYGASHGQAGGMTYDHKTGMLNFS
          130     140     150     160     170     180

          170
m215.pep  SKVKATIYDTKDMX
          |||||:|||||
a215      SKVKATIYDTKDMX
          190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 757>:

g216.seq (partial)

```

1  ..atgatatcga tttcgagctc ggtaccacgc gacgaaatca ccgccatcat
51  ccccgcactc aaacgcaaag acattaccct cgtctgcatc accgcccgcg
101 ccgattcaac catggcgcg ccatgccgata tccacatcac cgcacgggtt
151 tcgcaagaag cctgcccgtt ggggcttgcc ccgaccacca gcaccaccgc
201 cgttatggct ttgggcgacg cgttgggcgt cgtcctgctg cgcgcccgcg
251 cgttcacgcc cgacgacttc gccttgatcc accctgcccg cagcctcggc
301 aaacgcctgc ttttgccgct tgccgacatt atgcacaaag gcggcgccct
351 gcccgcgcgc cgactcggca cgcccttgaa aggagccatc gtcagcatga
401 gcgagaaagg tttgggcatg tgggcgggaa cggacgggca aaggctgtct
451 gaaaggcctt tttactga

```

This corresponds to the amino acid sequence <SEQ ID 758; ORF 216.ng>:

g216.pep (partial)

```

1  ..MISISSSVPS DEITAIPAL KRKDITLVC I TARP DSTMAR HADIHITASV
51  SQEACPLGLA PTTSTTAVMA LGDALAVLL RARAF TPDDF ALIHPAGSLG
101 KRLLLRVADI MHKGGGLPAV RLGTPLKGAI VSMSEKGLGM WAGTDGQRLS
151 ERPFY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 759>:

m216.seq

```

1  ATGGCAATGG CAGAAAACGG AAAATATCTC GACTGGGCAC GCGAAGTGTT
51  GCACGCCGAA GCGGAAGGCT TGCGCGAAAT TGCAGCGGAA TTGsACAAAA
101 ACTTCGTCCT TGCGGCAGAC GCGTTGTTGC ACTGCAAGGG CAGGGTCGTT
151 ATCACGGGCA TGGTCAAGTC GGGACATATC GGGCGCAAAA TGGCGGCAAC
201 TATGGCCTCG ACCGGCACGC CTGCGTTTTT CGTCCACCCT GCGGAAGCGG
251 CACACGgCGA TTTGGGTATG ATTGTGGACA rCGACGTGGT CGTCGCGATT
301 TCCAATTCCG GCGAAAGCGA CGAAATCGCC GCCATCATCC CCGCACTCAA
351 ACGCAAAGAC ATCACGCTTG TCTGCATCAC CGCCCGCCCC GATTCAACCA
401 TGGCGCGCCA TGCCGACATC CACATCACGG CGTCGGTTTC CAAAGAAGCC
451 TGCCCGCTGG GGCTTGCCCC GACCACCAGC ACCACGCGC TCATGGCTTT
501 GGGCGATGCG TTGGCGGTGCG TCctGCTGCG CgcACGCGCG TTCACGCCCC
551 ACGATTTCGC CTTGAGCCAT CCTGCCGGCA GCCTCGGCAA ACGCCTACTT
601 TTGCGCGTTG CCGACATTAT GCACAAAGGC GGCGGCCTGC CTGCCGTCCG
651 ACTCGGCACG CCCTTGAAAG AAGCCATCGT CAGCATGAGT GAAAAAGGGC
701 TGGGCATGTT GGCGGTAAAG GACGGGCAAG GCCGTCTGAA AGGCGTATTC
751 ACCGACGGCG ATTTGCGCCG CCTGTTTCAA GAATGCGACA ATTTTACCGG
801 TCTTTCGATA GACGAAGTCA TGCATACGCA TCCTAAAACC ATCTCCGGC
851 AACGTCTCGC CACCGAAGCC CTGAAAGTCA TGCAGGCAAA CCATGTGAAC
901 GGGCTTCTGG TTACCGATGC AGATGGCGTG CTGATCGGCG CGCTGAATAT
951 GCACGACCTG CTGGCGGCAC GGATTGTATA G

```

This corresponds to the amino acid sequence <SEQ ID 760; ORF 216>:

m216.pep

```

1  MAMAENGKYL DWAREVLHAE AEGLREIAAE LXKNFVLAAD ALLHCKGRVV

```

```

51  ITGMVKSGHI GRKMAATMAS TGTPAFFVHP AEAHGDLM IVDXDVVVAI
101 SNSGESDEIA AIIPALKRKD ITLVCITARP DSTMARHADI HITASVSKEA
151 CPLGLAPTTS TTAVMALGDA LAVVLLRARA FTPDDFALSH PAGSLGKRLL
201 LRVADIMHKG GGLPAVRLGT PLKEAIVSMS EKGLGMLAVT DGQRLKGVF
251 TDGDLRRLFQ ECDNFTGLSI DEVMHHPKT ISAERLATEA LKVMQANHVN
301 GLLVTDADGV LIGALNMHDL LAARIV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 216 shows 91.8% identity over a 147 aa overlap with a predicted ORF (ORF 216.ng) from *N. gonorrhoeae*:

m216/g216

```

              70      80      90      100      110      120
m216.pep      TMASTGTPAFFVHPAEAAHGDLMIVDXDVVVAISNSGESDEIAAIIPALKRKDITLVC
g216              ::|||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
              10      20      30
              MISISSVPSDEITAIIPALKRKDITLVC

              130      140      150      160      170      180
m216.pep      TARPDSMARHADIHITASVSKEACPLGLAPTSTTAVMALGDALAVVLLRARAFTPDDF
g216              |||||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
              40      50      60      70      80      90
              TARPDSMARHADIHITASVSQEACPLGLAPTSTTAVMALGDALAVVLLRARAFTPDDF

              190      200      210      220      230      240
m216.pep      ALSHPAGSLGKRLLLRVADIMHKGGLPAVRLGTPLKEAIVSMSEKGLGMLAVTDGQRL
g216              || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
              100      110      120      130      140      150
              ALIHPAGSLGKRLLLRVADIMHKGGLPAVRLGTPLKGAIVSMSEKGLGMWAGTDGQRLS

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 761>:

```

a216.seq
1  ATGGCGATGG CAGGAAACGA AAAATATCTT GATTGGGCAC GCGAAGTGTT
51  GCACACCGAA GCGGAAGGCT TGCGCGAAAT TGCGGCGGAT TTGGACGAAA
101 ACTTCGCCCT TGCGGCGGAC GCGTTGTTGC ACTGCAAAGG CAGGGTCGTT
151 ATCACGGGCA TGGGCAAGTC GGGACATATC GGGCGCAAAA TGGCGGCAAC
201 CATGGCCTCG ACCGGCACGC CCGCGTTTTT CGTCCACCCT GCGGAAGCGG
251 CACACGGCGA TTTGGGCATG ATTGTGGACA ACGACGTGGT CGTCGCGATT
301 TCCAATTCCG GTGAAAGCGA CGAAATCGCC GCCATCATCC CCGCGCTCAA
351 ACGCAAAGAT ATCAGCCTTG TCTGCATCAC CGCCCGCCCC GATTCAACCA
401 TGGCGCGCCA TGCCGACATC CACATCACGG CGTCGGTTTC CAAAGAAGCC
451 TGCCCGCTGG GGCTTGCCCC GACCACCAGC ACCACGCGCG TTATGGCTTT
501 GGGCGATGCG TTGGCGGTTG TCCTGTGTCG CGCCCGCGCG TTCACGCCCC
551 ACGACTTCGC CTTGAGCCAC CCTGCCGCGA GCCTCGGCAA ACGCCTACTT
601 TTGCGCGTTG CCGACATTAT GCACAAAGGC GGCGGCCTGC CTGCCGTCCG
651 ACTCGGCACG CCCTTGAAAG AAGCCATCGT CAGCATGAGT GAAAAAGGGC
701 TGGGCATGTT GGCGGTAACG GACGGGCAAG GCCGTCTGAA AGGCGTATTC
751 ACCGACGGCG ATTTGCGCCG CCTGTTTCAA GAATGCGACA ATTTTACCGG
801 TCTTTCGATA GACGAAGTCA TGCATACGCA TCCTAAAACC ATCTCCGCCG
851 AACGTCTCGC CACCGAAGCC CTGAAAGTCA TGCAAGCAAA CCATGTGAAC
901 GGGCTTCTGG TTACCGATGC AGATGGCGTG CTGATCGGCG CGCTGAATAT
951 GCACGACCTT TTGGCGGCGC GGATTGTATA G

```

This corresponds to the amino acid sequence <SEQ ID 762; ORF 216.a>:

```

a216.pep
1  MAMAGNEKYL DWAREVLHTE AEGLEIAAD LDENFALAAD ALLHCKGRVV
51  ITGMKSGHI GRKMAATMAS TGTPAFFVHP AEAHGDLM IVDNDVVVAI
101 SNSGESDEIA AIIPALKRKD ITLVCITARP DSTMARHADI HITASVSKEA
151 CPLGLAPTTS TTAVMALGDA LAVVLLRARA FTPDDFALSH PAGSLGKRLL
201 LRVADIMHKG GGLPAVRLGT PLKEAIVSMS EKGLGMLAVT DGQRLKGVF
251 TDGDLRRLFQ ECDNFTGLSI DEVMHHPKT ISAERLATEA LKVMQANHVN

```

301 GLLVTDADGV LIGALNMHDL LAARIV*

m216/a216 97.2% identity in 326 aa overlap

	10	20	30	40	50	60
m216.pep	MAMAENKYLWAREVLHAEAEGLREIAAELXKNFVLAADALLHCKGRVITGMVKSGHI					
a216	MAMAGNEKYLWAREVLHTEAEGLREIAADLDENFALAADALLHCKGRVITGMGKSGHI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m216.pep	GRKMAATMASTGTPAFFVHPAEAAHGDLMIVDXDVVAISNSGESDEIAAIIIPALKRKD					
a216	GRKMAATMASTGTPAFFVHPAEAAHGDLMIVDNDVVAISNSGESDEIAAIIIPALKRKD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m216.pep	ITLVCITARPDSTMARHADIHITASVSKEACPLGLAPTSTTAVMALGDALAVVLLRARA					
a216	ITLVCITARPDSTMARHADIHITASVSKEACPLGLAPTSTTAVMALGDALAVVLLRARA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m216.pep	FTPDDFALSHPAGSLGKRLLLRVADIMHKGGLPAVRLGTPLKEAIVSMSEKGLGMLAVT					
a216	FTPDDFALSHPAGSLGKRLLLRVADIMHKGGLPAVRLGTPLKEAIVSMSEKGLGMLAVT					
	190	200	210	220	230	240
	250	260	270	280	290	300
m216.pep	DGQGRKGVFTDGDRLRLFQECDNFTGLSIDEVMHHPKTISAERLATEALKVMQANHVN					
a216	DGQGRKGVFTDGDRLRLFQECDNFTGLSIDEVMHHPKTISAERLATEALKVMQANHVN					
	250	260	270	280	290	300
	310	320				
m216.pep	GLLVTDADGVLIGALNMHDLAARIVX					
a216	GLLVTDADGVLIGALNMHDLAARIVX					
	310	320				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 763>:

g217.seq

```

1  atggcggatg acggtttggt gcggaactg tccgaaaaac ccagccaaag
51  tgctctcttc ctgccatttg acccattcgt tttcgaggtt ttggactgcc
101 ttttggtcat cgggcccggc ttgaaacaat gtttcaagca aatcccggca
151 acgcgccacc cattcgccga ccgtcgagg ttgccgcat atccgggcaa
201 tatccgacag ggtttcgagg aaggcggaac aacgtccgaa catggcggtt
251 tgattcacgt cggcatacca cgcgctgaca tctgccaca tcgggttgcc
301 gccttcgggc agcatccagc ccaatatcat acggtctgcc gcctgcttcc
351 aggtaaacag ctgatccgtg ccgccgcgca tttctccgtc caatccccaa
401 tggacgttca aatcggcaac catatcgtgc aaaagcgga aatcgtcccc
451 ggtcagtcgg aaacggcgca acacggggcg ggtttccaaa agcgcgagca
501 ctttgccgac ttcaaaacgg ctttcagca agtcggacac gcaactccaa
551 gcataaaaaa acggttgccg gcggctgatt ttcacgtccg aaacggaata
601 cggcaatgcc tgcgcgcggg gttgcgcctg tccgaacacg gcttccataa
651 aaggcgataa ggggttcgata ttcgggggta a

```

This corresponds to the amino acid sequence <SEQ ID 764; ORF 217.ng>:

g217.pep..

```

1  MADDGLLRQL SEKPSQSALF LPFDPFVFEV LDCLLVIGPG LKQCFKQIPA
51  TRHPFADRRR LPPYPGNIRQ GFEEGGKTSE HGGLIHVGIP RADILPHRVA
101 AFGQHPAQYH TVCRLLPGKQ LIRAAAHFSV QSPMDVQIGN HIVQKRQIVP
151 GQSETAQHGR GFQKREHFAD FKTAFOQVGH ALQRIKKRLP AADFHVRNGI

```

201 RQCLRAGLRL SEHGFHKRRI GFDIRG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 765>:

m217.seq

```

1  ATGCGCGATG  ACGGTGTGCG  GCGGCAACTG  TCCGGAAAAT  TCGGCCAATT
51  CGGTTTCCGC  CTCCATTG  ACCCATTCGT  TTTCAAGGTT  TTGGACTGAC
101 TTTTGGTCAT  CGGCTTCAGC  TTGGAACAAT  GTTTCAGCA  AATCCCGGCA
151 ACGCGCCACC  CATTGCGCGA  CCGTTGCGGG  CTGCCGCCAT  ATCCGTACAA
201 TATCCGTCAG  GGTTCGAGG  AAGGCGGCAA  AACGTCCGAA  CATGGCGGTT
251 TGATTACAGT  CGGCATACCA  CGCGCTGACA  TCCTGCCACA  TCGGATTGCC
301 GCCTTTGGGC  AGCATCCAGC  CCAATATCAT  GCGTTCCTACC  GCCTGCTTCC
351 AGGTGAACAG  CTGATCCGTG  CCGCCGCGCA  TTTCTCCGTC  CAAACCCAG
401 TGGACGTTCA  AATCGGCAAC  CATGTCGTGC  AAAAGCGGTA  AATCGTCCTC
451 AGTCAGTCCG  AAACGGCGCA  ACACGGGCGC  GGTTTCTAAA  AGCACAAGCA
501 CTTTATCGAC  TTCAAATCGG  CTTTCCAACA  AGTCGAACAG  GCATGACAAA
551 GCATGAAACA  GCGGTTGGCG  GCGGCTGATT  TTCACGTCTG  ACACGGAATA
601 CGGCAATGCC  TGCGCACCgG  GctGCGCCTG  TCCGAACACG  GCTTCGATAA
651 AAGGCGTATA  GGATTCGATA  TTCGGGGTTA  A

```

This corresponds to the amino acid sequence <SEQ ID 766; ORF 217>:

m217.pep

```

1  MADDGVRRQL  SGKLRQGFGR  LPFDPFVFKV  LDXMLLVIGFS  LEQCFKQIPA
51  TRHPFADRCG  LPPYPYNIRO  GFEEGGKTSE  HGGLIHVGIP  RADILPHRIA
101 AFGQHPAQYH  AFYRLLPGEQ  LIRAAAHFSV  QTPVDVQIGN  HVVQKRXLIVL
151 SQSETAQHGR  GFXXKHKHFD  FKSFAQQVEQ  AXQSMKQRLA  AADFHVXHGI
201 RQCLRTGLRL  SEHGFDKRI  GFDIRG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 217 shows 80.5% identity over a 226 aa overlap with a predicted ORF (ORF 217.ng) from *N. gonorrhoeae*:

m217/g217

m217.pep	10	20	30	40	50	60
	MADDGVRRQLSGKLRQGFRLPFDPFVFKVLDXMLLVIGFSLEQCFKQIPATRHFPADRCG					
g217	MADDGLLRLQSEKPSQSALFLPFDPFVFEVLDCLLVIGPGLKQCFKQIPATRHFPADRRR					
	10	20	30	40	50	60
m217.pep	70	80	90	100	110	120
	LPPYPYNIROGFEEGGKTSEHGGLIHVGIPRADILPHRIAFAFGQHPAQYHAFYRLLPGEQ					
g217	LPPYPGNIRQGFEEGGKTSEHGGLIHVGIPRADILPHRVAAFGQHPAQYHTVCRLLPGKQ					
	70	80	90	100	110	120
m217.pep	130	140	150	160	170	180
	LIRAAAHFSVQTPVDVQIGNHVQKRXLIVLSQSETAQHGRGFXXKHKHFIDFKSAFQQVEQ					
g217	LIRAAAHFSVQSPMDVQIGNHIVQKRQIVPGQSETAQHGRGFQKREHFADFKTAFQQVGH					
	130	140	150	160	170	180
m217.pep	190	200	210	220		
	AXQSMKQRLAAADFHVXHGIHQCLRTGLRLSEHGFDKRRIGFDIRGX					
g217	ALQRIKKRLPAADFHVNRNGIRQCLRAGLRLSEHGFKRRIGFDIRG					
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 767>:

a217.seq

```

1  GTGGCGGATG  ACGGTGTGCA  GCGGCAACTG  TCCGGAAAAT  TCGGCCAATT
51  CGGTTTCCGC  CTGCCATTG  ACCCATTCGT  TTTGAGGCT  TTGGACTGCC
101 TTTTGGTCAT  CGCCTTCGAC  TTGGAACAAT  GTTTCAGCA  AATCCCGGCA
151 ACGCGCCACC  CATTGCTCAA  CCGTCGCAGG  TTGCCGCCAT  ATCCGTACAA

```



```

201 TATCCGTCAG GGTTCGAGG AAGGCGGCAA AACGTCCGAA CAGGGCGGTT
251 TGGTTCACGT CGGCATACCA CGCGCTGACC CCCTGCCACA TCGGATTGCC
301 GCCTTCGGGC AGCATCCAGC CCAATATCAT GCGTTCCTACC GCCTGCTTCC
351 AGGTGAACAG CTGATCCGTG CCGCGCGCA TTTCTCCGTC CAAACCCAG
401 CGGACGTTCA AATCGGCAAC CATGTCGTGC AAAAGCGGCA AATCGTCCTC
451 AGTCAGTCCG AAATGGCGCA ACACGGGCGC GGTTCCTAAA AGCACAAGCA
501 CTTTATCGAC TTCAAATCGG CTTTCCAACA AGTCGAACAG GCATGACAAA
551 GCATGAAACA GCGGTTGTCG GCGGCTGATT TTCACATCCG AAACGGAATA
601 CGGCAATGCC TGC GCGCGCCG GCTGCGCCTG TCCGAACACG GCTTCGATAA
651 AAGGCGTATA GGATTCGATA TTCGGGGTTA A

```

This corresponds to the amino acid sequence <SEQ ID 768; ORF 217.a>:

```

a217.pep
1 VADDGVQRQL SGKLRQFGFR LPFDPFVFEEA LDCLLVIAFD LEQCFKQIPA
51 TRHPFVNRRR LPPYPYNIRQ GFEEGGKTSE QGGLVHVGP RADPLPHRIA
101 AFGQHPAQYH AFYRLLPGEQ LIRAAAHFSV QTPADVQIGN HVVQKRQIVL
151 SQSEMAQHGR GF*KHKHFID FKSAFQQVEQ A*QSMKQRLS AADFHIRNGI
201 RQCLRAGLRL SEHGFDKRRRI GFDIRG*

```

m217/a217 90.3% identity in 226 aa overlap

m217.pep	MADDGVRRLSGKLRQFGFRLPFDPFVFEEALDCLLVIAFDLEQCFKQIPATRHPPFADRCG
a217	VADDGVQRQLSGKLRQFGFRLPFDPFVFEEALDCLLVIAFDLEQCFKQIPATRHPPFVNRRR
m217.pep	LPPYPYNIRQGFEEGGKTSEHGGLIHVGIPRADILPHRIA AFGQHPAQYHAFYRLLPGEQ
a217	LPPYPYNIRQGFEEGGKTSEQGGLVHVGP RADPLPHRIA AFGQHPAQYHAFYRLLPGEQ
m217.pep	LIRAAAHFSVQTPVDVQIGNHVQKRXIVLSQSETAQHGRGFXKHKHFIDFKSAFQQVEQ
a217	LIRAAAHFSVQTPADVQIGNHVQKRQIVLSQSEMAQHGRGFXKHKHFIDFKSAFQQVEQ
m217.pep	AXQSMKQRLAAADFHVXHGIRQCLRTGLRLSEHGFDKRRIGFDIRGX
a217	AXQSMKQRLSAADFHIRNGIRQCLRAGLRLSEHGFDKRRIGFDIRGX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 769>:

```

g218.seq
1 atggttgccg tggatcctta tacggcaaaa gtggtcaaca ccatgcccg
51 caatcagggg tggatcaca ctatggatga aatccacggc gatatgatgc
101 tcggtgcccg aggcgattat cttttggaaa cggcagcttc actgaccatt
151 attatggttg tcagcggctt gtacctttgg tgggcgaaac agcgcggcat
201 taaagcgatg ctgctgccgc caaaaagcag ggcgcgttct tggtgccgga
251 atctgcacgg cgcgtttgga acttgggtgt cgttgatttt actggtgttc
301 tgctgtcgg gtattgcttg ggcaggtatt tggggcgcca aattcgtgca
351 ggcttggaa cagttcccgc ccggcaaatg ggggtgtcga ccgaaccccg
401 tttcaatcgt gccgaccac gccgaggtat tgaatgacgg caaggttaa
451 gaagtgccgt ggattttgga gcttatgcct atgcctgtct cagggaacgac
501 tgtgggtgaa aacggcatta accccaccga gcccaataac attggaaacc
551 gtcgaccgtt tcgcgcggga aatcggtttc aaagggcggt atcagttgaa
601 tttgcccaca gccgaggacg ggggtatggac tttgtcgcag gattctatga
651 gttatga

```

This corresponds to the amino acid sequence <SEQ ID 770; ORF 218.ng>:

```

g218.pep
1 MVAVDPTYAK VVNTMPRNQG WYHTMDEIHG DMMLGAAGDY LLETAASLTI

```

```

51  IMVVSGLYLW WAKQRGIKAM LLPPKSRARS WWRNLHGAFG TWVSLILLLF
101 CLSGIAWAGI WGGKFVQAWN QFPAGKWGVE PNPVSIVPTH GEVLNDGKVK
151 EVPWILELMP MPVSGTTVGE NGINPTEPNN IGNRRPFRAG NRFQALSVE
201 FAQRRGRGMD FVAGFYEL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 771>:

```

m218.seq
1  ATGGTCCGGC TCGATCCTTA TACGGCAAAA GTGGTCAGTA CCATGCCCGC
51  CAATCAGGGT TGGTATTACA CGATGGATGA AATCCACAGC GATATGATGC
101 TCGGTGCCGC AGGCGATTAT CTTTGGAAA CGGCAGCTTC ACTGACCATT
151 ATTATGGTTG TCAGCGGCTT GTACCTTTGG TGGGTGAAAC GGC GCGGCAT
201 CAAGGCGATG CTGCTGCCGT CAAAAGGCAr GGC GCGTCT TGGTGGCGGA
251 ATCTGCACGG CACGTTTGA ACTTGGGTGT CGTTGATTTT GCTGTTGTC
301 TGCCTGTCGG GTATTGCTTG GCGGGTATT TGGGGCGGCA AGTTCGTACA
351 GGCTTGGAGT CAGTTCCTTG CCGGTAAATG GGGTGTGCGA CCGAACCCCG
401 TTTCAATCGT GCCGACCCAC GCGGAGGTAT TGAATGACGG CAAGGTTAAG
451 GAAGTGCCGT GGGTTTTGGA GCTTACGCCT ATGCCTGTTT CAGGGACGAC
501 yGtgGGCAA GACGGCATT ACCCTGACGA GCCGATGACA TTGGAACCCG
551 TCGACCGCTT TCGCGCGnGA AATCGGTTTC AAAGGGCGTT ATCAGTTGAA
601 TTTGCCCAA GCGGAGGACG GCGTATGGAC TTTGTCGCAG GATTCTATGA
651 GTTA

```

This corresponds to the amino acid sequence <SEQ ID 772; ORF 218>:

```

m218.pep
1  MVAVDPYTAK VVSTMPRNOG WYITMDEIHS DMMLGAAGDY LLETAASLTI
51  IMVVSGLYLW WVKRRGIKAM LLPSKGXARS WWRNLHGTFG TWVSLILLLF
101 CLSGIAWAGI WGGKFVQAWS QFPAGKWGVE PNPVSIVPTH GEVLNDGKVK
151 EVPWILELTP MPVSGTTVGK DGINPDEPMT LETVDRFARX NRFQALSVE
201 FAQRRGRGMD FVAGFYEL

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 218 shows 87.2% identity over a 218 aa overlap with a predicted ORF (ORF 218.ng) from *N. gonorrhoeae*:

```

m218/g218
10      20      30      40      50      60
m218.pep  MVAVDPYTAKVVSTMPRNOGWYITMDEIHS DMMLGAAGDY LLETAASLTI IMVVSGLYLW
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g218      MVAVDPYTAKVVNTMPRNOGWYHTMDEIHGDMMLGAAGDY LLETAASLTI IMVVSGLYLW
          10      20      30      40      50      60

70      80      90      100     110     120
m218.pep  WVKRRGIKAMLLPSKGXARSWWRNLHGTFGTWVSLILLLFCLSGIAWAGIWGGKFVQAWS
          |:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:
g218      WAKQRGIKAMLLPPKSRARSWWRNLHGAFGTWVSLILLLFCLSGIAWAGIWGGKFVQAWN
          70      80      90      100     110     120

130      140     150     160     170     180
m218.pep  QFPAGKWGVEPNPVSIVPTHGEVLNDGKVKEVPWVLELTPMPVSGTTVGK DGINPDEPMT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g218      QFPAGKWGVEPNPVSIVPTHGEVLNDGKVKEVPWILELMPMPVSGTTVGGENINPTEPNN
          130     140     150     160     170     180

190      200     210
m218.pep  LETVDRFARXNRFQALSVEFAQRRGRGMD FVAGFYEL
          : : | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g218      IGNRRPFRAGNRFQALSVEFAQRRGRGMD FVAGFYEL
          190     200     210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 773>:

a218.seq

```

1   ATGGTCGCGG TCGATCCTTA TACGGCAAAA GTGGTCAGTA CCATGCCGCG
51  CAATCAGGGT TGGTATTACG CGATGGATGA AATCCACAGC GATATGATGC
101 TCGGTTTCGAC AGGTGATTAT CTTTGGAAA CGGCTGCATC GCTGACGATT
151 ATCATGATAA TCAGCGGTTT GTACCTTTGG TGGGTGAAAC GGC GCGGCAT
201 CAAGGCGATG CTGCTGCCGC CAAAAGGCAG GGC GCGTCTT TGGTGGCGGA
251 ATCTGCACGG CGCGTTTGGA ACTTGGGTGT CGTTGATTTT ACTGTTGTTC
301 TGCCTGTCGG GTATTGCTTG GGCAGGTATT TGGGGCGGCA AGTTCGTGCA
351 GGCTTGGAGT CAGTTCCCGG CAGGCAAATG GGGTGTGCGA CCGAACCCCTG
401 TTTCAATCGT GCCGACCCAC GGCAGGTAT TGAATGACGG CAAGGTAAAG
451 GAAGTGCCGT GGGTTTTGGA GCTTACGCTT ATGCTGTGTT CAGGGACGAC
501 TGTGGGCAAA GACGGTATTA ACCCTGACGA GCCGATGACA TTGAAACCG
551 TCGACCGTTT TGC GCGG.GA AATCGGTTT AAAGGCGTT ATCAGCTGAA
601 TTTGCCCAAA GCGAGGACG GCGTATGGAC TTTGTCGCAG GATTCTATGA
651 GTTA

```

This corresponds to the amino acid sequence <SEQ ID 774; ORF 218.a>:

a218.pep

```

1   MVAVDPYTAK VVSTMPRNQG WYYAMDEIHS DMMLGSTGDY LLETAASLTI
51  IMIISGLYLW WVKRRGIKAM LLPPKGRARS WWRNLHGAFG TWVSLILLLF
101 CLSGIAWAGI WGGKFVQAWS QFPAGKWGVE PNPVSVVPTH GEVLNDGKVK
151 EVPPVLELTP MPVSGTTVGK DGINPDEPMT LETVDRFARX NRFQRLSAE
201 FAQRRGRMD FVAGFYEL

```

m218/a218 95.9% identity in 218 aa overlap

	10	20	30	40	50	60
m218.pep	MVAVDPYTAKVVSTMPRNQGWYYTMD	IEHSDMMLGAAGDY	LLETAASLTI	IMVVSGLYLW		
a218	MVAVDPYTAKVVSTMPRNQGWYYAMDEI	HSMDMMLGSTGDY	LLETAASLTI	IMIISGLYLW		
	10	20	30	40	50	60
m218.pep	WVKRRGIKAMLLPSKXARS	WWRNLHGTFGTWVSLILLF	CLSGIAWAGIWGGKFVQAWS			
a218	WVKRRGIKAMLLPPKGRARS	WWRNLHGAFGTWVSLILLF	CLSGIAWAGIWGGKFVQAWS			
	70	80	90	100	110	120
m218.pep	QFPAGKWGVEPNPVSVVPTHGEVLNDGKVK	KEVPWVLELTPMPVSGTTVGK	DGINPDEPMT			
a218	QFPAGKWGVEPNPVSVVPTHGEVLNDGKVK	KEVPWVLELTPMPVSGTTVGK	DGINPDEPMT			
	130	140	150	160	170	180
m218.pep	LETVDRFARXNRFQRLS	VEFAQRRGRMD	FVAGFYEL			
a218	LETVDRFARXNRFQRLS	AEFAQRRGRMD	FVAGFYEL			
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 775>:

```
g219.seq
1   atgacggcaa ggttaaggaa gtgccgtgga ttttggagct tatgcctatg
51  cctgtctcag ggacgactgt ggtgaaaac ggcattaacc ccaccgagcc
101 caataacatt ggaaaccgtc gaccgtttcg cgcgggaaat cggtttcaaa
151 gggcgttatc agttgaattt gcccaaaggc gaggacgggg tatggacttt
201 gtgcgaggat tctatgagtt atgacatgat cagcccgttt gccgaccgca
251 cggtagatat cgaccagtac agcggcgaga ttcttgccga catccgtttt
301 gacgattaca acccgttcgg caaatttatg gcggcaagca ttgcgctgca
351 tatggggact ttgggctggg ggagcgtggt ggcgaacgct gtgttctgcc
401 ttgccgtgat ttttatcggc atcagcggct gcgtgatgtg gtggaacgcg
451 cgtccgtccg gcgtggcggg cattgttcct ccggcgcaaa aaatcaaaact
501 gcccgtctgg tgggcgatgg cattgccgct gctgttgatt gcactgcttt
551 tcccgaccgc gctgcttgcc attgccgtga tttggctggt ggataccttg
601 ctgctgtcgc ggattcctgt gttgaggaaa tggtttaaat ga
```

This corresponds to the amino acid sequence <SEQ ID 776; ORF 219.ng>:

```
g219.pep
1   MTARLRKCRG FWSLCLCLSQ GRLVVKTALT PPSPITLETV DRFAREIGFK
51  GRYQLNLPKG EDGVWTLSDQ SMSYDMISPF ADRTVHIDQY SGEILADIRF
101 DDYNPFGKFM AASIALHMG T LGWWSVLANV VFCLAVIFIG ISGCVMWWR
151 RPSGVAGIVP PAQKIKLPVW WAMALPLLLI ALLFPTALLA IAVIWLLDTL
201 LLSRIPVLRK WFK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 777>:

```
m219.seq
1   ATGACGGCAA GGTAAAGGAA GTGCCGTGGG TTTTGGAGCT TACGCCTATG
51  CCTGTTTCAG GGACGACyGt gGCGAAAGAC GGCATTAACC CTGACGAGCC
101 GATGACATTG GAAACCGTCG ACCGCTTTGC GCGGnGAAAT CGGTTTCAAA
151 GGGCGTTATC AGTTGAATTT GCCCAAAGGC GAGGACGGCG TATGGACTTT
201 GTCGCAGGAT TCTATGAGTT ACGACATGAT CAGCCCCTTT GCCGACCGCA
251 CGGTACATAT CGACCACTAC AGCGGCAAAA TCCTTGCCGA CATCCGTTTT
301 GACGATTACA ACCCGTTCGG CAAATTTATG GCGGCAAGCA TTGCGCTGCA
351 TATGGGACT CTGGGCTGGT GGAGCGTGTG GCGCAACGTC TTGTTCTGCC
401 TTGCCGTCAT TTTTATCGGT ATCAGCGGCT GCGTGATGTG GTGGAACGC
451 CGTCCGACCG GAGCGGTGGG CATCGTTCCG CCGGCGCAGA AAGTCAAGCT
501 GCCGTTTGG TGGATGATGG CATTGCCGCT ATTGGCAATC GCACTGCTCT
551 TCCCGACCTC ACTGCTTGCC ATTGCCGTGA TTTGGCTGTT GGATACGCTG
601 CTGTTGTCGC GGATTCCTGT TTTGAGGAGA TGGTTTAAAT GA
```

This corresponds to the amino acid sequence <SEQ ID 778; ORF 219>:

```
m219.pep
1   MTARLRKCRG FWSLRLCLFQ GRXWAKTALT LTSRXHWKPS TALRGEIGFK
51  GRYQLNLPKG EDGVWTLSDQ SMSYDMISPF ADRTVHIDQY SGKILADIRF
101 DDYNPFGKFM AASIALHMG T LGWWSVLANV LFCLAVIFIG ISGCVMWWR
151 RPTGAVGIVP PAQVKLPVW WMMALPLLAI ALLFPTSLLA IAVIWLLDTL
201 LLSRIPVLRK WFK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 219 shows 86.9% identity over a 213 aa overlap with a predicted ORF (ORF 219.ng) from *N. gonorrhoeae*:

```
m219/g219
      10      20      30      40      50      60
m219.pep MTARLRKCRGFWSLRLCLFQGRXWAKTALTLSRXHWKPS TALRGEIGFKGRYQLNLPKG
g219      MTARLRKCRGFWSLCLCLSQGRLVVKTALTTPSPITLETVD RFAREIGFKGRYQLNLPKG
      10      20      30      40      50      60
      70      80      90     100     110     120
m219.pep EDGVWTLSDQSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFGKFM AASIALHMG T
g219      EDGVWTLSDQSMSYDMISPFADRTVHIDQYSGEILADIRFDDYNPFGKFM AASIALHMG T
```

505

	70	80	90	100	110	120
	130	140	150	160	170	180
m219.pep	LGWWSVLANVLFCLAVIFIGISGCVMWKRRPTGAVGIVPPAQKVKL PVWMMALPLLAI					
	: : : : :					
g219	LGWWSVLANVVFCLAVIFIGISGCVMWKRRPSGAVGIVPPAQKIKLPVWWMALPLLII					
	130	140	150	160	170	180
	190	200	210			
m219.pep	ALLFPTSLLAIAVIWLLDTLLLSRIPVLRWFVKX					
	: : : :					
g219	ALLFPTALLAIAVIWLLDTLLLSRIPVLRKWFK					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 779>:

```
a219.seq
1   ATGACGGCAA GGTAAAGGAA GTGCCGTGGG TTTTGGAGCT TACGCCTATG
51  CCTGTTTCAG GGACGACTGT GGGCAAAGAC GGTATTAACC CTGACGAGCC
101 GATGACATTG GAAACCGTCG ACCGTTTTGC GCGG.GAAAT CGGTTTCAAA
151 GGGCGTTATC AGCTGAATTT GCCCAAAGGC GAGGACGGCG TATGGACTTT
201 GTCGCAGGAT TCTATGAGTT ACGACATGAT CAGCCCGTTT GCTGACCGCA
251 CGGTGCATAT CGACCACTAC AGCGGCAAGA TTCTTGCCGA CATCCGTTTT
301 GACGATTACA ACCCGTTCGG CAAATTTATG GCGGCAAGCA TTGCGCTGCA
351 TATGGGGACT TTGGGCTGGT GGAGCGTGTT GGCGAACGTT TTGTTCTGCC
401 TTGCCGTGAT TTTTATCGGC ATCAGCGGCT GCGTGATGTG GTGGAAACGC
451 CGTCCGTCCG GCGCGGTGGG CATGGTTCGG CCGGCGCAAA AAATCAAGCT
501 GCCCGTCTGG TGGGCAATGG CGGTGCCGCT GCTGCTGATT GCATTGCTTT
551 TCCCGACCGC GTTGCTTGCC ATTGCCGTA TTTGGCTGTT GGATACGCTG
601 CTGTTGTTCG GGATTCCTGT TTTGAGGAGA TGGTTTAAAT GA
```

This corresponds to the amino acid sequence <SEQ ID 780; ORF 219.a>:

```
a219.pep
1   MTARLRKCRG FWSLRCLFQ GRLWAKTVLT LTR*HWKPS TVLRXEIGFK
51  GRYQLNLPKG EDGVWTLSD SMSYDMISPF ADRTVHIDQY SGKILADIRF
101 DDYNPFGKFM AASIALHMG LGWWSVLANV LFCLAVIFIG ISGCVMWKRR
151 RPSGAVGMVP PAQKIKLPVW WAMAVPLLI ALLFPTALLA IAVIWLLDTL
201 LLSRIPVLRW WFK*
```

m219/a219 94.8% identity in 213 aa overlap

	10	20	30	40	50	60
m219.pep	MTARLRKCRGFWSLRCLFQGRXWAKTALTLSRXHWKPSTALRGEIGFKGRYQLNLPKG					
	: : : :					
a219	MTARLRKCRGFWSLRCLFQGRWAKTVLTLSRXHWKPSTVLRXEIGFKGRYQLNLPKG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m219.pep	EDGVWTLSDSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFGKFMAASIALHMG					
	: : : :					
a219	EDGVWTLSDSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFGKFMAASIALHMG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m219.pep	LGWWSVLANVLFCLAVIFIGISGCVMWKRRPTGAVGIVPPAQKVKL PVWMMALPLLAI					
	: : : :					
a219	LGWWSVLANVLFCLAVIFIGISGCVMWKRRPSGAVGMVPPAQKIKLPVWWMAMAVPLLLI					
	130	140	150	160	170	180
	190	200	210			
m219.pep	ALLFPTSLLAIAVIWLLDTLLLSRIPVLRWFVKX					
	: : : :					
a219	ALLFPTALLAIAVIWLLDTLLLSRIPVLRWFVKX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 781>:

```
g221.seq
1  atgcacgacc acggcgccat ggatcgccgc ctccccgctt tcggaagtct
51  gatcgggcga gccgtaaatc adatcgacgc tgacggattt gaaccttgcc
101 tcacgggagg catcgatgac ttctttggtt tcttcgtagc tttggatgag
151 gttgactgcc gccctgcaact tggggtcgaa atcctgaatg ccgacgctca
201 tgcggttgaa gccgagtctg ccgagcatga ggacgggtgc gccggtgact
251 ttgcgcgggt cgatttcgat ggaatattcg ccggacggta tcagttcgaa
301 atgtttgcgg atcatgcgga agacacgttc gatctgttcg tcgctcaaaa
351 aggtcggcgt gccgccgccg aagtgcagtt gggcaagctg gtgccgtccg
401 ttcagatgtg gagcgagcag ttccatttct ttttcaagat attcgatgta
451 ggtatcggcg cggcttttgt ctttggtgat gattttgttg cagccgcagt
501 agtagcagat ggtgttgcaa aacggaatgt gaatgtaaag ggaaagcggg
551 ttgtttta
```

This corresponds to the amino acid sequence <SEQ ID 782; ORF 221.ng>:

```
g221.pep
1  MHDHGAMDRR LPAFGSLMRR AVNXIDADGF EPCLTGGIDD FFGFFVALDA
51  VDCRLHFGVE ILNADAHAVE AESAEHEDGV AADFARVDFD GIFAGRYQFE
101 MFADHAEDTF DLFVAQKGRR AAAEVQLGKL VPSVQMWSEQ FHFFFKIFDV
151 GIGAAVFVGD DFVAAAVVAD GVAKRNVNVK GKRFV*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 783>:

```
m221.seq
1  ATGGyGGTTT TGATGcwcmg AAGTCTGGTG CGGCAGGCCG TAAATCAAAT
51  CGACGCTGAC GGATTTGAAC CCCGCTTCGC GCGCCGCATC GATGACTTCT
101 TTGGTTTCTT CGTAACTTTG GATGCGGTTG ACCGCCGCCT GCACTTTGGG
151 GTCGAAATCC TGAATGCCGA TGCTCATGCG GTTGAAGCCG AGTCTGCCGA
201 GCATGAGGAC GGTGTCGCGG CTGACTTTGC GCGGGTCGAT TTCGATGGAG
251 TATTCCGCCG TGGGGATTAA CTCGAAATGT TTGCGTATCA TCGGGAAGAC
301 ACGTTCGATC TGTTCTGTCG TCAAAAAGGt GCGTGCCcCCG CCGAAGTGCA
351 GTTGGGCAAG CTGGTGCCGT CCGTTCAGAT GTGGAGCGAG CAGTTCCATT
401 TCTTTTTCAA GATATTCGAT GTAGGCATCG GCGCGGCTTT TGTCTTTGGT
451 GATGATTTTG TTGCAGCCGC AGTAGTAGCA GATGGTGTG CAGAACGGAA
501 TGTGAATGTA AAGGGAAAGC GGTGTGTTTA A
```

This corresponds to the amino acid sequence <SEQ ID 784; ORF 221>:

```
m221.pep
1  MXVLMXRSLV RQAVNQIDAD GFEPFRFARRI DFFGFFVTL DAVDRRLHFG
51  VEILNADAH VEAESAHEH GVAADFARVD FDGVFAGGDX LEMFAYHAED
101 TFDLFVAQKG ACPAEVQLGK LVPSVQMWSE QFHFFFKIFD VGIGAAVFVG
151 DDFVAAAVVA DGVAERNVNV KGKRFV*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 221 shows 87.6% identity over a 170 aa overlap with a predicted ORF (ORF 221.ng) from *N. gonorrhoeae*:

```
m221/g221

          10      20      30      40      50
m221.pep      MXVLMXRSLVRQAVNQIDADGFEPFRFARRIDFFGFFVTLDAVDRRLHFGVE
                ||:||:| | | | | | | | | | | | | | | | | | | | | | | |
g221           MHDHGAMDRRLPAFGSLMRRAVNXIDADGFEPCLTGGIDDFFGFFVALDAVDCRLHFGVE
                10      20      30      40      50      60

          60      70      80      90      100     110
m221.pep      ILNADAHAVEAESAEHEDGVAADFARVDFDGVFAGGDXLEMFAYHAEDTFDLFVAQKGA-
                ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
g221           ILNADAHAVEAESAEHEDGVAADFARVDFDGI FAGRYQFEMFADHAEDTFDLFVAQKGRR
                70      80      90      100     110     120

          120     130     140     150     160     170
```

```

m221.pep      CPAEVQLGKLVPSVQMWSEQFHFFFKIFDVGIGAAVFVGDDFVAAAVVADGVAERNVNVK
               |||||||||||||||||||||||||||||||||||||||||||||:|||||
g221          AAAEVQLGKLVPSVQMWSEQFHFFFKIFDVGIGAAVFVGDDFVAAAVVADGVAKRNVNVK
               130      140      150      160      170      180

m221.pep      GKRFVX
               |||||
g221          GKRFVX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 785>:

```
a221.seq
1  ATGGTGGTTT  TGATGCTCCG  AAGTCTGGTG  CGGCAGGCCG  TAAATCAAAT
51  CGACGCTGAC  GGATTTGAAC  CCCGCTTCGC  GCGCCGCATC  GATGACTTCT
101 TTGGTTTCTT  CGTAACTTTG  GATGCGGTTG  ACCGCCGCCT  GCACTTTGGG
151  GTCGAAATCC  TGAATGCCGA  TGCTCATGCG  GTTGAAGCCG  AGTCTGCCGA
201  GCATGAGGAC  GGTGTCGCGG  CTGACTTTGC  CGGGTTCGAT  TTCGATGGAG
251  TATTCGCCGG  TGGGGATTAA  CTCGAAATGT  TTGCGTATCA  TCGGAAGAC
301  ACGTTCGATT  TGGTCGTCGC  TCAAAAAGGT  CGGCGTGCCG  CCGCCGAAGT
351  GCAGTTGGGC  AAGCTGGTGC  CGTCCGTTCA  GATGTGGAGC  GAGCAGTTCC
401  ATTTCTTTT  CAAGAAATTC  GATGTAGGCA  TCGGCGCGGC  TTTTGTCTTT
451  GGTGATGATT  TTGTTGCAGC  CGCAGTAGTA  CGGATGGTG  TTGCAGAACG
501  GAATGTGAAT  GTAAGGGGAA  AGCGGTTTGT  TTAA
```

This corresponds to the amino acid sequence <SEQ ID 786; ORF 221.a>:

a221.pap

1	MVVLMLRSLV	RQAVNQIDAD	GFEPRFARRI	DDFFGFFVTL	DAVDRRLHFG
51	VEILNADAH	VEAESAEHD	GVAADFARV	FDGVFAGGD*	LEMFAHYAED
101	TFDLVVAQKG	RRAAAEVQLG	KLVPVSQMW	EQHFFFFKKF	DVGIGAAAFV
151	GDDEFAAAV	ADGVAERNVN	VKGKRFV*		

m221/a221 95.5% identity in 177 aa overlap

		10	20	30	40	50	60
m221.pep		MXVLMXRSLVRQAVNQIDADGFEPFRARRIDDFGFFVTLDVDRRLHFGVEILNADAH					
a221		MVVLMLRSLVRQAVNQIDADGFEPFRARRIDDFGFFVTLDVDRRLHFGVEILNADAH					
		10	20	30	40	50	60
		70	80	90	100	110	119
m221.pep		VEAESAEHEDGVAADFARVDFDGVFAGGDYLEMFAYHAEDTDLFVAQKGA-CPAEVQLG					
a221		VEAESAEHEDGVAADFARVDFDGVFAGGDYLEMFAYHAEDTDLVVAQKGRRAAAEVQLG					
		70	80	90	100	110	120
	120	130	140	150	160	170	
m221.pep		KLVPSPQMWSEQFHFFFKIFDVGIGAAFFVGDDFVAAAVVADGVAERNVNVKGRFVX					
a221		KLVPSPQMWSEQFHFFFKIFDVGIGAAFFVGDDFVAAAVVADGVAERNVNVKGRFVX					
		130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEO ID 787>:

```
g223.seq
  1  atggaattca ggcaccaggt agtggtagtt ggtgtcgaac catttggtca
 51  ttccgatggc gaattgggtct ttgttgccgc gcgccaggttg gaagaattgt
101  tccaaaggca ggttttggct atcgaagccg aaacggggcgg gaatcgcgcc
151  cgtggatact tgcaggtcga ggatgtgatg gtagaaagtg aaatcacgta
201  cagcaacgta atcagcgcta ggagcagctt ggtgtttcca gtttttctcg
251  cgcaggtctt tggcaacgct gagcagctct tgttcactga tctctttgcg
301  ccagtatttt tcttgggcga atttcaattc acggaaggcg ccgacacgcy
351  qgaagctcga
```

This corresponds to the amino acid sequence <SEQ ID 788; ORF 223.ng>:

g223.pcp..

1 MEFRHQVVVV GVEPFGHFDG ELVFVAARQL EELFQRQVLA IEAETGGNRA
51 RGYLQVEDVM VESEITYSNV ISVRSSLVFP VFLAQVFGNV EQLLFTDLFA
101 PVFFLGEFQF TEGADTREAA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 789>:

```
m223.seq
1 GTGGAATTCA GGCACCAAGT AGTGGTAGTT GGTGTCGAAC CATTTGGTCA
51 TTTTCGATAGC GAATTTGGTCT TGTGTAACCG CAGCCAGTTG GAAGAATTGT
101 TCCAAAGACA GGTTTTGGCT GTCGAAGCCG AAGCGGGCGG GAAATCGCGC
151 GGTGGCGACT TGCAGGTCGA GGATGTGGTC GTAGAAAGTG AAATCsCTAC
201 GGCAACGAAA TCGGCGTTGG CAGCGACCTG GTGTTTCCAG TTTTCTCGC
251 GCAAGTCTTT AGCAACAGCC AGCAATTCTT GCTCGCTGAT TTCTTTGCGC
301 CAGTATTTT CTTGTGCGAA TTTCAATTCG CGGAAGGCGC CGACACGCGG
351 GAAGCCTGA
```

This corresponds to the amino acid sequence <SEQ ID 790; ORF 223>:

m223.pep

1	VEFRHQVVVV	GVEPFGHFDS	ELVFVTARQL	EELFQRQVLA	VEAEAGGNRA
51	GGDLQVEDVV	VESEIXYGNE	<u>IGVGSDLVFP</u>	<u>VFLAQVFSNS</u>	QQFLLDFFA
101	PVFFLCEFOF	AEGADTREA*			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 223 shows 80.7% identity over a 119 aa overlap with a predicted ORF (ORF 223.ng) from *N. gonorrhoeae*:

```
m223/g223
```

	10	20	30	40	50	60
m223.pep	VEFRHQVVVVGVEPFGHFDSELVFVTARQLEELFQRQVLAVEAEAGGNRAGGDLQVEDDV					
	: : : : : :					
g223	MEFRHQVVVVGVEPFGHFDGELVFVAARQLEELFQRQVLAIEAETGGNRARGYLQVEDVM					
	10	20	30	40	50	60

	70	80	90	100	110	120
m223.pep	VESEIXYGNEIGVGS DLVPVFLAQVFSNSQQFLLADFFAPVFFLCE FQFAEGADTREAX					
	: :					
g223	VESEITYSNVISVRSSLVFPVFLAQVFNVEQLLFDTLDFAPVFFLG EFQFT EGADTREAX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 791>:

a223.seq	1	51	101	151	201	251	301	351
	GTGGAATTC	GGCACCAAGT	AGTGGTAGTT	GGTGTCTGAAC	CATT	TGGTCA		
	TTTCGATAGC	GAATTGGTCT	TTGTTACCGC	GCGCCAGTTG	GAAGAATTGT			
	TCCAAAGATA	GGTTTTGGCT	CTCGAAGCCG	AAGCGGGCTG	GAATCGCGCC			
	GGTGGCGACT	TGCAGGTCGA	GGATGTGGTC	GTAGAAAGTG	GAATCGCCTA			
	CGGCAACGTA	ATCGGCGTTG	GCAGCGGCCT	GGTGTCTTCCA	GTTTTTCTCG			
	CGCAAGTCTT	TAGCAACAGC	CAGCAATTCT	TGCTCGCTGA	TTTCTTTGCG			
	CCAGTATTTT	TCTTGTGCGA	ATTTCAATTC	GCGGAAGGCA	CCGACACGCG			
	GGAAGCTTGA							

This corresponds to the amino acid sequence <SEQ ID 792; ORF 223.a>:

a223.pep

1	VEFRHQVWVV	GVEPFGHFDS	ELVFVTARQL	EELFQR*VLA	VEAEAGGNRA
51	GGDLQVEDVV	VESEIAYGNV	IGVGSGLVFP	<u>VFLAQVFSNS</u>	QQFLADFFA
101	PVFFLCEFQF	AEGTDTREA*			

m223/a223 95.8% identity in 119 aa overlap

	10	20	30	40	50	60
m223.pep	VEFRHQVVVVVGVEPFGHFDSELVVFVTARQLEELFQRQVLAVEAEAGGNRAGGDLQVEDVV					
a223	VEFRHQVVVVVGVEPFGHFDSELVVFVTARQLEELFQRQVLAVEAEAGGNRAGGDLQVEDVV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m223.pep	VESEIXYNEIGVGSDDLVPVFLAQVFSNSQQFLADFPVFFLCEFQFAEGADTREAX					
a223	VESEIAYGNVIGVSGSLVPVFLAQVFSNSQQFLADFPVFFLCEFQFAEGDTTREAX					

70 80 90 100 110 120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 793>:

```
g225.seq
1  atggattctt ttttcaaacc ggcagtttgg gcggttttgt ggctgatgtt
51  tgccgtccgc cccgcccttg ccgacgagtt gaccaacctg ctcagcagcc
101  gcgagcagat tctcagacag tttgccgaag acgaacagcc cgtttttacc
151  gtcaaccgag cccccgcccg gcgggcgggc aatgccgacg aactcatcgg
201  cggcgcgatg gggcttaacg aacagcccgt tgtacgcgtc aaccgagccn
251  ccgcccggcg ggcgggcaat gccgacaaac tcatcggcag cgcgatgcgg
301  cttttgggta ttgcctaccg ctacggcggc acatcgggtg ctaccgggtt
351  tgactgcagc ggattcatgc agcacatctt caaacgcgcc atgggcatca
401  acctgccgcg cacgtcggcg gaacaggcgc ggatgggcgc acccgttgcc
451  cgaagcgaat tgcagcccgg ggatatggtg tttttccgca cgctcggcgg
501  cagccgcatt tcccatgtcg gactttatat cggcaacaac cgcttcatcc
551  acgcgccgcg cacggggaaa aatatcgaaa tcaccagcct gagccacaaa
601  tattggagcg gcaaatatgc gttcggccgc cgggtcaaga aaaacgaccc
651  gtcacgcttt ctgaactga
```

This corresponds to the amino acid sequence <SEQ ID 794; ORF 225.ng>:

```
g225.pep
1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  VNRAPARRAG NADELIGGAM GLNEQPVVRV NRAXARRAGN ADKLIGSAMR
101  LLGIARYYGG TSVSTGFDCS GFMQHIFKRA MGINLPRTSA EQARMGAPVA
151  RSELQPGDMV FFRTLGGSR I SHVGLYIGNN RFIHAPRTGK NIEITSLSHK
201  YWSGKYAFAR RVKKNPDSRF LN*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 795>:

```
m225.seq (partial)
1  ..TTTCAAACC CGGCAGTTTG GCGGGTTTGG TGGCTGAWGT TTGCCGTCCG
51  CCCC GCCCTT GCCGACGAGT TGACCAACCT GCTCAGCAGC CGCGAGCAGA
101  TTCTCAGACA GTTGCCGAA GACGAACAGC CCGTTTTACC CATCAACCGA
151  GCCCCGCCCG GCGGGCGGG CAATGCCGAC GAACTCATCG GCAGCGCGAT
201  GGGGCTTAAC GAACAGCCCG TTTTACCGGT CAACCGAGTC CCGCCCCGGC
251  GGGCGGGCAA TGCCGACGAA CTCATCGGCA ACGCGATGGG GCTTAACGAA
301  CAGCCCGTTT TACCCGTCAA CCGAGCCCCC GCGCGCGGG CCGGCAATGC
351  CGACGAATC ATCGGCAACG CGATGGGACT TTTGGGTATT GCCTACCGCT
401  ACGGCGGCAC ATCGGTTTCT ACCGGTTTGG ACTGCAGCGG CTTTCATGCAG
451  CACATCTTCA AACCGGCCAT GGGCATCAAC CTGCCGCGCA CGTCGGCAGA
501  ACAGGCACGG ATGGGTACGC CGGTTGCCCG AAGCGAATTG CAGCCCGGAG
551  ATATGGTGTT TTCCGACAG CTCGGCGGCA GCCGCATTTC CCATGTGCGA
601  CTTTATATCG GCAACAACCG CTTTCATCCAC GCGCCGCGCA CGGGGAAAAA
651  TATCGAAATC ACCAGCCTGA GCCACAAATA TTGGAGCGGC AAATACGCGT
701  TCGCCCGCCG GGTCAGAAA AACGACCCGT CCCGCTTCT GAACGTA
```

This corresponds to the amino acid sequence <SEQ ID 796; ORF 225>:

```
m225.pep (partial)
1  ..FSNPAVWAVL WLXFAVRPAL ADELTNLLSS REQILRQFAE DEQVLPINR
51  APARRAGNAD ELIGSAMGLN EQVLPVNRV PARRAGNADE LIGNAMGLNE
101  QVLPVNRAP ARRAGNADEL IGNAMLLGI AYRYGGTSVS TGFDCSGFMQ
151  HIFKRAMGIN LPRTSAEQAR MGTPVARSEL QPGDMVFFRT LGGSRI SHVG
201  LYIGNNRFIH APRTGKNIEI TSLSHKYWSG KYAFARRVKK NDPSRFLN*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 225 shows 83.5% identity over a 248 aa overlap with a predicted ORF (ORF 225.ng) from *N. gonorrhoeae*:

```
m225/g225
10 20 30 40 50
m225.pep FSNPAVWAVLWLXFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG
| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g225 MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPVNRAPARRAG
```

510

	10	20	30	40	50	60
m225.pep	60	70	80	90	100	110
	NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA					
	: :					
g225	NADELIG-----			GAMGLNEQPVVRVNRAXARRAGNA		
				70	80	90
m225.pep	120	130	140	150	160	170
	DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR					
	: : : :					
g225	DKLIGSAMRLGLIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGAPVAR					
	100	110	120	130	140	150
m225.pep	180	190	200	210	220	230
	SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR					
g225	SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR					
	160	170	180	190	200	210
m225.pep	240	249				
	VKKNDPSRFLNX					
g225	VKKNDPSRFLN					
	220					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 797>:

```

a225.seq
1  ATGGATTCTT TTTTCAAACC GGCAGTTTGG GCGGTTTTGT GGCTGATGTT
51  TGCCGTCCGC CCCGCCCTTG CCGACGAGTT GACCAACCTG CTCAGCAGCC
101 GCGAGCAGAT TCTCAGACAG TTTGCCGAAG ACGAACAGCC CGTTTTACCC
151 ATCAACCGAN CCCCCGCCG GCGGGCGGGC AATGCCGACG AACTCATCGG
201 CAGCGCGATG GGGCTTAACG AACAGCCCGT TTTACCCGTC AACCGANTCC
251 CCGCCCGGCG GCGGGGCAAT GCCGACNAAC TCATCGGCAA CGCGATGGGG
301 CTTAACGAAC AGCCCGTTTT ACCCGTCAAC CGAGTCCCCG CCCGGCGGGC
351 GGGCAATGCC GACGAACCTA TCGGCAACGC GATGGGGCTT AACGAACAGC
401 CCGTTTTACC CGTCAACCGA GCGCCCGCCC GCGGGCGCGG CAATGCCGAC
451 GAACTCATCG GCAACGCGAT GGGACTTTTG GGTATTGCCT ACCGCTACGG
501 CGGCACATCG ATTTCTACCG GTTTTGACTG CAGCGGCTTC ATGCAGCACA
551 TCTTCAAACG CGCCATGGGC ATCAACCTGC CGCGCACGTC GGCAGAACAG
601 GCGCGGATGG GTACGCCGGT TGCCCGAAGC GAATTGCAGC CCGGGGATAT
651 GGTGTNTTTC CGCACGCTCG GCGGCAGCCG CATTTCCTCAT GTCGGACTTT
701 ATATCGGCAA CAACCGCTTC ATCCACGCGC CGCGCACGGG GAAAAATATC
751 GAAATACCA GCCTGAGCCA CAAATATTGG AGCGGCAAAT ACGCGTTCGC
801 CCGCCGGGTC AAGAAAAACG ACCCGTCCCG CTTTCTGAAC TGA

```

This corresponds to the amino acid sequence <SEQ ID 798; ORF 225.a>:

```

a225.pep
1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  INRXPARRAG NADELIGSAM GLNEQPVLPV NRXPARRAGN ADXLIGNAMG
101 LNEQPVLPVN RVPARRAGNA DELIGNAMGL NEQPVLPVNR APARRAGNAD
151 ELIGNAMGLL GIAYRYGGTS ISTGFDCSGF MQHIFKRAMG INLPRTSAEQ
201 ARMGTPVARS ELQPGDMVXF RTLGGSRISH VGLYIGNNRF IHAPRTGKNI
251 EITSLSHKYW SGKYAFARRV KKNNDPSRFLN *

```

m225/a225 87.4% identity in 277 aa overlap

	10	20	30	40	50
m225.pep	FSNPAVWAVLWLXFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG				
	: : :				
a225	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRXPARRAG				
	10	20	30	40	50
m225.pep	60	70	79	80	
	NADELIGSAMGLNEQPVLPVNR-----				VPARRAGNA

```

a225      |||||
          NADELIGSAMGLNEQPVLFPVNRXPARRAGNADXLIGNAMGLNEQPVLFPVNRVPARRAGNA
          70      80      90      100      110      120

m225.pep  90      100      110      120      130      140
          DELIGNAMGLNEQPVLFPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF
          |||||

a225      130      140      150      160      170      180
          DELIGNAMGLNEQPVLFPVNRAPARRAGNADDELIGNAMGLLGIAYRYGGTSISTGFDCSGF

m225.pep  150      160      170      180      190      200
          MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF
          |||||

a225      190      200      210      220      230      240
          MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFXFRTLGGSRISHVGLYIGNNRF

m225.pep  210      220      230      240      249
          IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDSRFLNX
          |||||

a225      250      260      270      280
          IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDSRFLNX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 799>:

g225-1.seq

```

1  atggattctt ttttcaaacc ggcagtttgg gcggttttgt ggctgatgtt
51  tgcggtccgc cccgcccttg cgcacgagtt gaccaacctg ctcagcagcc
101  gcgagcagat tctcagacag ttgcccgaag acgaacagcc cgttttacct
151  gtcaaccgag ccccgcccg ggcggcgggc aatgccgacg aactcatcgg
201  cggcgcgatg gggcttaacg aacagcccgt tgtacgcgtc aaccgagccn
251  cgcgccggcg ggcgggcaat gccgacaaac tcacggcag cgcgatgcgg
301  cttttgggta ttgctaccg ctacggcggc acatcggtgt ctaccggtt
351  tgactgcagc ggattcatgc agcacatctt caaacgcgcc atgggcatca
401  acctgccgcy cagctcggcg gaacaggcgc ggatgggcgc acccggtgcc
451  cgaagcgaaat tgcagcccg ggatatggtg tttttccgca cgctcggcgg
501  cagccgcatt tcccatgtcg gactttatat cggcaacaac cgcttcatec
551  acgcgcgcgc cagggggaaa aatatcgaaa tcaccagcct gagccacaaa
601  tattggagcg gcaaatatgc gttcgccgc cgggtcaaga aaaacgaccc
651  gtcacgcttt ctgaactga

```

This corresponds to the amino acid sequence <SEQ ID 800; ORF 225-1.ng>:

g225-1.pep

```

1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  VNRAARRAG NADELIGGAM GLNEQPVVRV NRAKARRAGN ADKLIGSAMR
101  LLGIAYRYGG TSVSTGFDCS GFMQHIFKRA MGINLPRTSA EQARMGAPVA
151  RSELQPGDMV FFRTLGGSR I SHVGLYIGNN RFIHAPRTGK NIEITSLSHK
201  YWSGKYAFAR RVKKNDSRFL LN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 801>:

m225-1.seq

```

1  ATGGATTCTT TTTTCAAACC GGCAGTTTGG GCGGTTTTGT GGCTGATGTT
51  TGCCGTCCGC CCGGCCCTTG CCGACGAGTT GACCAACyTG CTCAGCAGCC
101  GCGAGCAGAT TCTCAGACAG TTGCCCAGAG ACGAACAGCC CGTTTTACCC
151  ATCAACCGAG CCCCCGCCG GCGGGCGGGC AATGCCGACG AACTCATCGG
201  CAGCGCGATG GGGCTTAACG AACAGCCCGT TTTACCCGTC AACCGAGTCC
251  CCGCCCGGCG GCGGGGCAAT GCCGACGAAC TCATCGGCAA CGCGATGGGG
301  CTTAACGAAC AGCCCCGTTT ACCCGTCAAC CGAGCCCCCG CCCGGCGGGC
351  GGGCAATGCC GACGAACCTA TCGGCAACGC GATGGGACTT TTGGGTATTG
401  CCTACCGCTA CGGCGGCACA TCGGTTTCTA CCGGTTTTGA CTGCAGCGGC
451  TTCATGCAGC ACATCTTCAA ACGCGCCATG GGCATCAACC TGCCGCGCAC
501  GTCGGCAGAA CAGGCACGGA TGGGTACGCC GGTGCGCCGA AGCGAATTGC
551  AGCCCGGAGA TATGGTGT TTCCGCACGC TCGGCGGCAG CCGCATTTC
601  CATGTCGGAC TTTATATCGG CAACAACCGC TTCATCCACG CGCCGCGCAC
651  GGGGAAAAAT ATCGAAATCA CCAGCCTGAG CCACAAATAT TGGAGCGGCA
701  AATACGCGTT CGCCCGCCGG GTCAAGAAAA ACGACCCGTC CCCTTTCTG
751  AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 802; ORF 217>:

m225-1.pep

```

1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  INRAPARRAG NADELIGSAM GLNEQPVLPV NRVPARRAGN ADELIGNAMG
101 LNEQPVLPVN RAPARRAGNA DELIGNAMGL LGIAYRYGGT SVSTGFDCSG
151 FMQHIFKRAM GINLPRTSAE QARMGTPVAR SELQPGDMVF FRTLGGSRIS
201 HVGLYIGNNR FIHAPRTGKN IEITSLSHKY WSGKYAFARR VKKNDPSRFL
251 N*

```

m225-1/g225-1 84.9% identity in 251 aa overlap

```

              10      20      30      40      50      60
m225-1.pep  MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
              |||||
g225-1      MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPVNRAPARRAG
              10      20      30      40      50      60

              70      80      90      100     110     120
m225-1.pep  NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
              |||||
g225-1      NADE-----LIGGAMGLNEQPVVRVNRAXARRAGNA
                      70      80      90

              130     140     150     160     170     180
m225-1.pep  DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
              |||||
g225-1      DKLIGSAMRLGLIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGAPVAR
              100     110     120     130     140     150

              190     200     210     220     230     240
m225-1.pep  SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
              |||||
g225-1      SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
              160     170     180     190     200     210

              250
m225-1.pep  VKKNDPSRFLNX
              |||||
g225-1      VKKNDPSRFLNX
              220

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 803>:

a225-1.seq

```

1  ATGGATTCTT TTTCAAACC GGCAGTTTGG GCGGTTTTGT GGCTGATGTT
51  TGCCGTCGCG CCCGCCCTTG CCGACGAGTT GACCAACCTG CTCAGCAGCC
101 GCGAGCAGAT TCTCAGACAG TTTGCCGAAG ACGAACAGCC CGTTTTACCC
151 ATCAACCGAN CCCCCGCCCG GCGGCGGGC AATGCCGACG AACTCATCGG
201 CAGCGCGATG GGGCTTAACG AACAGCCCGT TTTACCCGTC AACCGANTCC
251 CCGCCCGGCG GCGGGGCAAT GCCGACNAAC TCATCGGCAA CGCGATGGGG
301 CTTAACGAAC AGCCCGTTTT ACCCGTCAAC CGAGTCCCCG CCCGGCGGGC
351 GGGCAATGCC GACGAACCTA TCGGCAACGC GATGGGGCTT AACGAACAGC
401 CCGTTTTACC CGTCAACCGA GCGCCCGCCC GCGGGCGGGG CAATGCCGAC
451 GAACTCATCG GCAACGCGAT GGGACTTTTG GGTATTGCCT ACCGCTACGG
501 CGGCACATCG ATTTCTACCG GTTTGACTG CAGCGGCTTC ATGCAGCACA
551 TCTTCAAACG CGCCATGGGC ATCAACCTGC CGCGCACGTC GGCAGAACAG
601 GCGCGGATGG GTACGCCGGT TGCCCGAAGC GAATTGCAGC CCGGGGATAT
651 GGTGTNTTTC CGCACGCTCG GCGGCAGCCG CATTTCCCAT GTCGGACTTT
701 ATATCGGCAA CAACCGCTTC ATCCACGCGC CGCGCACGGG GAAAAATATC
751 GAAATCACCA GCCTGAGCCA CAAATATTGG AGCGGCAAAT ACGCGTTCGC
801 CCGCCGGGTC AAGAAAAACG ACCCGTCCCG CTTTCTGAAC TGA

```

This corresponds to the amino acid sequence <SEQ ID 804; ORF 225-1.a>:

a225-1.pep

```

1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  INRXPARRAG NADELIGSAM GLNEQPVLPV NRXPARRAGN ADXLIGNAMG
101 LNEQPVLPVN RVPARRAGNA DELIGNAMGL NEQPVLPVNR APARRAGNAD
151 ELIGNAMGLL GIAYRYGGTS ISTGFDCSGF MQHIFKRAMG INLPRTSAEQ
201 ARMGTPVARS ELQPGDMVXF RTLGGSRISH VGLYIGNNRF IHAPRTGKNI
251 EITSLSHKYW SGKYAFARRV KKNDDPSRFLN *

```

a225-1/m225-1 88.6% identity in 280 aa overlap

```

      10      20      30      40      50      60
a225-1.pep MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRXPARRAG
|||||
m225-1      MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
      10      20      30      40      50      60

      70      80      90     100     110     120
a225-1.pep NADELIGSAMGLNEQPVLPVNRXPARRAGNADXLIGNAMGLNEQPVLPVNRVPARRAGNA
|||||
m225-1      NADELIGSAMGLNEQ-----VLEPVNRVPARRAGNA
      70                                80      90

      130     140     150     160     170     180
a225-1.pep DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSISTGFDCSGF
|||||
m225-1      DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF
      100     110     120     130     140     150

      190     200     210     220     230     240
a225-1.pep MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVXFRTLGGSRISHVGLYIGNNRF
|||||
m225-1      MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF
      160     170     180     190     200     210

      250     260     270     280
a225-1.pep IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDP SRFLNX
|||||
m225-1      IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDP SRFLNX
      220     230     240     250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 805>:

g226.seq

```

1   ATGAGCGAAA TCCTCAGGCA GCCCAGCGTT CTGCTTTTCC TCACGCTTGC
51  CGTGTACGCG CTTGCGATTA TCGTGCGCAC GCGCACGGGC AATATCTTCT
101 GCAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC
151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAAT TCATTGATTT
201 TCGGCTGAAA cccGccgtCG TCGTGCTTGC CGTGCCGCTC TACCAAAACC
251 GCCGTAAAT CTTCAACCAG TGGCTGCCCC TCATCGTTTC GCAGCTTGCG
301 GGCAGCGTTA cggGCATTGT tacggggATG TATTTTgccg cttggctcgg
351 gccggatacc caattctcct tccgcctcgt tcttcaatat ctgttattta
401 caccctctgg aatcccaatt cacaccctgt atgcgcgggt tctcccgcca
451 tttctgttgc ctccgcctct cctgccgcgc ctccggccgc atacattcgg
501 ccggttcaca atacttccaa aaaaactacg gccgtttaag cccctcctcc
551 cagtggtggt cctttctcct Ccgggcctcg cccctcccct cttataa

```

This corresponds to the amino acid sequence <SEQ ID 806; ORF 226.ng>:

g226.pep

```

1   MSEILRQPSV LLFLTLAVYA LAIIVRTRTG NIFCNPVLSV TIVLIAYLKI
51  LGIDYAVYHN AAQFIDFRLK PAVVVLAVPL YQNRKIFNQ WLPVIVSOLA
101 GSVTGIVTGM YFAAWLGPD TQFSFPRLQY LLFTPSGIPI HTLYARVLPP
151 FLLPPPLLPR LGPHTLRRFT ILPKKLPRFK PLLPVVVLSP PGLAPPLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 807>:

m226.seq

```

1   ATGAACGAAA TCCTCAGGCA GCCCAGCGTT CTGCTTTTCC TCACGCTTGC
51  CGTGTACGCG CTTGCGATTA TCGTGCGCAC GCGCACGGGC AATATCTTCT
101 GCAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC
151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAAT TCATTGATTT
201 TTGGCTGAAA CCCGCCGTCG TCGTGCTTGC CGTGCCGCTC TACCAAAACC
251 GCCGTAAAT CTTCAACCAG TGGCTGCCCC TCATCGTTTC ACAGCTTGCG
301 GGCAGCGTTA CGGCATTGT TACAGGATG TATTTTGCCA AATGGCTGGG
351 CGCGGAACGC GAAGTCGTCC TCTCGCTCGC GTCCAAATCT GTTACCAACC
401 CCATCGCTAT TGAAATCACC CGCTCCATCG GCGGCATTCC CGCCATTACC
451 GCCGCCACCG TCATCATTGC CGGTCTGGTC GGACAGATTG CCGGTTACAA

```

501 AATGCTGAAG AACACGGTCG TCATGCCCTC GTCCGTGGGT ATGTCGCTCG
 551 GCACGGCTTC GCACGCGATG GGGATTGCCG CCTCGCTCGA ACGCAGCCGC
 601 CGTATGGCGG CATAACGCGG GCTGGGGCTG ACGTTCAACG GCGTACTGAC
 651 CGCGCTGATT GCGCCGCTGC TCATCCCCGT TTTGGGATTT TGA

This corresponds to the amino acid sequence <SEQ ID 808; ORF 226>:

m226.pep
 1 MNEILROPSV LLFLTLAVYA LAIIVRTRTG NIFCNPVLVS TIVLIAYLKI
 51 LGIDYAVYHN AAQFIDFWLK PAVVVLAVPL YQNRKIFNQ WLPVIVSOLA
 101 GSVTGIIVTGM YFAKWLGAER EVVLSLASKS VTNPIAIEIT RSIGGIPAIT
 151 AATVIIAGLV GQIAGYKMLK NTVVMPSSVG MSLGTASHAM GIAASLERSR
 201 RMAAYAGLGL TFNGVLTALI APLLIPVLGF *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 226 shows 94.2% identity over a 121 aa overlap with a predicted ORF (ORF 226.ng) from *N. gonorrhoeae*:

m226/g226

m226.pep	10	20	30	40	50	60
	MNEILRQPSVLLFLTLAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKILGIDYAVYHN					
g226	MSEILRQPSVLLFLTLAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKILGIDYAVYHN					
	10	20	30	40	50	60
m226.pep	70	80	90	100	110	120
	AAQFIDFWLKPAVVVLAVPLYQNRKIFNQWLPVIVSOLAGSVTGIIVTGM YFAKWLGAER					
g226	AAQFIDFRLKPAVVVLAVPLYQNRKIFNQWLPVIVSOLAGSVTGIIVTGM YFAAWLGPDT					
	70	80	90	100	110	120
m226.pep	130	140	150	160	170	180
	EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVVMPSSVG					
g226	QFSFPPRLQYLLFTPSGIPHTLYARVLPFPPLPRLPGLPHTLRRFTILPKKLRFK					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 809>:

a226.seq
 1 ATGAACGAAA TCCTCAGGCA GCCGAGCATC CTGCTTTTCC TCACGCTTGC
 51 CGTGACGCG CTTGCGATTA TCGTGCGCAC GCGCACGGGT AATATCTTCT
 101 GCAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC
 151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAGT TTATCGATTT
 201 CTGGCTCAAG CCCGCCGTCG TCGTGCTTGC CGTGCCGCTC TACCAAAACC
 251 GCCGTAAAAT CTTCAACCAA TGGCTGCCCG TCATCGTTTC GCAGCTTGGC
 301 GGCAGCGTTA CGGGCATTGT TACGGGGATG TATTTTGCCA AATGGCTGGG
 351 CGCGGAACGC GAAGTCGTCC TCTCGCTCGC GTCAAATCT GTTACCAATC
 401 CTATCGCCAT CGAAATCACC CGCTCCATCG GCGGCATTCC CGCCATTACC
 451 GCCGCCACCG TCATCATTGC CGGCCTGGTC GGACAGATTG CCGGTTACAA
 501 AATGTTGAAA AACACGGTCG TTATGCCCTC ATCTGTCGGA ATGTCGCTCG
 551 GCACGGCTTC GCACGCGATG GGCATTGCCG CCTCGCTCGA ACGCAGCCGC
 601 CGCATGGCGG CATAACGCGG GCTGGGGCTG ACGTTCAACG GCGTACTGAC
 651 CGCGCTGATT GCGCCGCTGC TTATCCCCGT TTTGGGATTT TGA

This corresponds to the amino acid sequence <SEQ ID 810; ORF 226.a>:

a226.pep
 1 MNEILROPSI LLFLTLAVYA LAIIVRTRTG NIFCNPVLVS TIVLIAYLKI
 51 LGIDYAVYHN AAQFIDFWLK PAVVVLAVPL YQNRKIFNQ WLPVIVSOLA
 101 GSVTGIIVTGM YFAKWLGAER EVVLSLASKS VTNPIAIEIT RSIGGIPAIT
 151 AATVIIAGLV GQIAGYKMLK NTVVMPSSVG MSLGTASHAM GIAASLERSR
 201 RMAAYAGLGL TFNGVLTALI APLLIPVLGF *

m226/a226 99.6% identity in 230 aa overlap

10 20 30 40 50 60

```

m226.pep  MNEILRQPSVLLFLT LAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKILGIDYAVYHN
|||||:|||||
a226      MNEILRQPSILLFLT LAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKILGIDYAVYHN
          10      20      30      40      50      60

          70      80      90      100     110     120
m226.pep  AAQFIDFWLKPAVVVLAVPLYQNRRIKIFNQWLPVIVSQLAGSVTGIVTGMYFAKWLGAER
|||||:|||||
a226      AAQFIDFWLKPAVVVLAVPLYQNRRIKIFNQWLPVIVSQLAGSVTGIVTGMYFAKWLGAER
          70      80      90      100     110     120

          130     140     150     160     170     180
m226.pep  EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVVMPSVSG
|||||:|||||
a226      EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVVMPSVSG
          130     140     150     160     170     180

          190     200     210     220     230
m226.pep  MSLGTASHAMGIAASLERSRRMAAYAGLGLTFNGVLTALIAPLLIPVLGFX
|||||:|||||
a226      MSLGTASHAMGIAASLERSRRMAAYAGLGLTFNGVLTALIAPLLIPVLGFX
          190     200     210     220     230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 811>:

```

g227.seq
1  atgaacatca tccgcgcgct cctcatcatc ctcggctgcc tcgccgccgg
51  cgaaaccgcc gttttcctag caggcatcaa actgcccgcc agcatcgctcg
101 gcatgggcgt gctgtttgct cttttgcagg cgggttggt caaaacgtct
151 tggctgcaac agcttaccga cgcgctgatg gcaaacctga cgctgttcct
201 cgtgccgccc tgcgtggcgg tcatcagcta ttgggatttg attgccgacg
251 attggttttc gatactggtt tccgcctccg ccagcacttt gtgcgtactg
301 ctggttacgg gcaaggttca ccgctggata cggagcatta tctga

```

This corresponds to the amino acid sequence <SEQ ID 812; ORF 227.ng>:

```

g227.pep
1  MNIIRALLII LGCLAAGETA VFLAGIKLPG SIVGMGVLF LLQAGWLKTS
51  WLQQLTDALM ANLTLFLVPP CVAVISYLDL IADDWF SILV SASASTLCVL
101 LVTGKVHRWI RSII*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 813>:

```

m227.seq (partial)
1  ..ACGTCTTkgc TGCAACAGCT TACCGACGCG CTGATGTCGA ACCTGACGCT
51  GTtCCTCGTG CCgCC.TGCG TGGCGGTCAT CAGCTATTTG GATTTGATTG
101 CCGACGATTG GTTTTCGATA CTGGTTTCCG CCTCCGCCAG cACTTTGTGC
151 GTAGTGCTGG TTACGGGCAA AGTCCACCGG TGGATACGGG GTATTATCCG
201 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 814; ORF 227>:

```

m227.pep (partial)
1  ..TSXLQQLTDA LMSNLTFLV PPCVAVISYL DLIADDWFSI LVSASASTLC
51  VLLVTGKVHR WIRGIIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 227 shows 95.5% identity over a 66 aa overlap with a predicted ORF (ORF 227.ng) from *N. gonorrhoeae*:

```

m227/g227

          10      20      30
m227.pep  TSXLQQLTDALMSNLTFLVPPCVAVISYL
          ||      ||      ||
g227      TAVFLAGIKLPGSIVGMGVLFALLQAGWLKTSWLQQLTDALMANLTLFLVPPCVAVISYL
          20      30      40      50      60      70

          40      50      60

```

516

```

m227.pep  DLIADDWFSILVSASASTLCVLLVTGKVHRWIRGIIRX
           |||||||||||||||||||||:||||
g227      DLIADDWFSILVSASASTLCVLLVTGKVHRWIRSIIX
           80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 815>:

```

a227.seq
1  ATGAACATCA TCCGCGCGCT CCTCATCATC CTCGGCTGCC TCGCCACCGG
51 CGAAACCGCC GTTTTCCTAG CAGGCATCAA ACTGCCCGGC AGCATCGTCG
101 GCATGGGCGT ACTGTTTTCG CTTTTCGAGG CGGGTTGGGT CAAAACGTCT
151 TGGCTGCAAC AGCTTACCGA CGCGCTGATG GCGAATCTGA CGTTGTTTCT
201 CGTGCCGCCG TGCCTGGCGG TCATCAGCTA TTTGGATTG ATTGCCGACG
251 ATTGGTTTTC GATACTGGTT TCCGCCTCCG CCAGCACTTT GTGCGTACTG
301 CTGTTTACAG GCAAGTTTCA CCGCTGGATA CGGAGCATT TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 816; ORF 227.a>:

```

a227.pep
1  MNIIRALLII LGCLATGETA VFLAGIKLPG SIVGMGVLEA LLOAGWVKTS
51 WLQQLTDALM ANLTLFLVPP CVAVISYLDL IADDWFSILV SASASTLCVL
101 LVTGKVHRWI RSII*

```

m227/a227 95.5% identity in 66 aa overlap

```

m227.pep                                     10      20      30
                                           TSXLQQLTDALMSNLTFLVPPCVAVISYL
a227      TAVFLAGIKLPGSIVGMGVLFALLQAGWVKTSWLQQLTDALMANLTLFLVPPCVAVISYL
           20      30      40      50      60      70

m227.pep           40      50      60
           DLIADDWFSILVSASASTLCVLLVTGKVHRWIRGIIRX
           |||||||||||||||||||||:||||
a227      DLIADDWFSILVSASASTLCVLLVTGKVHRWIRSIIX
           80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 817>:

```

m228.seq
1  ATGAAAAAAT TATTGATTGC CGCAATGATG GCGGCTGCCT TGGCAGCTTG
51 TTCGCAAGAA GCCAAACAGG AGGTTAAGGA AGCGGTTCAA GCCGTTGAGT
101 CCGATGTTAA AGACACTGCG GCTTCTGCCG CCGAGTCTGC CGCTTCTGCC
151 GTCGAAGAAG CGAAAGACCA AGTCAAAGAT GCTGCGGCTG ATGCAAAGGC
201 AAGTGCCGAG GAAGCTGTAA CTGAAGCCAA AGAAGCTGTA ACTGAAGCAG
251 CTAAAGATAC TTTGAACAAA GCTGCCGACG CGACTCAGGA AGCGGCAGAC
301 AAAATGAAAG ATGCCGCCAA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 818; ORF 228>:

```

m228.pep
1  MKKLLIAAMM AAALAACSQE AKQEVKEAVQ AVESDVKDTA ASAAESAASA
51 VEEAKDQVKD AAADAKASAE EAVTEAKEAV TEAAKDTLTK AADATQEAAD
101 KMKDAAK*

```

Computer analysis of this amino acid sequence gave the following results:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 819>:

```

a228.seq
1  ATGAAAAAAT TATTGATTGC CGCAATGATG GCGGCTGCCT TGGCAGCTTG
51 TTCGCAAGAA GCCAAACAGG AGGTTAAGGA AGCGGTTCAA GCCGTTGAGT
101 CCGATGTTAA AGACACTGCG GCTTCTGCCG CCGAGTCTGC CGCTTCTGCC
151 GTCGAAGAAG CGAAAGACCA AGTCAAAGAT GCTGCGGCTG ATGCAAAGGC
201 AAGTGCCGAG GAAGCTGTAA CTGAAGCCAA AGAAGCTGTA ACTGAAGCAG
251 CTAAAGATAC TTTGAACAAA GCTGCCGACG CGACTCAGGA AGCGGCAGAC
301 AAAATGAAAG ATGCCGCCAA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 820; ORF 228.a>:

a228.pep
 1 MKKLLIAAMM AAALAACSQE AKQEVKEAVQ AVESDVKDTA ASAAESAASA
 51 VEEAKDQVKD AAADAKASAE EAVTEAKEAV TEAAKDTLNK AADATQEAAD
 101 KMKDAAK*

m228/a228 100.0% identity in 107 aa overlap

	10	20	30	40	50	60
m228.pep	MKKLLIAAMMAAALAACSQEAKQEVKEAVQAVESDVKDTAASAAESAASAVEEAKDQVKD					
a228	MKKLLIAAMMAAALAACSQEAKQEVKEAVQAVESDVKDTAASAAESAASAVEEAKDQVKD					
	10	20	30	40	50	60
	70	80	90	100		
m228.pep	AAADAKASAEAVTEAKEAVTEAAKDTLNKAADATQEAADKMKDAAKX					
a228	AAADAKASAEAVTEAKEAVTEAAKDTLNKAADATQEAADKMKDAAKX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 821>:

g229.seq
 1 atggctgccg tatcgggcgg cggcgcggtc ttcctgataa tgcttcacaca
 51 tattgcccgc gttagcggtc agccgccagc gttagcccaa gcgtcgggag
 101 aaatcgccat tgaagccgcc ggcgaaattg tatcggtgct cgcccaagag
 151 gttttgcccg acaaacggca cggcgccgaa cgagcgcggt accgaacggt
 201 tttgatggcc gaacgacagg cgcaggttct gttagctgaa atctttgtta
 251 tcccaataat gcacgccgcg gctgatgccg ccgtagagga aatgatgccc
 301 gcccgcattg atttcgcgcg acacgcccga gccgtagcgc aaaccgtgtg
 351 ccttttgccg caggctgtcg gcggttttcg tccagcttct gcccgcaaat
 401 tcaatcggtt tttcgacga agcgtgtgtt atagcggatt aacaaaaatc
 451 aggacaaggc ggcgggcccgc aggcagtacg gatggtacgg aaccggttcg
 501 cccggtgctt ggacgcctta gggaaccgtt ccctttgagc cggggcgggg
 551 caaccggtac cgggttttgt tcatccgccca tattgtgttg a

This corresponds to the amino acid sequence <SEQ ID 822; ORF 229.ng>:

g229.pep
 1 MAAVSGGGAV FLIMLPHIAR VQROPFAFAQ ASGEIGIEAA GEIVSAAAOE
 51 VLPDKRHGAE RARYRTVLM AERQAQVFAE IFVIPIMHAA ADAAVEEMMP
 101 ARIDFARHAQ AVAQTVCLLR QAVGGFRPAS ARKFNRFGR SVVYSGLTGI
 151 RTRRRAAGST DGTEPVRPVL GRLREPFPLS RGGATRTGFC SSAILC*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 823>:

m229.seq (partial)
 1 ..GCTCAAGCGT TGGGAGAAAT CGGCATTGAA GCCGCCGACG AAATTGTATC
 51 GGCTGCCGCC TAAGAGGTTT TGCTCGACAA ACGGCACGAT GCCGAACGAG
 101 CGCGTTACCG AACGGTTTTT ATAGCCGAAC GACAGGCGCA GGCTCTGTTC
 151 GCTGAAATCT TTGTTATCCC AATAATGCAC GCCGCCGCCG CTGATGCCGC
 201 CGTAGAGGAA ATGATGCCTG CCCGCATTGA TTTCGCGCGA CACGCCTAAG
 251 CCCTAGCGCA AACCGTGTGC CTTTTCGCGC AGGCTGTCGG CGGTTTTCGT
 301 CCAGCTTCTG CCGCAAATT CAATCGTTTT TTCGGACGAA GCGTTGTTTA
 351 TAGCGGATTA ACAAAAATCA GGACAAGGCA ACGAAGCCGC AGACAGTACA
 401 AATAGTACGG AACCGATTCA CTGGGTGCTT CAGCACcTTA GAGAATCGTT
 451 CTCTTTTTTG TTCATCCGCT ATATTGTGTT GA

This corresponds to the amino acid sequence <SEQ ID 824; ORF 229>:

m229.pep (partial)
 1 ..AQALGEIGIE AADEIVSAAA XEVLLDKRHD AERARYRTVF IAERQAQALF
 51 AEIFVIPIMH AAAADA AVEE MPPARIDFAR HAXALAQTVC LLRQAVGGFR
 101 PASARKFNRF FGRSVVYSGL TKIRTRQRSA DSTNSTEPIH LVLQHLRESR
 151 SLFCSSAILC *

Computer analysis of this amino acid sequence gave the following results:

m229/g209

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 825>:

This corresponds to the amino acid sequence <SEQ ID 826; ORF 229.a>:

m229/a229 85.6% identity in 167 aa overlap

BNSDOCID: <WO_8957280A2 | >

```

          100      110      120      130      140      149
m229.pep  RQAVGGFRPASARKFNRRFFGRSVVYSGLTKIRTRQRSADSTNSTEPIHLVLQHLRES---
          |||||  |||||  |||||  |||||  |||||  |||||
a229      RQAVGGFRPASACKFNRRFFGRSVVYSGLTKIRTRRSADSTDSTEPIHLVLQHLRESSLX
          130      140      150      160      170      180

          150      160
m229.pep  -----RSLFCSSAILCX
          |: ||||:|
a229      AKARQRRTGFCSSSTI
          190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 827>:

```
g230.seq
1 atgttccatt ccatcgaaaa atacagaaca cccgcccaag tcttattagg
51 cctgattgca ttaacttttg tcggtctcgg cgtcagcacg gtttcccatc
101 cgggcgcgca ctacatcgtc caagtgggcg acgaaaaaat cagcgagcac
151 tcaatcaaca acgccatgca gaacgagcag gcgcgacggc gcagcccttg
201 gcgcgacgcg gtgttccaat cctgtctgca acgcgccttac ctgaaccagg
251 gcgcgaagct gatgggcatt tcggtttctt ccgaacaaat caagcagatg
301 attgtggacg atcccaattt ccacgacgca aacggcaaat tcagtacgcg
351 gcttttgagt caatacctgt cgcaacgcca tatgtctgaa gaccagtttg
401 tcgaagaaat ccgcgatcag tttgccttgc agaattttgg taaacctcgtc
451 caaaacggcg tattggtcgg cgacgcgcag gcggaacagc tgatcagggt
501 gacgcaggtc aaccgcacca tccgttcgca cactttcaac cccgacgagt
551 tcatcgccca agtcaaagcg tctgaagccg atttgcagaa attttataat
601 gcgaacaaaa aagactatct gctgccgcag gcggtcaaat tggaaatatgt
651 cgccttgaat ctgaaggatt ttgcagacaa gcagaccgtc agtgaaacgg
701 aagtgaaaaa tgcgtttgaa gagcgcgtgg cgcgtttgcc ggcacatgaa
751 gccaaacctt ctttcgagca ggaaaaagcc gccgtcgaaa acgaattgaa
801 aatgaaaaag gcggttgccg acttcaacaa ggcaaaaaga aagctgggcg
851 acgatgcgtt caatcatccc tcctcgcttg ccgaagccgc aaaaaacagc
901 ggtttgaaag tggaaaccca agaaaacttg ctgagcaggc aggacgcaca
951 aatgtccggc atgcccgaaa acctaatcaa tgccgtattc agcgacgacg
1001 tattgaagaa aaaacacaaat tccgaagtgc tgaccatcaa cagcgaaacc
1051 gcgtgggtcg tccgcgccaat agaagtcctgc gaagaaaaaa acctactggt
1101 tgaagaagcc aaagatgcgg tgcgtcaggc ctatatccgt accgaagccg
1151 caaaactttt gaaaacaatg taa
```

This corresponds to the amino acid sequence <SEQ ID 828; ORF 230.ng>:

g230.pap

1	<u>MFHSIEKYRT</u>	<u>PAQVLLGLIA</u>	<u>LTFVGFVST</u>	<u>VSHPGADYIV</u>	<u>QVGDEKISEH</u>
51	SINNAMQNEQ	ADGGSPWRDA	VFQSLQRAY	LKQGAQLMGI	SVSSEQIKQM
101	IVDDPNFHDA	NGKFSHALLS	QYLSQRHMSE	DQFVEEIRDQ	FALQNLVSLV
151	QNGVLVGDAQ	AEQLIRLTQV	NRTIRSHTFN	PDEFIAQVKA	SEADLQKFYN
201	ANKKDYLLPQ	AVKLEYVALN	LKDFADKQTV	SETEVKNAFE	ERVARLPAHE
251	AKPSFEQEKA	AVENELMKKK	AVADFNKAKE	KLGDADFNNP	SSLAEAAKNS
301	GLKVETQETW	LSRQDAQMSG	MPENLINAVF	SDDVLKKKHN	SEVLTTINSET
351	AWVVRAKEVR	EEKNLLFEEA	KDAVROAYIR	TEAAKLLKTM	*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 829>:

```
m230.seq (partial)
1 ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCAAG TCCTTTTGGG
51 CCTGATTGCA TTAACCTTCG TCGGCTTCGG GGTGAGCACG GTATCCCATC
101 CGGGTGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAaT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201 GCc.GACGCG GTGTTCCAAT CCCTGCTGCA ACGCGCCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTTCT CCGAACAAAT CAAGCAAATT
301 ATCGTGAGAC ATCCCAATTT CCACGACGCA AACGGCAAAT TCGACCACGC
351 GCTTTTAAAC CGTACCTTT CCCAACGCCA TATGTCTGAA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTTGGT AAACCTCGTC
```

```

451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACACAGGTC AACCGCACCA TCCGTTTCGA CACTTTCAAC CCCGACGAGT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA ATTTTATAAT
601 GCGAACAAAA AAGACTATCT GCTGCCGCGAG GCGGTCAAAT TGGAATATGT
651 CGCCTTGAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAACGg
701 AAGTGAAAAA TGCATTTGAA GAGCGCGTGG CGCGTTTGCC GGCAAATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAAAAGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAACAA GGCAAAGAA AAATTGGGCG
851 ACGATGC.GT CAACCATCCT TCyTCGCTTG CCGAAGCCGC CAAAAACAGC
901 GGTTCGAAAAG TCGAAACCCA AGAACTTGG CTGAGTAGGC AGGACGCGCA
951 AATGTCCGGT ATGCCCGAAA ACCTGATCAA TGCCGTATTG AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCG TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCCTGCCGTT
1101 TGCCGAAGCC AAAGACGCGG TACGTCAGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACCTT...

```

This corresponds to the amino acid sequence <SEQ ID 830; ORF 230>:

```

m230.pep (partial)
1 MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
51 SINNAIQNEQ ADGGGSPSDA VFQSLQRAY LKQGAQMGI SVSSEIQKI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHMSE DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELMKK AVADFNKAKE KLGDVAVNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLTINSET
351 AWVVRKEVR EEKTLPFMEA KDAVRQAYIR TEAAKL...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 230 shows 95.9% identity over a 386 aa overlap with a predicted ORF (ORF 230.ng) from *N. gonorrhoeae*:

```

m230/g230

      10      20      30      40      50      60
m230.pep MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ
          |||||
g230      MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISEHSINNAMQNEQ
          |||||

      10      20      30      40      50      60
m230.pep ADGGGSPSDAVFQSLQRAYLKQGAQMGI SVSSEIQKI IVDDPNFHDA NGKFDHALLN
          |||||
g230      ADGGSPWRDAVFQSLQRAYLKQGAQMGI SVSSEIQKMI VDDPNFHDA NGKFSHALLS
          |||||

      70      80      90      100     110     120
m230.pep RYLSQRHMSEDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRTIRSHTFN
          |||||
g230      QYLSQRHMSEDQFVEEIRDQFALQNLVSLVQNGVLVGDAQAEQLIRLTQVNRTIRSHTFN
          |||||

      130     140     150     160     170     180
m230.pep :|||||
g230      QYLSQRHMSEDQFVEEIRDQFALQNLVSLVQNGVLVGDAQAEQLIRLTQVNRTIRSHTFN
          |||||

      130     140     150     160     170     180
m230.pep :|||||
g230      QYLSQRHMSEDQFVEEIRDQFALQNLVSLVQNGVLVGDAQAEQLIRLTQVNRTIRSHTFN
          |||||

      190     200     210     220     230     240
m230.pep PDEFIAQVKVSEADLQKFYNANKKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE
          |||||
g230      PDEFIAQVKASEADLQKFYNANKKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE
          |||||

      190     200     210     220     230     240
m230.pep :|||||
g230      PDEFIAQVKASEADLQKFYNANKKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE
          |||||

      250     260     270     280     290     300
m230.pep ERVARLPANEAKPSFEQEKA AVENELMKKAVADFNKAKEKLGDVAVNHPSSLAEAAKNS
          |||||
g230      ERVARLPAHEAKPSFEQEKA AVENELMKKAVADFNKAKEKLGDVAVNHPSSLAEAAKNS
          |||||

      250     260     270     280     290     300

```

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	310	320	330	340	350	360
m230.pep	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSEVLTINSETAWVVRakeVR					
g230	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSEVLTINSETAWVVRakeVR					
	310	320	330	340	350	360
	370	380				
m230.pep	EEKTLPPFAEAKDAVRQAYIRTEAAKL					
	:					
g230	EEKNLLFEEAKDAVRQAYIRTEAAKLKTM					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 831>:

a230.seq (partial)

1	ATGTTCCATT	CCATCGAAAA	ATACAGAACG	CCGCCCCAAG	TCCTTTTGGG
51	CCTGATTGCA	TTAACCTTCG	TCGGCTTCGG	GGTCAGCACG	GTATCCCATC
101	CGGGTGCCGA	CTACATCGTC	CAAGTGGGCG	ACGAAAAAAT	CAGCGACCAC
151	TCCATCAACA	ACGCCATACA	GAACGAACAG	GCGGACGGCG	GCGGCCCTTC
201	GCGCGACGCG	GTGTTCCAAT	CCCTGCTACA	ACGCGCCTAC	CTGAAACAGG
251	GCGCGAAGCT	GATGGGCATT	TCGGTTTCTT	CCGAACAAAT	CAAGCAGATT
301	ATCGTGGACG	ATCCCAATTT	CCACGACGCA	AACGGCAAAT	TCGACCACGC
351	GCTTTTAAAC	CGCTACCTTT	CCCAACGTCA	TATGTCTGAA	GACCAAGTTG
401	TCGAAGAAAT	CCGCGATCAG	TTTGCCTTGC	AGAATTTGGT	AAACCTCGTC
451	CAAAACGGCG	TATTGGTCGG	CGACGCGCAG	GCGGAACAGC	TGATCAGGCT
501	GACGCAGGTC	AACCGCACCA	TCCGTTTCGA	CACCTTCAAC	CCCGACGAAT
551	TCATCGCCCA	AGTCAAAGTG	TCTGAAGCCG	ATTTGCAGAA	GTTTTATAAC
601	GCAAACAAA	AAGACTACCT	GCTTCCCAA	GCGGTCAAAT	TGGAATATGT
651	CGCCTTGAAT	CTGAAAGACT	TTGCAGACAA	ACAGACCGTC	AGCGAAACAG
701	AAGTGAAAA	TGCGTTTGAA	GAGCGCGTGG	CGCGTTTGCC	GGCAAATGAA
751	GCCAAACCTT	CTTTCGAGCA	GGAAAAAGCC	GCCGTCGAAA	ACGAATTGAA
801	AATGAAAAAG	GCGGTTGCCG	ACTTCAATAA	GGCAAAGAA	AAGCTGGGCG
851	ATGACGCGTT	CAACCATCCT	TCCTCGCTTG	CCGAAGCCGC	CAAAAACAGC
901	GGTTTGAAAG	TCGAAACCCA	AGAAACTTGG	CTGAGCAGGC	AGGATCGCGA
951	AATGTCCGGT	ATGCCCGAAA	ACCTGATCAA	TGCCGTATTC	AGCGACGACG
1001	TATTGAAGAA	AAAACACAAT	TCCGAAGTGC	TGACCATCAA	CAGCGAAACC
1051	GCGTGGGTCG	TCCGCGCCAA	AGAAGTCCGC	GAAGAGAAAA	CCCTGCCGTT
1101	TGCCGAAGCC	AAAGACGCGG	TACGTCAGGC	TTATATCCGT	ACCGAAGCCG
1151	CCAAACTT				

This corresponds to the amino acid sequence <SEQ ID 832; ORF 230.a>:

a230.pep (partial)

1	MFHSIEKYRT	PAQVLLGLIA	LTFVGFVST	VSHPGADYIV	QVGDEKISDH
51	SINNAIQNEQ	ADGGGSPSRDA	VFQSLQRAY	LKQGAklmgi	SVSSEQIKQI
101	IVDDPNFHDA	NGKFDHALLN	RYLSQRHMSE	DQFVEEIRDQ	FALQNLVNLV
151	QNGVLVGDAQ	AEQLIRLTQV	NRTIRSHTFN	PDEFIAQVKV	SEADLQKFYN
201	ANKKDYLLPK	AVKLEYVALN	LKDFADKQTV	SETEVKNAFE	ERVARLPANE
251	AKPSFEQEKA	AVENELKMKK	AVADFNKAKE	KLGDdafnHP	SSLAEAAKNS
301	GLKVETQETW	LSRQDAQMSG	MPENLINAVF	SDDVLKKKHn	SEVLTINSET
351	AWVVRakeVR	EEKTLPPFAE	KDAVRQAYIR	TEAAKL	

m230/a230 99.2% identity in 386 aa overlap

	10	20	30	40	50	60
m230.pep	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
a230	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m230.pep	ADGGGSPSDAVFQSLQRAYLKQGAklmgiSVSSEQIKQIIVDDPNFHdANGKFDHALLN					
a230	ADGGGSPSDAVFQSLQRAYLKQGAklmgiSVSSEQIKQIIVDDPNFHdANGKFDHALLN					
	70	80	90	100	110	120
	130	140	150	160	170	180

m230.pep	RYLSQRHMS	EDQFVEE	IRDQFAL	QNLVNLV	QNGVLVG	DAQAEQ	LIRLTQ	VNRTIR	SHTFN
a230	RYLSQRHMS	EDQFVEE	IRDQFAL	QNLVNLV	QNGVLVG	DAQAEQ	LIRLTQ	VNRTIR	SHTFN
	130	140	150	160	170	180			
m230.pep	PDEFIAQ	VKVSEAD	LQKFYN	NANKKDY	LLPQAV	KLEYVAL	NLKFAD	KQTVSE	TEVKNA
a230	PDEFIAQ	VKVSEAD	LQKFYN	NANKKDY	LLPQAV	KLEYVAL	NLKFAD	KQTVSE	TEVKNA
	190	200	210	220	230	240			
m230.pep	ERVARLP	PANEAKP	SFEQEK	AAVENEL	KMKKAV	ADFNKA	KEKLG	DDAVNH	PSSLAE
a230	ERVARLP	PANEAKP	SFEQEK	AAVENEL	KMKKAV	ADFNKA	KEKLG	DDAVNH	PSSLAE
	250	260	270	280	290	300			
m230.pep	GLKVETQ	ETWLSR	QDAQMS	GMPENL	INAVFS	DDVLKK	KHNSEV	LTINSE	TAWVVR
a230	GLKVETQ	ETWLSR	QDAQMS	GMPENL	INAVFS	DDVLKK	KHNSEV	LTINSE	TAWVVR
	310	320	330	340	350	360			
m230.pep	EECTLP	FAEAKD	AVRQAY	IRTEAA	KL				
a230	EECTLP	FAEAKD	AVRQAY	IRTEAA	KL				
	370	380							

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 833>:

g230-1.seq

```

1  ATGTTCCATT CCATCGAAAA ATACAGAACA CCCGCCCAAG TCTTATTAGG
51  CCTGATTGCA TTAACCTTTG TCGGCTTCGG CGTCAGCACG GTTTCCTCATC
101 CGGGCGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGAGCAC
151 TCAATCAACA ACGCCATGCA GAACGAGCAG GCGGACGCGC GCAGCCCTTG
201 GCGCGACGCG GTGTTCCAAT CCCTGCTGCA ACGCGCCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAGATG
301 ATGTGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCAGTCACGC
351 GCTTTTGAGT CAATACCTGT CGCAACGCCA TATGCTGAA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTGGT AAGCCTCGTC
451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACGCAAGTC AACCGCACCA TCCGTTGCGA CACTTTC AAC CCGACGAGT
551 TCATCGCCCA AGTCAAAGCG TCTGAAGCCG ATTTGCAGAA ATTTTATAAT
601 GCGAACAAAA AAGACTATCT GCTGCCGCGA GCGGTCAAAT TGGAATATGT
651 CGCCTTGAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAAACGG
701 AAGTGAAAAA TGCGTTTGAA GAGCGCGTGG CGCGTTTGCC GGCACATGAA
751 GCCAAACCTT CTTTCGAGCA GGA AAAAGCC GCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAACAA GGCAAAAGAA AAGCTGGGCG
851 ACGATGCGTT CAATCATCCC TCCTCGCTTG CCGAAGCCGC CAAAACAGC
901 GGTTTGAAAG TGGAACCCCA AGAACTTGG CTGAGCAGGC AGGACGCACA
951 AATGTCCGGC ATGCCCGAAA ACCTAATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCG TCCGCGCCAA AGAAGTCCGC GAAGAAAAAA ACCTACTGTT
1101 TGAAGAAGCC AAAGATGCGG TCGCTCAGGC CTATATCCGT ACCGAAGCCG
1151 CCAAACCTGC CGAAAACAAG GCAAAGAAG TGCTTACCCA ACTGAACGGC
1201 GGCAAGGCGA TTGACGTGAA ATGGTCGGAA GTGTCGGTT TGCGCGCGCA
1251 GCAGGCAAGG CAGTCCATGC CGCCGAGGC TTATGCGGAA CTGCTGAAAG
1301 CAAAACGGGC AAACGGCAAA CCCGCCTATG TCAGACTGAC CGGTCTGCCG
1351 GCACCCGTA TTGTCGAGGC GCAGGCAGTC ACGCTCCCG AGGATATTGC
1401 CGCACAGCTT CCTCCTGCGA AACAGGCTT GCGCAACAG CAGTCTGCCA
1451 ATACTTTCGA CTTGCTGATC CGCTATTTCA ACGGAAAAAT CAAACAGACT
1501 AAAGGAGCAC AATCGGTTGA CAACGGCGAT GGTCAAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 834; ORF 230-1.ng>:

g230-1.pep

```

1  MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISEH
51  SINNAMQNEQ ADGGSPWRDA VFQSLQRAY LKQGAKLMI SVSSEQIKQM
101  IVDDPNFHDA NGKFSHALLS QYLSQRHMS DQFVEEIRDQ FALQNLVSLV

```

```

151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKA SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPAHE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVL TINSET
351 AWVVRakeVR EEKNLLFEEA KDAVRQAYIR TEAAKLAENK AKEVLTQLNG
401 GKAVDVKWSE VSVLGAQQAR QSMPEAYAE LLKAKPANGK PAYVRLTGLP
451 APVIVEAQAV TPPEDIAAQL PPAKQALAAQ QSANTFDLLI RYFNGKIKQT
501 KGAQSVNDGD GQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 835>:

m230-1.seq

```

1 ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCAAG TCCTTTTGGG
51 CCGTATTGCA TTAACCTTCG TCGGCTTCGG GGTGAGCAG GTATCCCATC
101 CGGGTGCCGA CTACATCGTC CAAGTGGCGG ACGAAAAAAT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201 GCGCGACGCG GTGTTCCAAT CCCTGCTGCA ACGCGCCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAAATT
301 ATCGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCGACCACGC
351 GCTTTTAAAC CGCTACCTTT CCAACGCCA TATGCTGAA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTTGGT AAACCTCGTC
451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACACAGGTC AACCGCACCA TCCGTTCCGA CACTTTCAAC CCCGACGAGT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA ATTTTATAAT
601 CGGAACAAAA AAGCATATCT GCTGCCGCG GCGGTCAAAT TGGAAATATG
651 CGCCTTGAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAAACGG
701 AAGTGAAAAA TGCAATTTGAA GAGCGCGTGG CCGGTTTGCC GGCAAATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAAAAGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAACAA GGCAAAAGAA AAATTGGGCG
851 ACGATGCGTT CAACCATCCT TCCTCGCTTG CCGAAGCCGC CAAAAACAGC
901 GGTTTGAAAG TCGAAACCCA AGAAACTTGG CTGAGTAGGC AGGACGCGCA
951 AATGTCCGGT ATGCCCGAAA ACCTGATCAA TGCGGTATTG AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCG TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCCTGCCGTT
1101 TGCCGAAGCC AAAGACGCGG TACGTCAGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACCTTG CGAAAAACAAG GCAAAAGACG TGCTTACCCA ACTGAACGGC
1201 GGCAAGGCTG TTGACGTGAA ATGGTCGGAA GTGTCCGTTT TGGGCGCACA
1251 GCAGGCAAGC CAGTCCATGC CGCCCGAGGC TTATGCGGAA CTGCTGAAAG
1301 CAAAACCGGC AAACGGCAAA CCGCCTACG TCAGGCTGAT CGGTCTGCCG
1351 GCACCCGTGA TTGTCGAAGT ACAGGCTGTA ACCCCGCCGG ATGATATCGC
1401 CGCACAGCTT CCGCTTGCAA AACAGGCTTT GCGCAACAG CAGTCTGCCA
1451 ATACTTTTGA CTGTTGATA CGTTATTTCA ACGGCAAAAT CAAACAGACC
1501 AAAGGAGCGC AATCGGTCGA CAACGGCGAC GGTCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 836; ORF 230-1>:

m230-1.pep

```

1 MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
51 SINNAIQNEQ ADGGGSPSRDA VFQSLQRAY LKQGAklmgi SVSSEIQIKI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHMSE DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQKV SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVL TINSET
351 AWVVRakeVR EEKTLFPAEA KDAVRQAYIR TEAAKLAENK AKDVLTLQNG
401 GKAVDVKWSE VSVLGAQQAR QSMPEAYAE LLKAKPANGK PAYVRLIGLP
451 APVIVEQAV TPPDDIAAQL PLAKQALAAQ QSANTFDLLI RYFNGKIKQT
501 KGAQSVNDGD GQ*

```

m230-1/g230-1 96.3% identity in 512 aa overlap

	10	20	30	40	50	60
m230-1.pep	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
g230-1	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISEHSINNAMQNEQ					
	10	20	30	40	50	60
m230-1.pep	ADGGGSPSRDAVFQSLQRAYLKQGAklmgiSVSSEIQIKIIVDDPNFHDANGKFDHALLN					
g230-1	ADGGSPWRDAVFQSLQRAYLKQGAklmgiSVSSEIQIKMIIVDDPNFHDANGKFSHALLS					
	70	80	90	100	110	120
m230-1.pep	ADGGGSPSRDAVFQSLQRAYLKQGAklmgiSVSSEIQIKIIVDDPNFHDANGKFDHALLN					
g230-1	ADGGSPWRDAVFQSLQRAYLKQGAklmgiSVSSEIQIKMIIVDDPNFHDANGKFSHALLS					
	70	80	90	100	110	120
m230-1.pep	RYLSQRHMSEDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRTIRSHTFN					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 837>:

1	ATGTTCCATT	CCATCGAAAA	ATACAGAACG	CCGCCCCAAG	TCCTTTTGGG
51	CCGTGATTGA	TTAACCTTCG	TCGGCTTCGG	GGTCAGCACG	GTATCCCATC
101	CGGGTGGCGA	CTACATCGTC	CAAGTGGCGG	ACGAAAAAAT	CAGCGACATC
151	TCCATCAACA	ACGCCATACA	GACGAACAAG	CGGGACGGCG	CGGCGCCCTC
201	GCGCGACGCG	GTGTTCCAAT	CCCTGCTACA	ACGCGCCTAC	CTGAAACAGG
251	GCGCGAAGCT	GATGGGCATT	TCGGTTTCCT	CCGAACAAAT	CAAGCAGATT
301	ATCGTGGACG	ATCCCAATT	CACGACGACA	AACGGCAAA	TGCAGCACGC
351	GCTTTTAAAC	CGCTACCTTT	CCCAACGTCA	TATGCTGAA	GACCAGTTTG
401	TCGAAGAAAT	CCGCGATCAG	TTTGCCTTGC	AGAATTTGGT	AAACCTCGTC
451	CAAAACGGCG	TATTGTCGCG	CGACGCGCAG	GCGGAACAGC	TGATCAGGCT
501	GACGCAGGTC	AACCGCACCA	TCGGTTCGCA	CAGTTTCAAC	CCCGACGAAT
551	TCATCGCCCA	AGTCAAAGTG	TCTGAAGCCG	ATTGTCAGAA	GTTTTATAAC
601	GCAAAACAAA	AAGACTACCT	GCTTCCCAAA	GCGGCTCAAT	TGGAATATGT
651	CGCCTTGAAT	TGAAAGACT	TGTCAGACAA	ACAGACCGTC	AGCGAAACAG
701	AAGTGAAAAA	TGCGTTTGAA	GAGCGCGTGG	CGCGTTTGCC	GGCAAAATGAA
751	GCCAAACCTT	CTTTCGAGCA	GGAAAAAGCC	GCCGTCGAAA	ACGAATTGAA
801	AATGAAAAAG	GCGGTTTGGC	ACTTCAATAA	GCGAAAGAA	AAGCTGGGCG
851	ATGACGCGTT	CAACCATCCT	TCTTCGCTTG	CCGAAGCCGC	CAAAAACAGC
901	GGTTTGAAG	TGAAACCCCA	AGAAATCTTG	CTGAGCAGGC	AGGATCGCA
951	AATGTCGGGT	ATGCCCGGAA	ACCTGATCAA	TGCCGTATT	AGCGACGAGC
1001	TATTGAAGAA	AAAACACAAT	TCGGAATGTC	TGACCATCAA	CAGCGAAACC
1051	GCGTGGGTGC	TCCGCGCGCA	AGAAGTCCGC	GAAGAGAAAA	CCCTGCCGTT
1101	TGCCGGAAGC	AAAGACCGCG	TACGTACGCG	TTATATCCCT	ACCGAAGCCG
1151	CCAAACTTGC	GAAAAACAAG	GCAAAAGACG	TGCTTACCGA	ACTGAACCGC
1201	GGCAAGGCTG	TTGACGTGAA	ATGGTCGGAA	GTGTCGGTTT	TGGGCGCACA
1251	GCAAGCAAGG	CAGTCCATGC	CGCCCCGAGC	TTATTCGGAA	CTGCTGAAAG
1301	CAAAACCGCG	AAACGCGCAA	CCCCCTACG	TCAGGCTGAT	CGGTCTGCCG
1351	GCACCCGTGA	TTGTGCAAGT	ACAGGCTGTA	ACCCGCGCGG	ATGATATCGC
1401	CGCAGACGTT	CCGCTTGC AA	AACAGCTTTT	GGCGCAACAG	CAGTCTGCCA
1451	ATACTTTCCA	CTTGTTGATA	CGTTATTCTA	ACGGCAAAAT	CAAAACAGAC
1501	AAAGGAGCGC	AATCGTTCGA	CAACGCGCAC	GGTCAGTAA	

This corresponds to the amino acid sequence <SEQ ID 838; ORF 230-1.a>:

a230-1.pep

```
1 MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
51 SINNAIQNEQ ADGGGPSRDA VFQSLQRAY LKQGAQLMGI SVSSEQIKQI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHMSE DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHFTN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPK AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELMKKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLINSET
351 AWVVRKEVR EEKTLFFAEA KDAVRQAYIR TEAAKLAENK AKDVLTLQNG
401 GKAVDVKWE VSVLGAQQAQ QSMPEAYAE LLKAKPANGK PAYVRLIGLP
451 APVIVEVQAV TPPDDIAAQL PLAKQALAQQ QSANTFDLLI RYFNGKIKQT
501 KGAQSVNDNGD GQ*
```

a230-1/m230-1 99.8% identity in 512 aa overlap

a230-1.pep	10	20	30	40	50	60
m230-1	10	20	30	40	50	60
a230-1.pep	70	80	90	100	110	120
m230-1	70	80	90	100	110	120
a230-1.pep	130	140	150	160	170	180
m230-1	130	140	150	160	170	180
a230-1.pep	190	200	210	220	230	240
m230-1	190	200	210	220	230	240
a230-1.pep	250	260	270	280	290	300
m230-1	250	260	270	280	290	300
a230-1.pep	310	320	330	340	350	360
m230-1	310	320	330	340	350	360
a230-1.pep	370	380	390	400	410	420
m230-1	370	380	390	400	410	420
a230-1.pep	430	440	450	460	470	480
m230-1	430	440	450	460	470	480
a230-1.pep	490	500	510			
m230-1	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 839>:

g231.seq

```
1 atgtcaaaac gaaaatccat aaaccgtccg tatcaaaaac cggcggaact
51 gccgcggttg caaaaataatc cgccatttta cgtataaaac cgccgcctga
101 acttttttat cgcggcagac ggcggttgcg cgtctccgca aaaatgcagg
151 gcgcgcggtt ttcagacggc atttgccgtt caaggccgtg cgggtgtcttt
201 accaaatgcc caaccattcg ccacggaat ccatccaatc cttattgccc
251 ccgccgtcc tgcctgcccg gcggtacgcc caccggcgctt gcggattttt
301 agctttccac aatcctttgc gttccctttc cgcctgaatt tgagcgtcgg
351 catagtcggc aaaatccgcc ttatcctgct gttcttttagc ataactttta
401 taatgccacg ccgcccgcgc ctgcacctgc atcagggtca aatcggtttt
451 gccggcggat acctgcgcca cttcgcgctg atagcggtcg gtttcaaaca
501 cacgtacact gactttccta ccctccgcgc ccgcgcgcag gttgtcgcgc
551 gaacgtgtac cctaagcctg cgtcgcgcgc gatcagtgga agggatctcg
601 ccgaatttta tgtttcgcgc cttccgcgc gatcagtgga agggatctcg
651 cgtcatagac tttggacacc gtgcctgtgt agctgtggcc ggatttcgcc
701 gatgccgcgc gccgaacggg cgcgtcgaaa ccacgtccc ctgcagtgcc
751 gagtacgtcg agtacggcaa ccgccgtccg caccgcctca ctgtcatatc
801 ccgtataacc caacgcgccc aaaagcgaca gggcgacggg aagccatttc
851 atgatttttt taatctgcat atttttcaaa tgccgatgcc gtctgaacat
901 ctctga
```

This corresponds to the amino acid sequence <SEQ ID 840; ORF 231.ng>:

g231.pap

1	MSKRKSINRP	YQKPAELPPL	QNNPPFYRKN	RRLNFFIAAD	GGCASPQKCR
51	ARGFQTAFAV	QGRAVSLPNA	QPFAGHINPI	LIAPAAPACP	AVRPRRLRIF
101	SFPQSFAFPF	RLNLSVGIVG	KIRLILLFFS	ITFIMPRRPV	LHLHQVQIGF
151	AGGYLRHFAL	IAVGFKHTYT	DFPTLRRRAQ	VVARTCTVSL	FHLRCVDIRH
201	PNFMFRAVAV	DDVKGIAVID	FGHRACVAVA	GFRRCPSANG	RVETHVPCSA
251	EYVEYGNRRP	HRLTVISRIT	QRAQKRQGDG	KPFHDFFNLI	IFQMPMPSEH
301	L*				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 841>:

```
m231.seq (partial)
      1  ATGTCAAAC  GAAAATCCAT  AAACCGTCCG  TATCAAAAAC  CGGCGGAAC
     51  GCCGCCGTTG  CAAAATAATC  CGCCATTTTA  CCGTAAAAAC  CGCCGCCTGA
    101  ACTTTTTTAT  CGCGGCAGAC  GCGCGTTGCG  CGTCTCCGCA  AAAATGCAGG
    151  GCGCGCGGTT  TTCAGACGGC  ATTTGCCGTT  CAAAGCCGTG  CGGTGTCTTT
    201  ACCAAATGCC  CAACCATTGC  GC....
```

This corresponds to the amino acid sequence <SEQ ID 842; ORF 231>:

```
m231.pep (partial)
1  MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
51 ARGFQTAFAV QSRVSLPNA QPFG....
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 231 shows 98.6% identity over a 73 aa overlap with a predicted ORF (ORF 231.ng)

from *N. gonorrhoeae*:

m231/g231

```

                10      20      30      40      50      60
m231.pep      MSKRKSINRPYQKPAELPPLQNNPPFYRKNNRRLNFFIAADGGCASPQKCRARGFQTAFV
                |||||
g231           MSKRKSINRPYQKPAELPPLQNNPPFYRKNNRRLNFFIAADGGCASPQKCRARGFQTAFV
                10      20      30      40      50      60

                70
m231.pep      QSRVSLPNAQPFG
                |:|||||:
g231           QGRAVSLPNAQPFAHGIHPILIAPAAPACPAVRPRRLRIFSFQSFAPFRLNLSVGIVG
                70      80      90      100     110     120

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 843>:

a231.seq (partial)

```

1 ATGTCAAAAC GAAAATCCAT AAACCGTCCG TATCAAAAC CGGCGGAAC
51 GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGNGGCAGAC GCGGTTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CCGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCCC
251 CCGCGCTCC TGCCTGCCG GCGGTACGCC CACGGCGCTT GCGGATTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
351 CATAATCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACTTTTA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT
451 GCCGACAGAA ACCTGCGCCA CTTCGCGCTG GTAGCGGTCG GTGTGGAACA
501 CCGGACGCT GACTTTCTTG CCTTCCGCCG CCGCGCGCAG GTTGTGCGCG
551 GAACGCGTGC CGTAAGCCTG TTTCATCTCC GGCGCGTCGA TATACGCCAT
601 CCGGATTTTG TGTTTCGCGC CGTCGCGGTC GATAACGTGA AGGGTGTGCG
651 CGTCATAGAC TTTGGACACC GTGCCTGTGT AGCGGTGGCC GGATTTCGCC
701 GATGCTCGGC GCGGGGCGGG CGCGTCGGAA CCCGCGTCCC CTGCCGCGCC
751 GAGTACGTCG AGTACGGCAA CCGCCGTCCG CACCGCCTCG CTGCCGTACC
801 CCGTATAACC CAACGCACCC AAAAGCGACA AGGCGACGGG AAGCCATTTT
851 ATGATTTTTT TAATCTGCAT ATTTTTCAAA TGCCGATGCC GTCTGAACAT
901 ATC

```

This corresponds to the amino acid sequence <SEQ ID 844; ORF 217.a>:

a231.pep (partial)

```

1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIXAD GGCASPQKCR
51 ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF
101 SFPQSFAFPF RLNLVGIIG KIRLILFFS ITFIMPRRPV LHLHQVQIGF
151 ADRNLRHFAL VAVGVEHADA DFPAFRRRAQ VVARTRAVSL FHLRRVDIRH
201 PDFVFRAVAV DNVKGVAVID FGHRACVAVA GFRRCSAAGG RVGTRVPCRA
251 EYVEYGNRRP HRLAAVPRIT QRTQKRQGDG KPFHDFFNH IFQMPMPSEH
301 I

```

m231/a231 98.6% identity in 73 aa overlap

	10	20	30	40	50	60
m231.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIXADGGCASPQKCRARGFQTAFV					
a231	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIXADGGCASPQKCRARGFQTAFV					
	10	20	30	40	50	60
	70					
m231.pep	QSRVSLPNAQPFQ					
a231	QSRVSLPNAQPFQFAHGIHPILIAPAAPACPAVRPRRLRIFSFPQSFAFPFRLNLVGIIG					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 845>:

g231-1.seq

```

1 ATGTCAAAAC GAAAATCCAT AAACCGTCCG TATCAAAAC CGGCGGAAC
51 GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGCGGCAGAC GCGGTTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAGCCGTG CCGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGAAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCCG GCGGTACGCC CACGGCGCTT GCGGATTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
351 CATAGTCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACTTTTA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT
451 GCCGGCGGAT ACCTGCGCCA CTTCGCGCTG ATAGCGGTCG GTTTCAAACa
501 CaCgTaCaat gagtttcgta ccctccGCGG ccgcgcgCAG GTTgtcgcGC
551 GAACgTGTA CGTAagcgtg Ttcatctcc GGTGcgtcGA TATACGCCaT
601 cCgAATTTta tGtttcgcgc cgtcgcCgtc gATGACGTGA AGGgtatcGC
651 CgtcATAGAC TTTGGACACC Gtgctgcgt AGctGTGGCC GGATttcgc

```

This corresponds to the amino acid sequence <SEQ ID 846; ORF 231-1.ng>:

g231-1.pep

```

1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIXAD GGCASPQKCR
51 ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF

```

101 SFPOSFAFFP RLNLVGIIVG KIRLILLFFS ITFIMPRRPV LHLHQVQIGF
151 AGGYLRHFAL IAVGFKHTYN EFRTLRRRAQ VVARTCTVSV FHLRCVDIRH
201 PNFMFRAVAV DDVKGIIVID FGHRACVAVA GFR

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 847>:

m231-1.seq

```
1 ATGTCAAAAC GAAAATCCAT AAACCGTCCG TATCAAAAC CGGCGGAACT
51 GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGCGGCAGAC GGCGGTTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TFCAGACGGC ATTTGCCGTT CAAAGCCGTG CGGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCTCG GCGGTACGCC CACGGCGCTT GCGGATTTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
351 CATAATCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACTTTAA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTC AATCGGTTTT
451 GCCGACAGAA ACCTGCGCCA CTTGCGCTG GTAGCGGTCG GTATCGAACA
501 CCGGCACGCT GACTTTCCTG CTTCCGCGC CCGCGCGCAG GTTGTGCGCG
551 GAACGCGTGC CGTAAGCCTG TTTCATCTCC GGCGCGTCGA TATACGCCAT
601 CCGGATTTTG TGTTTCGCGC CGTCGCCGTC GATAACGTGA AGGGTGTCGC
651 CGTCATAGAC TTTGGACACC GTGCCTGTGT AGCGGTGGCC GGATTTCGCC
701 GATGCTCGGC GCGGGCGGGG CGCGTCGGAA CCCGCGTCCC CTGCCGCGCC
751 GAGTACGTCG AGTACGGCAA CCGCCGTCG CACCGCTCG CTGCCGTACC
801 CCGTATAACC CAACGCACCC AAAAGCGACA GGGCGACGGG AAGCCATTTC
851 ATGATTTTTT TAATCTGCAT ATTTTCAAA TGCCGATGCC GTCTGAACAT
901 ATCGGAATCG GATTTCAGAC GGCATCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 848; ORF 231-1>:

m231-1.pep

```
1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPOKCR
51 ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAAPACS AVRPRRLRIF
101 SFPOSFAFFP RLNLVGIIVG KIRLILLFFS ITFIMPRRPV LHLHQVQIGF
151 ADRLNRHFAL VAVGIEHAHA DFPFERRRAQ VVARTRAVSL FHLRRVDIRH
201 PDFVFRAVAV DNVKGVAVID FGHRACVAVA GFRCSAAG RVGTRVPCRA
251 EYVEYGNRRP HRLAAVPRIT QRTQKRQGDG KPFHDFNLH IFQMPMPSEH
301 IGIQFQTAS*
```

g231-1/m231-1 87.0% identity in 262 aa overlap

	10	20	30	40	50	60
g231-1.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPOKCRARGFQTAFV					
m231-1	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPOKCRARGFQTAFV					
	10	20	30	40	50	60
g231-1.pep	QGRAVSLPNAQPFAHGIHPILIAPAAPACPAVRPRRLRIFSFPQSFAFFPRLNLVGIIVG					
m231-1	QSRVSLPNAQPFAHGIHPILIAPAAPACSAVRPRRLRIFSFPQSFAFFPRLNLVGIIVG					
	70	80	90	100	110	120
g231-1.pep	KIRLILLFFSITFIMPRRPVLHLHQVQIGFAGGYLRHFALIAVGFKHTYNEFRTLRRRAQ					
m231-1	KIRLILLFFSITFIMPRRPVLHLHQVQIGFADRLNRHFALVAVGIEHAHADFPFERRRAQ					
	130	140	150	160	170	180
g231-1.pep	VVARTCTVSVFHLRCVDIRHPNFMFRAVAVDDVKGIIVIDFGHRACVAVAGFRXCPSANG					
m231-1	VVARTRAVSLFHLRRVDIRHPDFVFRAVAVDNVKGVAVIDFGHRACVAVAGFRCSAAGG					
	190	200	210	220	230	240
g231-1.pep	CVETHVPCSAEYVVXGNRRPHR					
m231-1	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITQRTQKRQGDGKPFHDFNLHIFQMPMPSEH					
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 849>:

a231-1.seq

```
1 ATGTCAAAAC GAAAATCCAT AAACCGTCCG TATCAAAAC CGGCGGAACT
51 GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGCGGCAGAC GGCGGTTGCG CGTCTCCGCA AAAATGCAGG
```

```

151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CCGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCCCG GCGGTACGCC CACGGCGCTT GCGGATTTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
351 CATAATCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACTTTTA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT
451 GCGGACAGAA ACCTGCGCCA CTTGCGCTG GTAGCGGTCG GTGTCGAACA
501 CCGGACGCT GACTTTCCTG CCTTCCGCGC CCGCGCGCAG GTTGTCGCGC
551 GAACGCGTGC CGTAAGCCTG TTTCATCTCC GCGCGGTCGA TATACGCCAT
601 CCGGATTTTG TGTTCGCGC CGTCGCGCTC GATAACGTGA AGGGTGTGCG
651 CGTCATAGAC TTTGGACACC GTGCCTGTGT AGCGGTGGCC GGATTTCGCC
701 GATGCTCGGC GCGGGGCGGG CGCGTCGGAA CCCGCGTCCC CTGCCGCGCC
751 GAGTACGTCG AGTACGGCAA CCGCCGTCG CACCGCTCG CTGCCGTACC
801 CCGTATAACC CAACGCACCC AAAAGCGACA AGGCGACGGG AAGCCATTTC
851 ATGATTTTTT TAATCTGCAT ATTTTCAA TGCCGATGCC GTCTGAACAT
901 ATCGGAATCG GATTTCAGAC GGCATCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 850; ORF 231-1.a>:

a231-1.pep

```

1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
51 ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF
101 SFPQSFAFPF RLNLVGIIG KIRLILFFS ITFIMPRRPV LHLHQVQIGF
151 ADRLNRHFAL VAVGVEHADA DFPFRRAQ VVARTRAVSL FHLRRVDIRH
201 PDFVFRVAV DNVKGVAVID FGHRACVAV GFRCSAAGG RVGTRVPCRA
251 EYVEYGNRRP HRLAAVPRIT QRTQKRQGDG KPFHDFNLH IFQMPMPSEH
301 IGIGFQTAS*

```

a231-1/m231-1 99.0% identity in 309 aa overlap

a231-1.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV
m231-1	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV
a231-1.pep	QSRVSLPNAQPFAHGIHPILIAPAAPACPAVRPRRLRIFSFPQSFAFPFRLNLVGIIG
m231-1	QSRVSLPNAQPFAHGIHPILIAPAAPACSAVRPRRLRIFSFPQSFAFPFRLNLVGIIG
a231-1.pep	KIRLILFFSITFIMPRRPVLHLHQVQIGFADRLNRHFALVAVGVEHADADFPFRRAQ
m231-1	KIRLILFFSITFIMPRRPVLHLHQVQIGFADRLNRHFALVAVGIEHADADFPFRRAQ
a231-1.pep	VVARTRAVSLFHLRRVDIRHPDFVFRVAVDNLVKGVAIDFGHRACVAVAGFRCSAAGG
m231-1	VVARTRAVSLFHLRRVDIRHPDFVFRVAVDNLVKGVAIDFGHRACVAVAGFRCSAAGG
a231-1.pep	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITQRTQKRQGDGKPFHDFNLHIFQMPMPSEH
m231-1	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITQRTQKRQGDGKPFHDFNLHIFQMPMPSEH
a231-1.pep	IGIGFQTASX
m231-1	IGIGFQTASX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 851>:

g232.seq

```

1 atgatgggca acagcctgat tgaatccggt acgtttgtcg ccatcctgtt
51 tggtcagatt ttgggaacgg cggttgccgg cgcgccgct tatattgtcg
101 ggatactggt ttgctggtc gccgtcggag gaacggccgg cagcctgttt

```

```

151 atgccgtccg taccgcgcaa ggctgccgat acccaaatcg agtgggaatat
201 tgtccgtggg acaaaatccc tgctgcgtga aacgggtgcgg cacaatccccg
251 tttttaccgc cattatcggc atctcgtggg tttggtttgt cggcgcggtt
301 tataccacgc aactgccgac ctttacccaa atccatttgg gcggcaacga
351 taatgttttt aacctgatgc ttgctttgtt ttccatcggt attgccgccc
401 gttcgggtact gtgtgccaag ttcggcaggg aacgggtgat gttggcttgg
451 gtaacgggtt gtgcgttggg ttcgacgggt tgcggcctgg ttttggtgtg
501 gctgacgcac ggacaccggt ttgaagggct gaacggcatt ttttggtttt
551 tatcgcaagg atgggcatac cccgtgatgg cgggtgatgac gctgatcggc
601 tttttcggcg gatTTTTtctc cgttccgctc tatacctggc tgcaaacccg
651 cagcagcgag actttccgcg cccgcgcggt tgcgcgcaac aatatcggtta
701 acggcatctt tatggtttcc gccgcggtt tgagcgcggt attgctgttt
751 ttgtttgaca gcatttccct gctgtatctg attgtcgctt tgggcaatat
801 tccgttggcg gtatttttga ttaagcgcg aaggcggttt ttaggcgcgg
851 cggcaatcag gaaaaaacct tga

```

This corresponds to the amino acid sequence <SEQ ID 852; ORF 232.ng>:

g232.pep

```

1  MMGNSLIESG TFVAILFGQI LGTAVAGAPP YIVGILVLLV AVGGTAGSLF
51  MPSVPAKAAD TQIEWNIVRG TKSLIRETVR HNPVFTAIIG ISWFWFVGAV
101 YTTQLPTFTQ IHLGGNDNVF NLMLALFSIG IAAGSVLCAK FGRERLMLAW
151 VTVGALGSTV CGLVLVWLTH GHRFEGLNGI FWFLSQGWAY PMAVMTLIG
201 FFGGFFSVPL YTWLQTASSE TFRARAVAN NIVNGIFMVS AAVLSAVLLF
251 LFDSISLLYL IVALGNIPLA VFLIKRERRF LGAAAIRKKP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 853>:

m232.seq

```

1  ATGATGGGCA ACAGCCTGAT TGAATCGGGT ACGTTTGTCTG CCATCCTGTT
51  CGGTCAGATT TTGGGAACGG CGGTGGCAGG TGTACCGCCT TATATTGTCTG
101 GGATACTGGT TTTGCTGGTC GCCGTCGGAG GCACGGTCGG CAGCCTGTTT
151 ATGCCGTCCT TACCCGCCAA GGCTGCCGAT ACACAAATTG AGTGAATAT
201 TGTCCGTGGC AAAAAATCCC TGCTGCGTGA AACGGTGCGG CACAAGCCCCG
251 TTTTACCAGC CATTATCGGT ATTTCTGTGT TTTGGTTTGT CGGCGCGGTT
301 TATACCACGC AACTGCCGAC CTTTACCCAA ATCCATCTGG GCGGCAACGA
351 CAATGTTTTC AACCTGATGC TTGCTCTGTT TTCCATCGGT ATTGCCGCCG
401 GTTCGGTACT GTGTGCCAAG TTCAGCAkGG AACGCCTGAT GTTGCTTGG
451 GTAACGGTTG GTGCGTTGGG TTTGACGGTT TCGCGCTTGG TTTTGGTGTG
501 GCTGACGCAC GGACACCGTT TTGAAGGGCT GAACGGCATT TTTTGTGTTT
551 TATCGCAAGG ATGGGCATAT CCCGTGATGG CGGTGATGAC GCTGATCGGC
601 TTTTTCGGCG GATTTTTTCTC CGTTCGCTC TATACct(g)TG CAAACCGCCa
651 TAGCGAGaTT TCCGCGCCCG GCCGTTGCCG CCAACAATAT CGTTAACGGT
701 ATTTTATGTT TTTCCGCTGC CGTTTTGAGC GCGGTGTTGC TGTTTTGTG
751 TGACAGCATT TCCTTGTGTT ATCTGATTGT CGCTTTGGGC AATATTCCGT
801 TGTCGGTATT TTTGATTAAG CGCGAAAGGC GGTTTTTAGG CGCGCGGCA
851 ATCAGGAAAA AACCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 854; ORF 232>:

m232.pep

```

1  MMGNSLIESG TFVAILFGQI LGTAVAGVPP YIVGILVLLV AVGGTVGSLF
51  MPSVPAKAAD TQIEWNIVRG TKSLIRETVR HKPVFTAIIG ISWFWFVGAV
101 YTTQLPTFTQ IHLGGNDNVF NLMLALFSIG IAAGSVLCAK FSXERLMLAW
151 VTVGALGLTV CGLVLVWLTH GHRFEGLNGI FXFLSQGWAY PMAVMTLIG
201 FFGGFFSVPL YTVQTAIARF PRPAVAANNI VNGIFMVSA VLSAVLLFLF
251 DSISLLYLIV ALGNIPLSVF LIKRERRFLG AAAIRKKP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 232 shows 94.1% identity over a 290 aa overlap with a predicted ORF (ORF 232.ng) from *N. gonorrhoeae*:

m232/g232

```

10      20      30      40      50      60
m232.pep  MMGNSLIESGTFVAILFGQILGTAVAGVPPYIVGILVLLVAVGGTVGSLFMPSVPAKAAD
          |||||:|||||:|||||:|||||:|||||:|||||
g232      MMGNSLIESGTFVAILFGQILGTAVAGAPPYIVGILVLLVAVGGTAGSLFMPSVPAKAAD

```

531

	10	20	30	40	50	60
	70	80	90	100	110	120
m232 . pep	TQIEWNIVRGTKSLLRETVRHKPVFTAIIGISWFWFVGAVYTTQLPTFTQIHLGGNDNVF					
g232	TQIEWNIVRGTKSLLRETVRHNPVFTAIIGISWFWFVGAVYTTQLPTFTQIHLGGNDNVF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m232 . pep	NLMLALFSIGIAAGSVLCAKFSXERLMLAWVTVGALGLTVCGLVLVWLTHGHRFEGLNGI					
g232	NLMLALFSIGIAAGSVLCAKFSRERLMLAWVTVGALGSTVCGLVLVWLTHGHRFEGLNGI					
	130	140	150	160	170	180
	190	200	210	220	230	
m232 . pep	FXFLSQGWAYPVMAMVTLIGFFGGFFSVPLYT-VQTAIARFPRP-AVAANNIVNGIFMVS					
g232	FWFLSQGWAYPVMAMVTLIGFFGGFFSVPLYTWLQTASSETFRARAANAANNIVNGIFMVS					
	190	200	210	220	230	240
	240	250	260	270	280	289
m232 . pep	AAVLSAVLLFLFDSISLLYLIALGNIPLSVFLIKRERRFLGAAAIRKKPX					
g232	AAVLSAVLLFLFDSISLLYLIALGNIPAVFLIKRERRFLGAAAIRKKP					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 855>:

```

a232 . seq
1  ATGTACGCTA  AAAAAGGCGG  TTTGGGACTG  GTTAAAAGCC  GCCGTTTCGC
51  ACCTCTTTTC  GCTACGCAGT  TTCTCGGCGC  GTTCAACGAC  AATGTGTTC
101  AAACCGCGCT  GTTTGTGATG  ATTGGGTTTT  ACGGTTTGGG  GCAAAACGGC
151  TTCCTGCCTG  CCGGACAGAT  GTTGAACCTG  GGCGCGTTGC  TGTATTATTT
201  GCCGTATTTT  CTGTTTTTCT  CGCTGTCGGG  GCAGTTGGGT  AACAAATTCG
251  ACAAGGCCGT  TTTGGCGCGT  TGGGCCAAGG  TGCTGGAAAT  GATCATTATG
301  GCGGTGGCGG  CATACGGGTT  TTATATCCGG  TCTGCCCCGC  TGCTTTTGGC
351  GTGTCTGTTT  TGCATGGGCG  CGCAATCGAC  GCTGTTCCGG  CCGCTGAAAT
401  ACGCCATCCT  GCCCATTAT  CTCGACGACA  AAGAGTTGAT  GATGGGCAAC
451  AGCCTGATTG  AATCGGGTAC  GTTGTGCGCC  ATCCTGTTTC  GTCAGATACT
501  GGGGACTGCG  GTGGCAGGTG  TACCGCCTTA  TATTGTCGGG  ATACTGGTTT
551  TGCTGGTCCG  CGTAGGAGGC  ACGGTCGGCA  GCCTGTTTAT  CCGCTCCGTA
601  CCCGCCAAGG  CTGCCGATAC  ACAAATTGAG  TGGAAATATT  TCCGGGGTAC
651  AAAATCCCTG  CTGCGTGAAA  CGGTGCGGCA  CAAGCCCGTT  TTTACCGCCA
701  TTATCGGTAT  TTCGTGGTTT  TGGTTTGTTC  GCGCGGTTTA  TACCACGCAA
751  CTGCCGACCT  TTACCCAAAT  CCATCTAGGC  GGCAACGACA  ATGTTTTCAA
801  CCTGATGCTT  GCCCTGTTTT  CCATCGGTAT  TGCCGCCGGT  TCGGTACTGT
851  GTGCCAAGTT  CAGCAGGGAA  CGGCTGAGGT  TGGCTTGGGT  AACGGTTGGT
901  GCGTTGGGTT  TGACGGTTTG  CGGCTTGGTT  TTGGTGTGGC  TGACGCACGG
951  ACACCGTTTT  GAAGGGCTGA  ACGGCATTTT  TTGGTTTTTA  TCGCAAGGAT
1001  GGGCATATCC  CGTGATGGCG  GTGATGACGC  TGATCGGCTT  TTTCGGCGGA
1051  TTTTCTCCG  TTCCGCTCTA  TACCTGGCTG  CAAACCGCCA  GTAGGAGAC
1101  TTTCCGCGCC  CGCGCCGTTG  CCGCCAACAA  TATCGTTAAC  GGTATTTTAA
1151  TGGTTTCCGC  TGCCGTTTTG  AGCGCGGTGT  TGCTGTTTTT  GTTTGACAGC
1201  ATTTCTTGT  TGTATCTGAT  TGTCGCTTTG  GGCAATATTC  CGTTGTCGGT
1251  ATTTTGTATT  AAGCGCGAAA  GCGGTTTTTT  AGGCGCGGCG  GCAATCAGGA
1301  AAAAACCTTG  A

```

This corresponds to the amino acid sequence <SEQ ID 856; ORF 232.a>:

```

a232 . pep
1  MYAKKGLGL  VKSRRFAPLF  ATQFLGAFND  NVFKTALFVM  IGFYGLGQNG
51  FLPAGQMLNL  GALLFILPYF  LFSSLSGQLG  NKFDKAVLAR  WAKVLEMIIM
101  AVAAYGFYIR  SAPLLLACLF  CMGAQSTLFG  PLKYAILPDY  LDDKELMMGN
151  SLIESGTFVA  ILFGQILGTA  VAGVPPYIVG  ILVLLVAVGG  TVGSLFMPVS
201  PAKAADTQIE  WNIVRGTKSL  LRETVRHKPV  FTAIIGISWF  WFGAVYTTQ
251  LPTFTQIHLG  GNDNVFNML  ALFSIGIAAG  SVLCAKFSRE  RLRLAWVTVG

```

301 ALGLTVCGLV LVWLTHGHRF EGLNGIFWFL SQGWAYPVMA VMTLIGFFGG
 351 FFSVPLYTWL QTASSETFRA RAVAANNIVN GIFMVSAAVL SAVLLEFLDS
 401 ISLLYLIVAL GNIPLSVFLI KRERRFLGAA AIRKKP*

m232/a232 95.9% identity in 290 aa overlap

m232.pep					10	20	30
					MMGNSLIESGTFVAILFGQILGTAVAGVPP		
a232	ACLFCMGAQSTLFGPLKYAILEDYLDKELMMGNSLIESGTFVAILFGQILGTAVAGVPP						
	120	130	140	150	160	170	
m232.pep		40	50	60	70	80	90
		YIVGILVLLVAVGGTVGSLFMPSVPAKAADTQIEWNIVRGTKSLLRETVRHKPVFTAIIG					
a232	YIVGILVLLVAVGGTVGSLFMPSVPAKAADTQIEWNIVRGTKSLLRETVRHKPVFTAIIG						
	180	190	200	210	220	230	
m232.pep		100	110	120	130	140	150
		ISWFWFVGAVYTTQLPTFTQIHLGGNDNVFNMLALFSIGIAAGSVLCAKFSXERLMLAW					
a232	ISWFWFVGAVYTTQLPTFTQIHLGGNDNVFNMLALFSIGIAAGSVLCAKFSRERLRLAW						
	240	250	260	270	280	290	
m232.pep		160	170	180	190	200	210
		VTVGALGLTVCGLVLVWLTHGHRFEGLNGIFXFLSQGWAYPVMAVMTLIGFFGGFFSVPL					
a232	VTVGALGLTVCGLVLVWLTHGHRFEGLNGIFWFLSQGWAYPVMAVMTLIGFFGGFFSVPL						
	300	310	320	330	340	350	
m232.pep		220	230	240	250	260	
		YT-VQTAIARFPRP-AVAANNIVNGIFMVSAAVLSAVLLFLFDSISLLYLIVALGNIPLS					
a232	YT-VQTAIARFPRP-AVAANNIVNGIFMVSAAVLSAVLLFLFDSISLLYLIVALGNIPLS						
	360	370	380	390	400	410	
m232.pep		270	280	289			
		VFLIKRERRFLGAAAIRKKPX					
a232	VFLIKRERRFLGAAAIRKKPX						
	420	430					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 857>:

g233.seq

```

1  atgaaacgca aaaatatcgc gctgattccc gccgccggca tcgggggtgcg
51  ttctcgtgcg gacaaacca agcaatatgt cgaaatcgga agcaaaaccg
101 ttttagaaca tgtacttggg atttttgaac ggcatgaggc cgtcgatttg
151 accgtcgttg tcgtctcgcc cgaagacacg tttgccgata aggttcagac
201 ggcatttcca caggttcggg tgtggaaaaa cgggtggacag acccgcgccg
251 aaactgtccg caacggtgtg gcaaaactgt tggaaaccgg tttggcggcg
301 gaaaccgaca atattctggt acacgatgcc gcccgctgct gcctgccgtc
351 tgaagctctg gcgcggttga tagaacaggc gggcaacgcc gccgaaggcg
401 ggattttggc agttcccgtt gccgatacgc tcaagcgcgc agaaagcgga
451 caaatcagtg caactgtcga cgttcgggg ctttggcagg cgcaaacgcc
501 gcagcttttt caagcgggtt tgctgcaccg cgcattggct gcggaaaact
551 tgggcggcat taccgatgaa gcgtccgccg tggaaaaact ggggtgtgct
601 ccgctactga tacaggcgca cgcgcgcaat ttgaaactga cgcagccgca
651 ggacgcatac atcgtcaggc tgctgctcaa tgccgtctga
  
```

This corresponds to the amino acid sequence <SEQ ID 858; ORF 233.ng>:

g233.pep

```

1  MKRKNIALIP AAGIGVRFGA DKPKQYVEIG SKTVLEHVLG IFERHEAVDL
51  TVVVVSPEDT FADKVQTAFF QVRVWKNNGQ TRAETVRNGV AKLLETGLAA
101 ETDNILVHDA ARCCLPSEAL ARLIEQAGNA AEGGILAVPV ADTLKRAESG
  
```


151 QISATVDRSG LWQAQTPQLF QAGLLHRLA AENLGGITDE ASAVEKLGVR
 201 PLLIQGDARN LKLTQPDAY IVRLLLNAV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 859>:

m233.seq (partial)
 1 ATGAAGCGCA AAAATATCGC GCTGATTCCC GCCGCCGGCA TCGGGGCGCG
 51 TTTCGGTGCG GACAAACCCA AGCAATATGT CGAAATCGGA AGCAAAACCG
 101 TTTTAGAACA TACGATTGGG ATTTTGAAC GGCATGAGGC CGTCGATTG
 151 ACCGTCGTTG TCGTCTCGCC CGAAGACACG TTTGCCGATA AGGTTTCAGAC
 201 GGCATTTCCTA CAGGTTCTGGG TGTGGAAAAA CGGCGGACAG ACCCGCGCCG
 251 AAACCGTCCG CAACGGTGTG GCAAACTGT TGGAAACCGG TTTGGCGGCG
 301 GAAACCGACA ATATTCTGGT ACACGATGCC GCGCGTTGCT GCCTGCCGTC
 351 TGAAGCTTTG ACGCGGTTGA TAGAACAGGC GGGCAACGCC GCCGAAGGCG
 401 GGATTTTGGC AATTCCCAT TCCGATACGC TCAAGTGCGC GGACGGTGGG
 451 AACATT....

This corresponds to the amino acid sequence <SEQ ID 860; ORF 233>:

m233.pep (partial)
 1 MKRKNIALIP AAGIGARFGA DKPKQYVEIG SKTVLEHTIG IFERHEAVDL
 51 TVVVVSPEDT FADKVQTAFP QVRVWKNNGQ TRAETVRNGV AKLLETGLAA
 101 ETDNILVHDA ARCLPSEAL TRLIEQAGNA AEGGILAIPI ADTLKCADGG
 151 NI....

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 233 shows 93.4% identity over a 152 aa overlap with a predicted ORF (ORF 233.ng) from *N. gonorrhoeae*:

m233/g233

m233.pep	10	20	30	40	50	60
	MKRKNIALIP AAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT					
g233	MKRKNIALIP AAGIGVRFADKPKQYVEIGSKTVLEHVLGIFERHEAVDLTVVVVSPEDT					
	10	20	30	40	50	60
m233.pep	70	80	90	100	110	120
	FADKVQTAFPQVRVWKNNGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCLPSEAL					
g233	FADKVQTAFPQVRVWKNNGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCLPSEAL					
	70	80	90	100	110	120
m233.pep	130	140	150			
	TRLIEQAGNA AEGGILAIPIADTLKCADGGNI					
g233	ARLIEQAGNA AEGGILAVPVADTLKRAESQISATVDRSGLWQAQTPQLFQAGLLHRLA					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 861>:

a233.seq
 1 ATGAAGCGCA AAAATATCGC GCTGATTCCC GCCGCCGGCA TCGGGGCGCG
 51 TTTCGGTGCG GACAAACCCA AGCAATATGT CGAAATCGGA AGCAAAACCG
 101 TTTTAGAACA TACGATTGGG ATTTTGAAC GGCATGAGGC CGTCGATTG
 151 ACCGTCGTTG TCGTCTCGCC CGAAGACACG TTTGCCGATA AGGTTTCAGAC
 201 GGCATTTCCTA CAGGTTCTGGG TGTGGAAAAA CGGCGGACAG ACCCGCGCCG
 251 AAACGTGTCG CAACGGTGTG GCAAAATTGT TGGAAACCGG TTTGGCGGCG
 301 GAAACCGACA ATATTCTGGT ACACGATGCC GCGCGTTGCT GCCTGCCGTC
 351 TGAAGCTTTG ACGCGGTTGA TAGAACAGGC GGGCAACGCT GCCGAAGGTG
 401 GGATTTTGGC AATTCCCGTT GCCGATACGC TCAAGTGCGC GGACGGTGGG
 451 AACATTAGTG CAACCGTCGA CGGACGAGC CTTTGGCAGG CGCAAACGCC
 501 GCAGCTTTTC CGCGCCGGGC TGCTGCACCG CGCATTGGCT GCGGAAACT
 551 TGGACGGCAT TACCGATGAA GCGTCCGCCG TGGAAAAATT GGGCATCCGC
 601 CCTTTGCTGG TGCAGGGCGA CGCGCGCAAT TTGAACTGA CGCAGCCGCA
 651 GGACGCATAC ATCGTCAGGC TGCTGCTCGA TGCCGTCTGA

This corresponds to the amino acid sequence <SEQ ID 862; ORF 233.a>:

```
a233.pep
1  MKRKNIALIP AAGIGARFGA DKPKQYVEIG SKTVLEHTIG IFERHEAVDL
51  TVVVVSPEDT FADKVQTAFF QVRVWKNNGQ TRAETVRNGV AKLLETGLAA
101 ETDNILVHDA ARCCLPSEAL TRLIEQAGNA AEGGILAI PV ADTLKCADGG
151 NISATVERTS LWQAQTPQLF RAGLLHRLA AENLDGITDE ASAVEKLGIR
201 PLLVQGDARN LKLTQPDQDAY IVRLLLDAV*
```

m233/a233 99.3% identity in 152 aa overlap

```

10      20      30      40      50      60
m233.pep MKRKNIALIPAAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT
|||||
a233      MKRKNIALIPAAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT
10      20      30      40      50      60

70      80      90      100     110     120
m233.pep FADKVQTAFFQVRVWKNNGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL
|||||
a233      FADKVQTAFFQVRVWKNNGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL
70      80      90      100     110     120

130     140     150
m233.pep TRLIEQAGNAEAGGILAIPIADTLKCADGGNI
|||||
a233      TRLIEQAGNAEAGGILAIPIADTLKCADGGNISATVERTSLWQAQTPQLFRAGLLHRLA
130     140     150     160     170     180

a233      AENLDGITDEASAVEKLGIRPLLVQGDARNLKLTQPDQDAYIVRLLLDAVX
190     200     210     220     230
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 863>:

```
g234.seq
1  atgaaaaccg tttccgccgc catcgctttt gccgccgctg ccgtttcact
51  gaccggctgt gcgaccgagt cctcacgcag cctcgagggt gcaaaagtcg
101 cctcctgcaa tacgcaatat cagggtgttc gcaccccgat ttccgctcga
151 acattcgaca accgctccag cttccaaaaa ggcattttct cgcacagtga
201 agaccgtctg ggcagccagg caaaaacccat cctggtaaca cacctgcaac
251 aaaccaaccg cttcaacgta ctgaaccgca ccaaccttag cgcattgaaa
301 caggaaatccg gcatttcccg caaagcgtag aacctgaaag gcgcagatta
351 tgtcgttacc ggcgatgtaa ccgaattcgg acgcagagat gtcggcgatc
401 atcagctctt cggcattttg ggtcgcggca aatcgcaaat cgcctatgca
451 aaagtggctc tgaatatcgt caacgtcaat acttccgaaa tcgtctattc
501 cacacagggc gcgggcgaaat acgcactttc caaccgcgaa atcatcggtt
551 tcggcggcac ttccgggtac gatgcgactt tgaacggcaa agttttagac
601 ttggcaatcc gcgaagccgt cgacaacttg gttcaggctg tcgacaacgg
651 cgcattggcaa tccaaccgtt aa
```

This corresponds to the amino acid sequence <SEQ ID 864; ORF 234.ng>:

```
g234.pep
1  MKTVSAAIAF AAAAVSLTGC ATESSRSLEV AKVASCNTQY HGVRTPISVG
51  TFDNRSSFQK GIFSDSEDRL GSQAKTILVT HLQOTNRNFV LNRTNLSALK
101 QESGISGKAQ NLKGADYVVT GDVTEFGRRD VGDHQLFGIL GRGKSQIAYA
151 KVALNIVNVN TSEIVYSTQG AGEYALSNRE IIGFGGTSY DATLNGKVLD
201 LAIREAVDNL VQAVDNGAWQ SNR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 865>:

```
m234.seq (partial)
1  ...GGCGCGGGCG AATACGCACT TTCCAACCGt GAAATCATCG GTTTCGGCGG
51  CACTTCCGGC TACGATGCGA CTTTGAACGG CAAAGTTTTA GACTTGGCAA
101 TCCGCGAAGC .gtCAACAGC CTGGTTCAGG CTGTTGACAA CGGCGCATGG
151 CAACCCAACC GTTAA
```

This corresponds to the amino acid sequence <SEQ ID 866; ORF 234>:

m234.pep (partial)
 1 ..GAGEYALSNR EIIGFGGTSG YDATLNGKVL DLAIREAVNS LVQAVDNGAW
 51 QPNR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 234 shows 94.4% identity over a 54 aa overlap with a predicted ORF (ORF 234.ng) from *N. gonorrhoeae*:

m234/g234

					10	20	30
m234.pep					GAGEYALSNREIIGFGGTSGYDATLNGKVL		
g234	LGRGKSQIAYAKVALNIVNVNTSEIVYSTQ	GAGEYALSNREIIGFGGTSGYDATLNGKVL					
	140	150	160	170	180	190	

		40	50
m234.pep	DLAIREAVNSLVQAVDNGAWQPNRX		
	:		
g234	DLAIREAVDNLVQAVDNGAWQSNRX		
	200	210	220

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 867>:

a234.seq (partial)
 1 AACCGCACCT ATTTGAACGC ATTAAAACAG GAATCCGGCA TTTCCGGCAA
 51 AGCGCATAAC CTGAAAGGCG CAAATTATGT CGNNACCGGC GATGTAACCG
 101 AATTCGGACG CANAGATGTC GGCGATCATC AGCTCTTCGG CATTTTGGGT
 151 CGCGGCAAAT CGCAAATCGC CTATGCAAAA GTGGCTCTGA ATATCGTCAA
 201 CGTCAATACT TCCGAAATCG TCTATTCCGC ACAGGGCGCG GGCGAATACG
 251 CACTTTCCAA CCGTGAAATC ATCGGTTTCG GCGGCACTTC CGGCTACGAT
 301 GCGACTTTGA ACGGCAAAGT TTTAGACTTG GCAATCCGCG AAGCCGTCAA
 351 CAGCCTGGTT CAGGCTGTTG ACAACGGCGC ATGGCAACCC AACCGTTAA

This corresponds to the amino acid sequence <SEQ ID 868; ORF 234.a>:

a234.pep (partial)
 1 NRTYLNALKQ ESGISGAHN LKGANYVXTG DVTEFGRXDV GDHQLFGILG*
 51 RGKSQIAYAK VALNIVNVNT SEIVYSAQGA GEYALSNREI IGFGGTSGYD*
 101 ATLNGKVL DL AIREAVNSLV QAVDNGAWQP NR*

m234/a234 100.0% identity in 54 aa overlap

					10	20
30						
m234.pep					GAGEYALSNREIIGFGGTSGYDATLNGKVL	
a234	LGRGKSQIAYAKVALNIVNVNTSEIVYSAQ	GAGEYALSNREIIGFGGTSGYDATLNGKVL				
	50	60	70	80	90	100

		40	50
m234.pep	DLAIREAVNSLVQAVDNGAWQPNRX		
a234	DLAIREAVNSLVQAVDNGAWQPNRX		
	110	120	130

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 869>:

g235.seq

```

1  atgaaacctt tgatttttagg gcttgccgcc gtgttggttc tgtctgcctg
51  ccaagttcga aaagctcccg acctcgacta cacgtcattc aaagaaagca
101 aaccggcttc aatttttggtg gttccgccgc tgaacgagtc gcctgatgtc
151 aacggcactt gggggatgct ggcttcgacc gccgcgccga tttccgaagc
201 cggctattac gtctttcccg ccgcagtcgt ggaggaaacc ttcaaagaaa
251 acggcttgac caatgccgcc gatattcacg ccgtccggcc ggaaaaactg
301 catcaaattt tcggcaatga tgcggttttg tacattacgg ttaccgaata
351 cggcacttca tatcaaattt tagacagcgt gacgaccgta tccgccaaag
401 cacggctggt cgattcccg c acgggaaaag agttgtggtc ggggtcggcc
451 agcatccgcg aaggcagcaa caacagcaac agcggcctgt tgggggcttt
501 ggtcggcgca gtggtcaatc agattgccaa cagcctgacc gaccgcgggt
551 atcaggtttc caaaaccgcc gcatacaacc tactgtcgcc ctattcccg
601 aacggtatct tgaaagggtcc gagattcgtc gaagagcagc ccaaataa

```

This corresponds to the amino acid sequence <SEQ ID 870; ORF 235.ng>:

g235.pep

```

1  MKPLILGLAA VLALSACQVR KAPDLDTYSF KESKPASILV VPPLNESPDV
51  NGTWGMLAST AAPISEAGYY VFPAAVVEET FKENGLTNAI DIHAVRPEKL
101 HQIFGNDAVL YITVTEYGTS YQILDSVTTV SAKARLVDSR NGKELWSGSA
151 SIREGSNNSN SGLLGALVGA VVNQIANSLT DRGYQVSKTA AYNLLSPYSR
201 NGILKGPRFV EEQPK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 871>:

m235.seq

```

1  ATGAAACCTT TGATTTTAGG GCTTGCCGCC GTGTTGGCGC TGTCTGCCTG
51  CCAAGTTCOA AAAGCGCCCG ATTCGACTA CACGTCAATC AAGGAAAGCA
101 AACCGGCTTC AATTTTGGTG GTTCCGCCGC TGAACGAATC GCCCGATGTC
151 AACGGAACAT GGGGTGTACT GGCTTCGACC GCCGCGCCGC TTCCGAAGC
201 CGGCTATTAC GTCTTCCCGC CCGCAGTCGT GGAGGAAACC TTCAAACAAA
251 ACGGCTTGAC CAATGCCGCC GATATTCACG CCGTCCGGCC GGAAAACTG
301 CATCAGATTT TCGGCAATGA TGCGGTTTTG TACATTACGG TTACCGAATA
351 CGGCACTTCA TATCAAATT TAGACAGCGT GACGACCGTA TCCGCCAAAG
401 CACGGCTGGT CGATTCCCGC AACGGAAAAG AGTTGTGGTC GGGTTCGGCC
451 AGCATCCGCG AAGGCAGCAA CAACAGCAAC AGCGGCCTGT TGGGGGCTTT
501 GGTCAGCGCA GTGGTCAATC AGATTGCCAA CAGCCTGACC GACCGCGGTT
551 ATCAGGTTTC CAAAACCGCC GCATACAACC TGCTGTCGCC CTATTCTCAC
601 AACGCGATCT TGAAAGGTCC GAGATTCGTT GAAGAGCAGC CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 872; ORF 235>:

m235.pep

```

1  MKPLILGLAA VLALSACQVQ KAPDFDYTSF KESKPASILV VPPLNESPDV
51  NGTWGVLAST AAPLSEAGYY VFPAAVVEET FKQNGLTNAI DIHAVRPEKL
101 HQIFGNDAVL YITVTEYGTS YQILDSVTTV SAKARLVDSR NGKELWSGSA
151 SIREGSNNSN SGLLGALVSA VVNQIANSLT DRGYQVSKTA AYNLLSPYSH
201 NGILKGPRFV EEQPK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 235 shows 96.7% identity over a 215 aa overlap with a predicted ORF (ORF 235.ng) from *N. gonorrhoeae*:

m235/g235

	10	20	30	40	50	60
m235.pep	MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST					
	: : : : :					
g235	MKPLILGLAAVLALSACQVRKAPDLDTYSFKESKPASILVVPPLNESPDVNGTWGMLAST					
	10	20	30	40	50	60
	70	80	90	100	110	120
m235.pep	AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS					
	: : : : :					
g235	AAPISEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS					
	70	80	90	100	110	120
	130	140	150	160	170	180

537

```

m235.pep  YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
          |||||
g235      YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
          |||||
          130      140      150      160      170      180

          190      200      210
m235.pep  DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
          |||||
g235      DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPKX
          |||||
          190      200      210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 873>:

```

a235.seq
1  ATGAAACCTT TGATTTTAGG GCTTGCCGCC GTGTTGGCGC TGTCTGCCTG
51  CCAAGTTCAA AAAGCGCCCG ATTCGACTA CACGTCATTC AAGGAAAGCA
101 AACCGGCTTC AATTTTGGTG GTTCCGCCGC TGAACGAATC GCCCGATGTC
151 AACGGAACAT GGGGTGTACT GGCTTCGACC GCCGCGCCGC TTTCCGAAGC
201 CGGCTATTAC GTCTTCCCGC CCGCAGTCGT GGAGGAAACC TTCAAACAAA
251 ACGGCTTGAC CAATGCCGCC GATATTCACG CCGTCCGGCC GGAAAACTG
301 CATCAGATT TCGGCAATGA TGCGGTTTGT TACATTACGG TTACCGAATA
351 CGGCACTTCA TATCAAATTT TAGACAGCGT GACGACCGTA TCCGCCAAAG
401 CACGGCTGGT CGATTCCCGC AACGAAAAAG AGTTGTGGTC GGGTTCGGCC
451 AGCATCCGCG AAGGCAGCAA CAACAGCAAC AGCGGCCTGT TGGGGGCTTT
501 GGTCAGCGCA GTGGTCAATC AGATTGCCAA CAGCCTGACC GACCGCGGTT
551 ATCAGGTTTC TAAAACCGCC GCATACAACC TGCTGTCGCC CTATTCTCAC
601 AACGGCATCT TGAAGGTCC GAGATTCGTC GAAGAGCAGC CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 874; ORF 235.a>:

```

a235.pep
1  MKPLILGLAA VLALSACQVQ KAPDFDYTSF KESKPASILV VPPLNESPDV
51  NGTWGVLAST AAPLSEAGYY VFPAAVVEET FKQNGLTNAA DIHAVRPEKL
101 HQIFGNDAVL YITVTEYGTS YQILDSVTTV SAKARLVDSR NGKELWSGSA
151 SIREGSNNSN SGLLGALVSA VVNQIANSLT DRGYQVSKTA AYNLLSPYSH
201 NGILKGPRFV EEQPK*

```

m235/a235 100.0% identity in 215 aa overlap

```

m235.pep  10      20      30      40      50      60
          MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
          |||||
a235      10      20      30      40      50      60
          MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST

m235.pep  70      80      90      100     110     120
          AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
          |||||
a235      70      80      90      100     110     120
          AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS

m235.pep  130     140     150     160     170     180
          YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
          |||||
a235      130     140     150     160     170     180
          YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT

m235.pep  190     200     210
          DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
          |||||
a235      190     200     210
          DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 875>:

g236.seq

```

1  ATGGCGCGTT TCGCCTTCTC CGCCGACATT CTCCGCACAG CGTTTGCAGA
51  CGGTTTTATA ACCTGCAACC GCGCCACAT CGCGGGTGTA ATGCCAGCAG
101 CGTTTCGCATT TTTCGCCGTC GCTGGCTTTG GCGGCAACGG CAAGTTCATC
151 ACCGACTTTC ACTTCTGCTT TAGACACCAG CAGGGCAAAG CGCAATTCTT
201 CGCCCAAAGC ATTACAGATAG CCGGCCATTT CTTCCGGCGC GGTAATTTTCG
251 GCTTCCGCCT GCAAggacga accgacagTT TTGTcggcGC GCAAAGGCTC
301 GAtagcggcg gTTACTGCTT CGCGCGCTTC GCGGATTGCC GTCCATTTTT
351 TCACCAgTTC GGCTTCGGCT TTTTCGTGA TGGCCGGGAA CTCGTGCCAA
401 GTATGGAAGA GGACGCTGTC TTCTTCGCCG CCGCCGATGA TGTCCCAACG
451 TTCTTCGCCG GTGAAGCACA AAATCGGTGC AATCAAGAGA ACCAGGCTGC
501 GCGTGATGTG GTACAGGGCG GTTTGCGCGC TCGCGCGGGC GCGGCTGTGC
551 GCTTTGGTGG TGTAGAGGCG GTCTTTCAGG ATGTCGAGGT AGAACGCGCC
601 CAAGTCTTCC GAGCAGAAAG AAACAATGTC TTTACGGCG AAGTGGAAAG
651 CATAGCGCGG ATAGTAACCG CCTGCCAAAC GCTCTTGCA CCGCCGCGCC
701 AATACCAAGG CGTAGCGGTC GATTTCACC ATATCCGCTT GTTGACCGG
751 ATCTTCAATC GGATTAAAGT CGCTCAAATT GGCAAacagG AAGCTCAAGG
801 TATTGCGGAT GCGGCGGTAG CTTTCGGTAA CGCGTTTGAG GATTTCCTTG
851 GAAatcgCCA ATtcgcgcgt gTAATCGGTG GATGCCGCCC ACAGGCGCAG
901 GATGTCCGCG CCGAATTCGT TATAGACTTC CTGCGCGCG ACGACGTGCG
951 CGATGGATTT CGACATTTTG CGGCCGTTTT GGTCAACCAC GAAACCGTGG
1001 GTCAGCAGCT GTTTATACGG TGC GCGTCCC ATGGATGA

```

This corresponds to the amino acid sequence <SEQ ID 876; ORF 236.ng>:

g236.pep

```

1  MARFAFSADI LRTAFADGFI TCNRAHIAGV MPAAFAFFAV AGFGNGKFI
51  TDFHFCFRHQ QGKAOFFAQS IQIAGHFFRR GNFGFRLQGR TDSFVGAQRL
101 DSGGYCFARF ADCRPFFHQF GFGFFVDGRE LVPSMEEDAV FFAAADVPR
151 FFAGEAQNRC NQENQAARDV VQGGLRAAAG AAVGFGGVEA VFQDVEVERA
201 QVFRAERNNV FHGEVEGIAR IVTACQTLLO PPRQYQGVAV DFHHIRLLHG
251 IFNRIKVAQI GKQEAQGIAD AAVAFGNAFE DFFGNRQFAA VIGGCRPQAO
301 DVRAEFVIDF LRRDDVADGF RHFAAVLVNH ETVGQQLFIR CASHG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 877>:

m236.seq (partial)

```

1  ..TTGCACGGAC GAACCGACGG TTTTGTGCGC GCGCAAAGGC TCGATGGCGG
51  CGGTTACCGC TTCGCGGGCT TCGCGGATTG CCGTCCATTT TTTCACCACT
101 TCGGCTTCGG TTTTTCGTT GATGGTCGGG AACTCGTGCC AAGTATGGAA
151 GAGGACGCTG TCKTCTTCGC CGCCGCCGWT GAyGTCCAC GCTTCTTCGC
201 CGGTGAAGCA CAAAATCGGT GCAATCAAGA GAACCAACT CCGTGTGATG
251 TGATACAGGG CAGTTTGTGC GCTGCGCGT GCATGGCTGT CTGCTTTGGT
301 GGTGTAGAGG CGGTCTTTCA GGATGTCGAG GTAGAACGCA CCCAAGTCTT
351 CCGAGCAGAA AGAAACArTG TCTTTTACGG CAAAGTGGaA kGCATAACGC
401 GGATAGTAAT CGCCTGCCAG AACTCTTGC AGCTGACGTG CCAATACCAC
451 GGCGTAGCGG TCGATTTCCA CCATATCCGC CTGTTGCACG GCATCTTCAA
501 TCGGATTAAA GTCGCTCAAG TTGGCAAACA AAAAGCTCAA GGTATTGCGG
551 ATACGGCGGT AgCTTTCGGT TACGCGTTTG AGGATTTCTT TGGAAATCGC
601 CAATTGCGCG CTGTAATCGG TAGATGCCGC CCACAGGCGC AGGATGTCTG
651 CGCCGAATTC GTTATAAACC TCTTGCGGTG CAACGACGTT GCCGATGGAT
701 TTCGACATTT TTTTGCCTTC GCCGTCGACA ACGAAACCAT GGGTCAGCAG
751 CTGTTTATAC GCGCGCGGAC CCATTGA

```

This corresponds to the amino acid sequence <SEQ ID 878; ORF 236>:

m236.pep (partial)

```

1  ..LHGRTDGFVG AQRLDGGGYR FAGFADCRPF FHQFGFGFFV DGRELVPSME
51  EDAVXFAXAX DVPRFFAGEA QNRNQNENQT ACDVIQSLC AAACMAVCFG
101 GVEAVFQDVE VERTQVFAE RNxVfYgKVE XITRIVIAcQ TLLQLTCQYH
151 GVAVDFHHIR LLHGIFNRIK VAQVGKQKAQ GIADTAVAFG YAFEDFFGNR
201 QFAAVIGRCR PQAQDVCAEF VINLLRCNDV ADGFRHFFAF AVDNETMGQQ
251 LFIRATH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 236 shows 82.9% identity over a 258 aa overlap with a predicted ORF (ORF 236.ng) from *N. gonorrhoeae*:

m236/g236

[illegible]

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 879>:

```
a236.seq
1 ATGGCGCGT TCGCCTTCTC CGCCGACATT CTCTGCACAG CGTTTGCA
51 CGGTTTCATG GCCTGCAACC GCGCCCACAT CGCGGGTGTA GTGCCAGCAG
101 CGTTCGCATT TTTCCACCAT ACTGGCTTTA GCGGCAACGG CAAGTTCGCT
151 GCCTACTTTT ACTTCTGCTT TAGACACCAG CAAAGCAAAG CGCAATTCCT
201 CGCCCAAAGC ATTCAGATAG CCGGCCATTT TTTCCGGCGC GTAAATTTTC
251 GCTTCGGCTT GCAAGGACGA ACCGACGGTT TTGTCGGCGC GCAAAGGCTC
301 GATGGCGGCG GTTACCGCTT CGCGGGCTTC GCGGATTGCC GTCCATTTTT
351 TCACCAGTTT GGCTTCGGCT TTTTCGTTGA TGGTCCGGGA CTCGTGCCAA
401 GTATGGAATA GCACGTGTCT TTCTCGCCG CGCCCGATGA TGTCCCACGC
451 TTCTTCGCCG GTGAAGCACA AATCCGGTGC AATCAAGAGA ACCAGGCTGC
501 GCGTGATGTG GTACAGGGCG GTTTGCGCGC TCGCGCGGGC GCGGCTGTCT
551 GCTTTGGTGG TATAGAGCGG GTCTTTCAGG ATATCGAGGT AGAACGCGCC
601 CAAGTCTTCC GAGCAGAAAG AAACCATTTC TTTACGGCA AAGTGAAGG
651 CATAACCGCG ATAAAAATCA CGGGCAACGC GTTCTTGCAG CCGCTTGCC
701 AACACCAAGG CATTCCGCTC GATTCCACC GATTCCGCTT GTTGCACGGC
751 ATCTTCAATA GGATTGAAGT CGCTCAAGTT GGCAAACAAA AAGCTCAAGG
801 TATTGCGGAT ACGGCGGTAG CTTTCGGTTA CGCGCTTGAG GATTTCCTTG
851 GAAATCGCCA ATTCGCGCCT GTAATCGGTG GATGCCGCCC ACAGGCGCAG
901 GATGTCGCGC CGAACTCGT TATACACTTC TTGCGGCGCG ACGACGTTGC
951 CGATGGATTG CAGCATTTTG CGCCCGTTTT GATCCACCAC GAAACCATGG
1001 GTCAGCAGCT GTTTGTACGG CGCGCGACCC ATTGA
```

This corresponds to the amino acid sequence <SEQ ID 880; ORF 236.a>:

a236.pep	1	MARFAFSADI	LCTAFADGFM	ACNRAHIAGV	VPAAFAFFTI	TGFSGNCKFA
	51	AYFHCFRHIQ	QSKAQFFFAQS	IQIAGHFRR	GNFGFLQHR	TDGFVGAQRL
	101	DGGGYRFAGF	ADCRPFHFQF	GFGFVDGREG	LVPSMEKHAV	FCAAADVDPV
	151	FFAGEAQNRC	NQENQAARDV	VQGGRLAAAG	AAVGFGGIEA	VFQDIEVERA
	201	QVFRAENNHF	FHGKVEGIR	IKITGNAFLQ	PPCQHQIAFV	DFHHIRLLHG
	251	IFNRIEVAQV	GKQKAQGIAD	TAVAFGYALE	ETFGNRQFAV	VIGGCRPQAO
	301	DVRAELVIHF	LRRDDVADGF	RHEAPVLTHH	DDMGOOLEVR	RATH*

m236/a236 81.0% identity in 258 aa overlap

```

m236.pep                               LHGRTDGFVGAQRLDGGGYRFAGFADCRPF
                                     |:|||||||||
a236    FRHQQSKAQFFAQSIQIAGHFFRRGNFGFLQGRTDGFVGAQRLDGGGYRFAGFADCRPF
          60      70      80      90      100     110

                40      50      60      70      80      90
m236.pep    FHQFGFGFFVDGRELVPSMEEDAVXFAXDVPRFFAGEAQNRCNQENQTACDVIQGSCLC
            |||||
a236    FHQFGFGFFVDGRELVPSMEKHAVFCAAADDVPRFFAGEAQNRCNQENQAARDVVQGGCLR
          120     130     140     150     160     170

                100     110     120     130     140     150
m236.pep    AAACMAVCFGGVEAVFQDVEVERTQVFRAERNXVFYGVKEXITRIVIAQCOTLLQLTCQYH
            ||| || |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
a236    AAAGA AVGFGGIEAVFQDIEVERAQVFRAERNHHFFHGKVEGITRIKITGNAFLQPPCQHQQ
          180     190     200     210     220     230

                160     170     180     190     200     210
m236.pep    GVA VDFHHIRLLHGIFNRIKVAQVGKQKAQGIADTAVAFGYAFEDFFGNRQFAAVIGRCR
            |:|||||||||:|||||||||:|||||||||:|||||||||:|||||||||
a236    GIA VDFHHIRLLHGIFNRIEVAQVGKQKAQGIADTAVAFGYALEDDFFGNRQFAAVIGGCR
          240     250     260     270     280     290

                220     230     240     250     259
m236.pep    PQA QDVCAEFVINLLRCNDVADGFRHF FAFVDNETMGQQLFIRRATHX
            ||||| :|::|::|:|::|::|:|::|::|:|::|::|:|::|::|
a236    PQA QDVRAELVIHF LRRDDVADGFRHFAPVL IHHETMGQQLFVR RATHX
          300     310     320     330     340

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 881>:

g237.seq					
1	atgcggggaca	agggttggcgg	taatatcgca	ctccccgcc	cacgaatat
51	cgattctaac	atcgggcaagc	tgcggaaaaa	ctttaagcat	atcttgccg
101	acaagctcgg	tcatacgcgc	aggattgtcg	ataaatctgt	tatccttacc
151	gccgaaaagc	agcctgcggt	cgcgcgtgag	gcggttaata	tccaaaaata
201	ggcgggttgt	gcatactgcc	atatgtgtgc	ggataagccc	ttttgtgcgc
251	gcgccaagg	gttcgggtggc	aataataaag	gtgctgacgg	caatcgccct
301	gcgttccaaa	ggcgggaata	tggggttcaa	accgacataa	gtattgacgg
351	catagaccac	atTTTTTtac	tgcacgctgc	cttcggggcgt	gtaaaccagc
401	caaccgtttt	gatacgggtc	gatgcgcgtc	atcgggggatt	gctcgaaaaa
451	ctgcgcgcgc	gcttcggcag	cggcgctggc	aacaccaaac	gtgtaattga
501	gcggatgaag	atgcccggac	aagggatcga	actgtgcgcc	ttgtacata
551	tcgctgtcaa	gctgctgttt	caactcggct	ttatcccaa	gttgataatg
601	actcgaccgc	taatgcccgt	gggcgtgttc	atgccactgc	tgcaactctt
651	cccaatgctg	cggacggacg	gcaaccgtgg	cataaccgcg	ctgccaatcg
701	caatcgatgg	catgttttgcg	gacgcgttcg	tccaccagt	cgaccgcctt
751	caaagactgt	tgccaaaacc	attgcgcctg	ctccaaccgc	acctgttttt
801	caatttcccc	cataccgcag	gcgtagtcgc	tgataaactg	cccgccactc
851	ctgcgggacg	cgccgaagcc	gatacgtgcg	gcttccaaaa	cgacgggctt
901	atgtccgtgt	tccgccagcg	gcaatgcggt	acacaaaacc	ctcaaaccgc
951	cgccgataat	gcagggtttcg	gcttttcagc	ggcattggag	tttcggataa
1001	acagtatcgc	gattaaccga	actaaaaata	taagaaggca	gatattcttg
1051	aaaatcaggg	cgaatcattg	tgtttgcctt	atcgggtata	tttccggacg
1101	gaatgataca	gactgtcggg	ccatatcgtc	caaacagaaa	atcgggttga

This corresponds to the amino acid sequence <SEQ ID 882; ORF 237.ng>:

g237.pap

1 MRDKVGGNIA LPAPRIFDSN IGKLRKNFKH ILADKLGHTR RIVDKFVILT
51 AEKQPAVRAE AVIIQNMAVV AYCHIVADKP FCARAQGGFGG NNGGADGNRL

101 AFQRPEYRVQ TDISIDGIDH IFTLDAAFGR VNQPTVLIRF DARHRGLEN
 151 LRAFGSGAG NTORVIERMK MPQGIELCA LVHIAVKLLF QLGFI PKLIM
 201 TRTVMPLGVF MPLLQLFPML RTDGNRGITA LPIAIDGMFA DAFVHQFDRL
 251 QRLLPKPLRL LQADLFFNFP HTAGVVADNL PATPAGRAEA DTCGFQNDGF
 301 MSVFRQRQCG TOTAQTAADN AGFGQTALF FRINSMRINR TKIIRQIFL
 351 KIRANHCVCF IGYIFGRNDT DCRAISSKQK IG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 883>:

m237.seq
 1 ATGCGGGACA AGGTTGGCGG TAATGTCGCA CTCCCCGCCC CACGAATATT
 51 CGATTTTACG ATCGGCAAGC TGCGGAAAAA CTTTAAGCAT ATCTTGGCGG
 101 ACAAGCTCGG TCATACGCTC AGGATTGTCG ATAAACTCGT TATCCTTACC
 151 GCCGAAAAGC AGTCTGCCGT CCGCGCTGAG GCGGTAATAA TCCAAAATAT
 201 GGCGGTTGTC GCATACTGCC ATATTGTTAC GGATAAGCCC TTTTGGCGCG
 251 GCGGCAAGG GTTCGGTCCG AATAATAAAG GTGCTGACAG CAATCGCCTT
 301 GCGTTCCAAA GGCCGGAATA TCGGGTTCAA ACCTGCATAA GTATTGACAG
 351 CATAGACCAC ATTTTTCAC TCGACGCTGC CTTCGGGCGT GTAAACCAGC
 401 CAACCGTTT GATGCGGTTT GATGCACGTC ATCGGGGATT GCTCGAAAAT
 451 CTGCGCACCG GCTTCGGCAG CGGCACGAGC GATGCCCCAA GTGTAAGTGA
 501 GCGGATGCAG GTGTCCGGAT AAGGGGTCGA ATTGTGCCCC TTGGTACATA
 551 TCGCTGTCAA GCTGCTGTTT CAACTCGGCT TTATCCCAA GTTGATAATG
 601 ACTCGCACCG TAATGCCGTT GGGCGTGTTC ATGCCACTGC TGCAACTCTT
 651 CCCAATGCTG CGGACGGACG GCAACCGTGG CATAACCGCG CTGCCAATCA
 701 CAATCGACGG CATGTTTTCG GACGCGTTCG TCCACAGTT CGACCGCCTG
 751 CAAAGACTGT TGCCAAAACC ATTGCGCCTG CTCCAAGCCG ACCTGTTTTT
 801 CAATTTCCCC CATAACCGAG nCGTAATCGC TGATAACCTG CCCGCCACTC
 851 CGTCCCGACG CGCCGAAACC GATACGCGCG GCTTCCAACA CAACCGTTTC
 901 ATGTCCCTGC TCCGCCAAGG GCAATGCAGT GCACAAACCA CCCAATCCGC
 951 CGCCGATGAT ACAGGTATCG GTTTTCAGAC GGCATTGAAG TTtCGGATAA
 1001 ACAGTATGAG GATTAACCGA ACTGAAATAA TAAGAAGGCA GATATTCTTG
 1051 AAAATCAGGG CGAATCATTG TGTGCTTTT ATCAGGTGTA TTTTCGGACG
 1101 GAATGATACA GGCTGTCGGG CCATATCGTC CAWACAGAAA ATCGGTTGA

This corresponds to the amino acid sequence <SEQ ID 884; ORF 237>:

m237.pep
 1 MRDKVGGNVA LPAPRIFDFD IGKLRKNFKH ILADKLGH TL RIVDKLVILT
 51 AEKQSAVRAE AVIIQNMAVV AYCHIVTDKP FCARPQGFGR NNKGADSNRL
 101 AFQRPEYRVQ TCISIDSIDH IFALDAAFGR VNQPTVLMRF DARHRGLEN
 151 LRTGFGSGTS DAQSVSERMQ VSGXGVELCP LVHIAVKLLF QLGFI PKLIM
 201 TRTVMPLGVF MPLLQLFPML RTDGNRGITA LPITIDGMFA DAFVHQFDRL
 251 QRLLPKPLRL LQADLFFNFP HTAXVIADNL PATPSRAET DTRGFOHNR
 301 MSLRQGCQS AQTTSAAAD TGIGFQTALK FRINSMRINR TEIIRQIFL
 351 KIRANHCVCF IRCIFGRNDT GCRAISSKQK IG*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 237 shows 86.1% identity over a 382 aa overlap with a predicted ORF (ORF 237.ng) from *N. gonorrhoeae*:

m237/g237

	10	20	30	40	50	60
m237.pep	MRDKVGGNVALPAPRIFDFDIGKLRKNFKHILADKLGH TL RIVDKLVILTAEKQSAVRAE					
g237	MRDKVGGNIALPAPRIFDSNIGKLRKNFKHILADKLGH TR RIVDKFVILTAEKQPAVRAE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m237.pep	AVIIQNMAVVAYCHIVTDKPFCARPQGFGRNNKGADSNRLAFQRPEYRVQTCISIDSIDH					
g237	AVIIQNMAVVAYCHIVADKPFCARQGFGRNNKGADGNRLAFQRPEYRVQTDISIDGIDH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m237.pep	IFALDAAFGRVNQPTVLMRFDARHRGLENLRTGFGSGTSDAQSVSERMQVSGXGVELCP					

[illegible]

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 885>:

```

a237.seq
1      ATGCGGGACA AGGTTGGCGG TAATGTCGCA CTCCCCGCCC CACGAATATT
51     CGATTTTGAC ATCGGCAAGC TGCGGAAAAA CTTTAAGCAT ATCTTGCGCG
101    ACAAGCTCGG TCATACGCGC GGGATTGTCT ATAAACTCGT TATCCTTACC
151    GCCGAAAAGC AGTCTGCCGT CCGCGCTGAG CGGTAATATA TCCAAATAT
201    GACGGTTGTC GCATACTGCC ATATTGTTGC GGATAAGCCC TTTTGCACGC
251    GCGCCAAGG GTTCTGTGGC AATAATAAAG GTGCTGACAG CAATCGCCTT
301    GCGCTCCAA GGCTTGAATA TCGATTCAA ACCGGCATAA GTATTGACGG
351    CGTACACCAG ATTTTTCGAT TCGAGCTGCG CTTCGGGGGT GTAAACACGC
401    CAACCGTTTT GATAAGGTTT AATGCGTATC ATGGGAGAAT GCTCAAAAAT
451    CTTCGTACCA GCTTCGGCAG CGGCGCGGGC GATGCCCAAC GTGTAATTGA
501    GCGGATGGAG ATGCCCGGAC AAGGGATCGA ACTGTGCGCC TTGGTACATA
551    TCGCTGTCAA GTTGTGCTT CAGTTTCAGT TTATCCCAGA GTTGATAATG
601    AGTTGCACCG TAATATTTTT GGGCGTGCTC ATGCCATTGT TGCATTCTT
651    CCCAATGCTG CGAACGGATG GCAACCGTGG CATAACCGCG TGCCAATCG
701    CAATCAATGG CATGTTTGCG GACGCGTTCG TCCACCAGTT CGACCGCCTG
751    CAAAGACTGT TGCCAAAACC ATTGCGCTTG CTCCAAACCG ACCTGTTTTT
801    CAATTTCTCT CATACCGCAG GCGTAATCGC TGATAACCTG CCCGCCACTC
851    CGTCCCGACG CGCGGAAAAC GATACGCGCG GCTTCCAACA CACCGCTTTC
901    ATGTCCCTGC TCCGCCAAGG GCAATGCAGT GCACAAACCA CTCAATCCGC
951    CGCCGATGAT ACAGGTATCG GTTTTCAGAC GGCATTGAAG TTTCGGATAA
1001   ACAGTATGAG GATTAACCGA ACTGAAATAA TAAGAAGGCA GATATTCTTG
1051   AAAATCAGGG CGAATCATTT TGTTTGCTTT ATCGGGTATA TTTTCGGACG
1101   GAATGATACA GGCTGTCGAG CCATATCGTC CAACAGAAAA ATTCGGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 886; ORF 237.a>:

a237.pap

1	MRDKVGGNVA	LPAPRIFDFD	IGKLRKNFKH	ILADKLGHTR	GIVDKLVILT
51	AEKQSAVRAE	AVIIQNMVTV	AYCHIVADKP	FCTRAQGQGC	NNKGADSNRL
101	ALQRLERYIQ	TGISIDGVHQ	IFAFDAAFGC	VNQPTVLIRF	NAYHGRLMLN
151	LRTSFGSGAG	DAQRVIERME	MPQGQIELCA	LVHIAVKLLL	QFSVIPLEIM
201	<u>SCTVIFLGLV</u>	<u>MPLLQFFPML</u>	RTDGNRGITA	LPIAINGMFA	DAFVHQFDRL
251	QRLLPKPLRL	LQTDLFNFEL	HTAGVIADNL	PATPSRAAET	DTRGFQHNRF
301	MSLLRQGCQS	AQTTQSAADD	TGIGFQTALK	FRINSMRINR	TEIIRRQIFL
351	KIRANHCVCF	IGYIFGRNDT	GCRAISSKOK	IG*	

m237/a237 85.6% identity in 382 aa overlap

m237.pep	10	20	30	40	50	60
	MRDKVGGNVALPAPRIFDFDIGKLRKNFKHILADKLGHTLRIVDKLVILTAEKQSAVRAE					
a237	MRDKVGGNVALPAPRIFDFDIGKLRKNFKHILADKLGHTRGIVDKLVILTAEKQSAVRAE					
	10	20	30	40	50	60
m237.pep	70	80	90	100	110	120
	AVIIQNMAVVAYCHIVTDKPFPCARPQGFRNNKGADSNRLAFQRPYRVQTCISIDSIDH					
a237	AVIIQNMTVVAYCHIVADKPFCTRAQGFSGNNKGADSNRLALQRLRYRIQTGISIDGVHQ					
	70	80	90	100	110	120
m237.pep	130	140	150	160	170	180
	IFALDAAFGRVNQPTVLMRFDARHRLLENLRTGFGSGTSDAQSVSERMQVSGXGVELCP					
a237	IFAFDAAFGGVNQPTVLIRFNAYHGRMLKNLRTSFGSGAGDAQRVIERMEMPGQGIELCA					
	130	140	150	160	170	180
m237.pep	190	200	210	220	230	240
	LVHIAVKLLFQLGFIPKILMTRTMPLGVFMPLQLFPMRLTDGNGRITALPITIDGMFA					
a237	LVHIAVKLLQFSVIPELIMSCTVIFLGVLMPLQLQFFPMLRTDGNGRITALPIAINGMFA					
	190	200	210	220	230	240
m237.pep	250	260	270	280	290	300
	DAFVHQFDRLQRLLPKPLRLQLADLFFNFPHPTAXVIADNLPATPSRRAETDRGFQHNRF					
a237	DAFVHQFDRLQRLLPKPLRLQLADLFFNFPHPTAXVIADNLPATPSRRAETDRGFQHNRF					
	250	260	270	280	290	300
m237.pep	310	320	330	340	350	360
	MSLLRQGQCSAQTTQSAADDTGIGFQTALKFRINSMRINRTEIIRROIFLKIRANHCVCF					
a237	MSLLRQGQCSAQTTQSAADDTGIGFQTALKFRINSMRINRTEIIRROIFLKIRANHCVCF					
	310	320	330	340	350	360
m237.pep	370	380				
	IRCFGRNDTGCRAISSXQKIGX					
a237	IGYIFGRNDTGCRAISSKQKIGX					
	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 887>:

g238.seq

```

1  atgaatttgc ctattcaaaa attcatgatg ctgttggcag cggcaatatc
51  gatgctgcat atccccatta gtcatgcgaa cggtttggat gcccgtttgc
101 gcgatgatat gcaggcaaaa cactacgaac cgggtggcaa ataccatctg
151 tttggtaatg ctcgcggcag tgtaaataat cgggttgcg ccgtccaaac
201 atttgatgca actgcggtcg gcccatact gcctattaca cacgaacgga
251 caggatttga aggtgttatc ggctatgaaa cccatttttc aggacacgga
301 cacgaagtac acagtccgtt cgataatcat gattcaaaaa gcacttctga
351 tttcagcggc ggcgtagacg gcggttttac cgtttaccaa cttcatcgga
401 cagggtcgga aatacatccc gcagacggat atgacgggcc tcaaggcggc
451 ggttatccgg aaccacaagg ggcaagggat atatacagct accatatcaa
501 aggaacttca accaaaacaa agataaacac tgttccgcaa gccccttttt
551 cagaccgctg gctaaaagaa aatgccggtg ccgcttcggg ttttctcagc
601 cgtgcggatg aagcaggaaa actgatatgg gaaaacgacc ccgataaaaa
651 ttggcgggct aaccgtatgg atgatattcg cggcatcgtc caagggtcgg
701 ttaatccttt ttaacgggt tttcaagggt tagggattgg ggcaattaca
751 gacagtgcgg taagcccggg cacagataga gccgctcagc agactctaca
801 aggtattaat gatttaggaa atttaagtcc ggaagcaciaa cttgccgcgc

```

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851 cgagcctatt acaggacagt gcctttgcgg taaaagacgg catcaattcc
901 gccagacaat gggctgatgc ccatccgaat ataacagcaa cagcccaaac
951 tggccttgcc gtagcagagg ccgcaggtag ggtttggcgc ggtaaaaaag
1001 tagaacttaa cccgaccaa tgggattggg ttaaaaaatac cggctataaa
1051 aaacctgctg cccgccatat gcagactgta gatggggaga tggcaggggg
1101 gaatagaccg cctaaatcta taacgtcggg aggaaaagct aatgctgcaa
1151 cctatcctaa gttggttaat cagctaaatg agcaaaactt aaataacatt
1201 gcggctcaag atccaagatt gagtctagct attcatgagg gtaaaaaaaa
1251 ttttccaata ggaactgcaa cttatgaaga ggcagataga ctaggtaaaa
1301 tttgggttgg tgagggtgca agacaaacta gtggaggcgg atgggttaagt
1351 agagatggca ctcgacaata tcggccacca acagaaaaaa aatcacaatt
1401 tgcaactaca ggtattcaag caaatTTTga aacttatact attgattcaa
1451 atgaaaaaag aaataaaatt aaaaatggac atttaaatat taggtaa

```

This corresponds to the amino acid sequence <SEQ ID 888; ORF 238.ng>:

g238.pep

```

1  MNLP IQKFMM LLAA AISMLH IPISHANGLD ARLRDDMQAK HYPEGGKYHL
51  FGNARGSVKN RVCAVQTFDA TAVGPILPIT HERTGFEGVI GYETHFSGHG
101 HEVHSPFDNH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP ADGYDGPQGG
151 GYPEPQGARD IYSYHIKGTs TKTKINTVPQ APFSDRWLKE NAGAASGFLS
201 RADEAGKLIW ENDPDKNWRA NRMDDIRGIV QGAVNPFLTG FQGVGIGAIT
251 DSAVSPVTDt AAQQTlQGIN DLGNLSPEAQ LAAASLLQDS AFAVKDGINs
301 ARQWADAHpN ITATAQTALA VAEAAGTVWR GKKEVLNPTK WDWVKNTGYK
351 KPAARHMqTV DGEMAGGNRP PKSITSEGKA NAATYPKLVN QLNEQNLNNI
401 AAQDPRLSLA IHEGKKNFPI GTATYEEADR LGKIWVGEga RQTSGGGWLS
451 RDGTRQYRPP TEKKSQFATT GIOANFETYt IDSNEKRNKI KNHGLNIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 889>:

m238.seq

```

1  ATGAATTTGC CTATTCAAAA ATTcATGATG CTGTTTGCAG CAGCAATATC
51  GTTGCTGCAA ATCCCCATTA GTCATGCGAA CGGTTTGGAT GCCCGTTTGC
101 GCGATGATAT GCAGGCAAAA CAcTACGAAC CGGGTGGTAA ATACCATCTG
151 TTGGTAATG CTcGCGGCAG TGTAAAAAG CGGGTTTACG CCGTCCAGAC
201 ATTTGATGCA ACTGCGGTCA GTCCTGTACT GCCTATTACA CACGAACGGA
251 CAGGGTTTGA AGGTGTTATC GGTATGAAA CCCATTTTTC AGGGCACGGA
301 CATGAAGTAC ACAGTCCGTT CGATCATCAT GATTCAAAAA GCACTTCTGA
351 TTTCAGCGGC GGTGTAGACG GCGGTTTAC TGTTTACCAA CTTcATCGAA
401 CAGGGTCGGA AATCCATCCG GAGGATGGAT ATGACGGGCC GCAAGGCAGC
451 GATTATCCGC CCCCCGGAGG AGCAAGGGAT ATATACAGCT ATTATGTCAA
501 AGGAACtTCA ACAAAAACAA AGACTAATAT TGTCCCTCAA GCCCATTtTT
551 CAGACCGTTG GCTAAAAGAA AATGCCGGTG CCGCCTCTGG TTTTTTCAGC
601 CGTGCGGATG AAGCAGGAAA ACTGATATGG GAAAGCGACC CCAATAAAAA
651 TTGGTGGGCT AACCGTATGG ATGATGTTcG CGGCATCGTC CAAGGTGCGG
701 TTAATCCTTT TTAATGGGT TTTCAAGGAG TAGGGATTGG GGCAATTACA
751 GACAGTGCAG TAAGCCCGGT CACAGATACA GCCGCGCAGC AGACTCTACA
801 AGGTATTAAT GATTTAGGAA AATTAAGTCC GGAAGCACA CTTGCTGCCG
851 CGAGCCTATT ACAGGACAGT GCTTTTGCgG TAAAAGACGG TATCAACTCT
901 GCCAAACAAT GGGCTGATGC CCATCCAAAT ATAACAGCTA CTGCCCCAAC
951 TGCCCTTTCC GCAGCAGAGG CCGCAGGTAC GGTTTGGAGA GGTAAAAAG
1001 TAGAACTTAA CCCGACTAAA TGGGATTGGG TTAAAAATAC CGGTTATAAA
1051 AAACCTGCTG CCCGCCATAT GCAGACTTTA GATGGGGAGA TGGCAGGTGG
1101 GAATAAACCT ATTAAATCTT TACCAACAG TGCCGCTGAA AAAAGAAAAc
1151 AAAATTTTGA GAAGTTTAAT AGTAActGGA GTTCAGCAAG TTTTGATTCA
1201 GTGCACAAAA CACTAACTCC CAATGCACCT GGTATTTTAA GTCCTGATAA
1251 AGTTAAAACT CGATACACTA GTTTAGATGG AAAAATTACA ATTATAAAAG
1301 ATAACGAAAA CAActATTTT AGAATCCATG ATAATTCACG AAAACAGTAT
1351 CTTGATTCAA ATGGTAATGC TGTGAAAACC GGTAAATTAC AAGGTAAGCA
1401 AGCAAAAGAT TATTTACAAC AACAAACTCA TATCAGGAAC TTAGACAAAT
1451 GA

```

This corresponds to the amino acid sequence <SEQ ID 890; ORF 238>:

m238.pep

```

1  MNLP IQKFMM LFAAAISLLQ IPISHANGLD ARLRDDMQAK HYPEGGKYHL
51  FGNARGSVKK RVYAVQTFDA TAVSPVLPIT HERTGFEGVI GYETHFSGHG
101 HEVHSPFDHH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP EDGYDGPQGS

```

Homology with a predicted ORF from *N. gonorrhoeae*

m238/g238

BNSDOCID: <WO 8957280A2 | >

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 891>:

```
a238.seq (partial)
1 ATGAATTGCT CTATCAAAA ATTCATGATG CTGTTTGCG CAGCAATATC
51 GTTGCTGCAA ATCCCCATTA GTCATGCGAA CGGTTTGGAT GCCCGTTTGC
101 GCGATGATAT GCAGGCAAAA CACTACGAAC CGGGTGGTAA ATACCATCTG
151 TTTGGTAATG CTCGCGGCAG TGTAAAAAAT CGGGTTTACG CCGTCCAAAC
201 ATTTGATGCA ACTGCGGTCG GCCCCATACT GCCTATTACA CACGAACGGA
251 CAGGATTTGA AGGCATTATC GGTATGAAA CCCATTTTTC AGGACATGGA
301 CATGAAGTAC ACAGTCCGTT CGATAATCAT GATTCAAAAA GCACTTCTGA
351 TTTCAGCGGC GCGGTAGACG GTGGTTTTAC CGTTTACCAA CTTTCATCGGA
401 CAGGGTCGGA AATCCATCCG GAGGATGGAT ATGACGGGCC GCAAGGCAGC
451 GATTATCCGC CCCCCGGAGG AGCAAGGGAT ATATACAGCT ACTATGTCAA
501 AGGAACTTCA AAAAAACAA AGAGTAATAT TGTTCCTCCG GCCCATTTT
551 CAGACCGCTG GCTAAAAGAA AATGCCGCTG CCGCCTCTGG TTTTTCAGC
601 CGTGCTGATG AAGCAGGAAA ACTGATATGG GAAAGCGACC CCAATAAAAA
651 TTGGTGGGCT AACCGTATGG ATGATATTCG CGGCATCGTC CAAGGTGCGG
701 TTAATCCTTT TTAATGGGT TTTCAAGGAG TAGGGATTGG GGCAATTACA
751 GACAGTGCAG TAAGCCCGGT CACAGATACA GCCGCGCAGC AGACTCTACA
801 AGGTATTAAT CATTTAGGAA ATTTAAGTCC CGAAGCACAA CTTGCGGCTG
851 CAACCGCATT ACAAGACAGT GCTTTTGCAG TAAAAGACGG TATCAATTCC
901 GCCAGACAAT GGGCTGATGC CCATCCGAAT ATAAGTCAA CAGCCCAAAC
951 TGCCCTTGCC GTAGCAGAGG CCGCAACTAC GGTTTGGGGC GGTAAAAAAG
1001 TAGAACTTAA CCCGACCAA TGGGATTGGG TAAAAAATAC CGGCTATAAA
1051 ACACCTGCTG TTCGCACCAT GCATACTTTG GATGGGGAAA TGGCCGGTGG
1101 GAATAGACCG CCTAAATCTA TAACGTCCAA CAGCAAAGCA GATGCTTCCA
1151 CACAA
```

This corresponds to the amino acid sequence <SEQ ID 892; ORF 238.a>:

```
a238.pep (partial)
1 MNLPIQKFMM LFAAAISLLQ IPISHANGLD ARLRDDMQAK HYPEGGKYHL
51 FGNARGSVKN RVYAVQTFDA TAVGPILPIT HERTGFEGII GYETHFSGHG
101 HEVHSPFDNH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP EDGYDGPQGS
151 DYPPPGGARD IYSYVKGTS TKTKSNIVPR APFSDRWLKE NAGAASGFFS
201 RADEAGKLIW ESDPNKNWWA NRMDDIRGIV QGAVNPFLMG FQGVGIGAIT
251 DSAVSPVTDI AAQOTLQGIN HLGNLSPFAQ LAAATALQDS AFAVKDGIN
301 ARQWADAHPN ITATAQTALA VAEAATTVWG GKKVELNPTK WDWVKNTRYK
351 TPAVRTMHTL DGEMAGGNRP PKSITSNSKA DASTQ
```

m238/a238 91.9% identity in 385 aa overlap

m238.pep	10	20	30	40	50	60
	MNLPIQKFMM	LFAAAISLLQ	IPISHANGLD	ARLRDDMQAK	HYPEGGKYHL	FGNARGSVK
a238	10	20	30	40	50	60
	MNLPIQKFMM	LFAAAISLLQ	IPISHANGLD	ARLRDDMQAK	HYPEGGKYHL	FGNARGSVK
m238.pep	70	80	90	100	110	120
	RVYAVQTFDA	TAVSPVLPIT	HERTFEGVIG	YETHFSGHG	HEVHSPFDH	DSKSTSDFSG
a238	70	80	90	100	110	120
	RVYAVQTFDA	TAVGPILPIT	HERTFEGVIG	YETHFSGHG	HEVHSPFDH	DSKSTSDFSG
m238.pep	130	140	150	160	170	180
	GVDGGFTVYQ	LHRTGSEIHP	EDGYDGPQGS	DYPPPGGARD	IYSYVKGTS	TKTKTNIVPQ
a238	130	140	150	160	170	180
	GVDGGFTVYQ	LHRTGSEIHP	EDGYDGPQGS	DYPPPGGARD	IYSYVKGTS	TKTKSNIVPR
m238.pep	190	200	210	220	230	240
	APFSDRWLKE	NAGAASGFFS	RADEAGKLIW	ESDPNKNWWA	NRMDDVRGIV	QGAVNPFLMG
a238	190	200	210	220	230	240
	APFSDRWLKE	NAGAASGFFS	RADEAGKLIW	ESDPNKNWWA	NRMDDIRGIV	QGAVNPFLMG
m238.pep	250	260	270	280	290	300
	FQGVGIGAIT	DSAVSPVTDI	AAQOTLQGIN	DLGKLSPEAQ	LAAASLLQDS	AFAVKDGIN

```

a238      |||||
          FQGVGIGAITDSAVSPVTDAAQOTLQGINHLGNLSPEAQLAAATALQDSFAFAVKDGIN
          250      260      270      280      290      300

          310      320      330      340      350      360
m238.pep  AKQWADAHPNITATAQTALSAAEAAGTVWRGKKVELNPTKWDWVKNTGYKKPAARHMQTL
          |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a238      ARQWADAHPNITATAQTALAVAEAATTVWGGKKVELNPTKWDWVKNTGYKTPAVRTMHTL
          310      320      330      340      350      360

          370      380      390      400      410      419
m238.pep  DGEMAGGNKPIKSLP-NSAAEKRKQNFENSNWSSASFDSVHKTLTPNAPGILSPDKVK
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a238      DGEMAGGNRPPKSITSNSKADASTQ

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 893>:

```

g239.seq
1   atgttccacc ataaaggtat tgcccgaaac cggcggatgg aggttttgtt
51  tttctgccgc cgccctgata gcttcgtgat tcgccaaacg cgccctgttg
101 agcctcattt gcgcataatc ctgctccaag gcgatttcct gttttttcgc
151 cttgtccaaa gctgtgaagt tgagcctgta ctggttttgc tgcatacaca
201 cggaaaaagc ggaaacgcac accgcaagca gcagaaagaa attcgatttg
251 ttcattgccg ttcagacgtt tttctctgtt attattccgg tatcggaccg
301 gcagtcgcgt ccgccacacg caaaactgcg ctctcgccc tcgggttggc
351 ggcaatttcc gcttcacccg gctttaatgc cctgcccacg attttcaggg
401 gcggatcggg caaatccgct tctctgaccg ccgcccagct cggcaggggc
451 tcgtgttgcg aatatttttt gacaaactgc ttcacaatgc ggtcttccaa
501 cgaatggaaa gcaatgaccg ccaaacgcc gccctctttc agacggcaca
551 tgacctgcgg caataccgcc cctacttctt caagctcgcg gttaataaag
601 atgcggattg cctggaaggt gcgcgtcgca ggatcctgcc cccgctcgcg
651 agtacggacg tttgtgcca cgatctgcgc cagcttgcgg gttgtatcga
701 ttggactttc cgcccgttgc gcgacaatgg ccgcgacaat ctggcggcta
751 aaccgctctt caccataa

```

This corresponds to the amino acid sequence <SEQ ID 894; ORF 239.ng>:

```

g239.pep
1   MFHHKGIARN RRMEVLFFCR RPDRFVIROT RLLQPHLR II LLQGDFLFFR
51  LVQSCEVEPV LVLHHLHNGKS GNAHRKQOKE IRFVHCRSDV FLCYYSIGIP
101 AVRSATRKTA LLALGLAAIS ASPGFNALPT IFRGSGKSA SLTAAQLGRG
151 SCCEYFLTNC FTMRSSNEWK AMTAKRPPSF RRMTCGNTA PTSSSRLIK
201 MRIAWKVRVA GSCPRSRVRT FCATICASLR VVSIGLSARC ATMARTIWR
251 NRSSP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 895>:

```

m239.seq
1   ATGCTCCACC ATAAAGGTmy kGCCCCGAAAC CGGCKGATGG AGGTTTTGTT
51  TTTCTGCCGC CGCCCTGATC GCTTCGTGGT TCGCCAAACG CGCCTGTTGC
101 AGCCTCATTG GCGCATAATC CTGCTCCAAG GCGATTTCCT GTTTTTTCGC
151 CTTATCCAAA GCTGTGAAAT TGAGCCTGTA CTGGTTTTGC TGCATCACAA
201 CGGAAAAAGC GGAAACGCAC ACCGCAAGCA GCAGAAGGAA ATTCAATTG
251 TTCATTGCCA TTCAGACGTT TTTCTCTGTG ATTGTTCCGG TATCGGACCG
301 GCAGTCCGCT CCGCCACACG CAAAACCGCA CTTCTCGCCC TCGGATTGGC
351 GGCAATTTCC GCCTCACCCG GCTTTAATGC CCTGCCCACG ATTTTCAGGG
401 GCAGCTCGGG CAAATCCGCT TCCCTGACCG CCGCCCAGCG CGGCAGGGGC
451 GCGTGTTCG AATATTTTTT GACAACTGC TTCACAATGC GATCTTCCAA
501 CGAATGGAAA GCAATGACCG CCAAACGTCC GCCCTCTTTC AGACGCACA
551 TGACCTGCGG CAATACTGCC CCTACTTCTT CAAGCTCGCG GTTAATAAAG
601 ATGCGGACCG CCTGGAAGGT GCGCGTCGCA GGATCCTGCC CCCGCTCGCG
651 AGTACGGACG TTTGTGCCA CGATCTGCGC CAGCTTGCGG GTTGATCGA
701 TTGGACTTTC CGCCCGTTGC GCAACAATGG CGCGCGCAAT CCGGCGGCTa
751 AACCGCTCTT cACCATAA

```

This corresponds to the amino acid sequence <SEQ ID 896; ORF 239>:

m239.pep
 1 MLHHKGXARN RXMEVLFFCR RPDRFVVRQT RLLOPHLRRI LLQGDFFLFFR
 51 LIQSCEIEPV LVLLHHNGKS GNAHRKQOKE IQFVHCHSDV FLCDCSGIGP
 101 AVRSATRKA LLALGLAAIS ASPGFNALPT IFRGSSGKSA SLTAAQRGRG
 151 ACCEYFLTNC FTMRSSNEWK AMTAKRPPSF RRHMTGNTA PTSSSSRLIK
 201 MRTAWKVRVA GSCPRSRVRT FCATICASLR VVSIGLSARC ATMARAIRRL
 251 NRSSP*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 239 shows 93.7% identity over a 255 aa overlap with a predicted ORF (ORF 239.ng) from *N. gonorrhoeae*:

m239/g239

m239.pep	10	20	30	40	50	60
	MLHHKGXARNRXMEVLFFCRPDRFVVRQTRLLQPHLRRIILQGDFFLFFRLIQSCEIEPV					
g239	MFHHKGIARNRRMEVLFFCRPDRFVIRQTRLLQPHLRRIILQGDFFLFFRLVQSCEVEPV					
	10	20	30	40	50	60
m239.pep	70	80	90	100	110	120
	LVLLHHNGKSGNAHRKQOKEIQFVHCHSDVFLCDCSGIGPAVRSATRKTALLALGLAAIS					
g239	LVLLHHNGKSGNAHRKQOKEIRFVHCRSDVFLCYSGIGPAVRSATRKTALLALGLAAIS					
	70	80	90	100	110	120
m239.pep	130	140	150	160	170	180
	ASPGFNALPTIFRGSSGKSASLTAAQRGRGACCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
g239	ASPGFNALPTIFRGSSGKSASLTAAQLGRGSCCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
	130	140	150	160	170	180
m239.pep	190	200	210	220	230	240
	RRHMTGNTAPTSSSSRLIKMRTAWKVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC					
g239	RRHMTGNTAPTSSSSRLIKMRIAWKVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC					
	190	200	210	220	230	240
m239.pep	250					
	ATMARAIRRLNRSSPX					
g239	ATMARTIWRLNRSSPX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 897>:

a239.seq

```

1 ATGCTCCACC ATAAAGGTAT TGCCCGAAAC CGGCGGATGG AGGTTTGTGT
51 TTTCTGCCGC CGCCCTGATC GCTTCGTGGT TCGCCAAACG CGCCTGTTGC
101 AGCCTCATTT GCGCATAATC CTGCTCCAAG GCGATTTCCT GTTTTTTCGC
151 CTTATCCAAA GCTGTGAAGT TGAGCCTGTA CTGGTTTTGC TGCATCACAA
201 CGGAAAAGC GGAAACGCAC ACCGCAAGCA GCAGAAGGAA ATTCAATTG
251 TTCATTGCCA TTCAGACGTT TTTCTCTGTG ATTGTTCCGG TATCGGACCG
301 GCAGTCCGCT CCGCCACACG CAAAACCGCA CTTCTCGCCC TCGGATTGGC
351 GGCAATTTCC GCCTCACCCG GCTTTAATGC CCGCCCGCGG ATTTTCAGGG
401 GCGGCTCGGG CAAATCCGCT TCCCTGACCG CCGCCAGCGG CGGCAGGGGC
451 GCGTGTGCG AATATTTTTT GACAACTGC TTCACAATGC GGTCTTCCAA
501 CGAATGGAAA GCAATGACCG CCAAACGTCC GCCCTCTTTC AGACGACACA
551 TGACCTGCGG CAATACTGCC CTAATTCTT CAAGCTCGCG GTTAATAAAG
601 ATGCGGATTG CCTGGAAGGT GCGCGTCGCA GGATCCTGCC CCCGCTCGCG
651 AGTACGACG TTTGTGCCA CGATCTGCGC CAGCTTGCAG GTTGATCGA
701 TTGGACTTTC CGCCGTTGC GCAACAATGG CGCGCGCAAT CTGGCGGCTA
751 AACCGCTCTT CACCATAA

```


This corresponds to the amino acid sequence <SEQ ID 898; ORF 239.a>:

```
a239.pep
  1 MLHHKGIARN RRMEVLFFCR RPDRFVVRQT RLLQPHLRRI LLQGDFLFFR
 51 LIQSCEVEPV LVLLHHNGKS GNAHRKQOKE IQFVHCHSDV FLCDCSGIGP
101 AVRSATRKA LLALGLAAIS ASPGFNALPA IFRGSGSKSA SLTAAQRGRG
151 ACCEYFLTNC FTMRSSNEWK AMTAKRPPSF RRHMTCGNTA PTSSSSRLIK
201 MRIAWKVRVA GSCPRSRVRT FCATICASLR VVSIGLSARC ATMARAIWRL
251 NRSSP*
```

m239/a239 97.3% identity in 255 aa overlap

```

      10      20      30      40      50      60
m239.pep MLHHKGXARNRXMEVLFFCRRPDRFVVRQTRLLQPHLRRIILQGDFFRLIQSCEIEPV
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a239      MLHHKGIARNRRMEVLFFCRRPDRFVVRQTRLLQPHLRRIILQGDFFRLIQSCEVEPV
          10      20      30      40      50      60

      70      80      90     100     110     120
m239.pep LVLLHHNGKSGNAHRKQOKEIQFVHCHSDVFLCDCSGIGPAVRSATRKTALLALGLAAIS
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a239      LVLLHHNGKSGNAHRKQOKEIQFVHCHSDVFLCDCSGIGPAVRSATRKTALLALGLAAIS
          70      80      90     100     110     120

     130     140     150     160     170     180
m239.pep ASPGFNALPTIFRGSSGKSASLTAAQRGRGACCEYFLTNCFTMRSSNEWKAMTAKRPPSF
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a239      ASPGFNALPAIFRGSGKSASLTAAQRGRGACCEYFLTNCFTMRSSNEWKAMTAKRPPSF
          130     140     150     160     170     180

     190     200     210     220     230     240
m239.pep RRHMTCGNTAPTSSSSRLIKMRTAWKVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a239      RRHMTCGNTAPTSSSSRLIKMRIAWKVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC
          190     200     210     220     230     240

      250
m239.pep ATMARAIIRRLNRSSPX
          ||||| ||||| ||||| |||||
a239      ATMARAIWRLNRSSPX
          250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 899>:

```
g240.seq
  1 atgatagaag tcatacattt cttcggcgcc gaaacgcgca gacagtttgc
 51 ttgtgccgac gttggacgat ttctgcataa tgccgcgcac atccaaagag
101 gggtaaacat gggatatcat gcgcacggga gacggtccga ttttataagg
151 ctgcgtattc agccgttcgt tcaaatcggg ttgcccgcga tccaatgcct
201 tcgcaatcac gaacggtttg attgccgaac cagggttcgat catatcgggt
251 acggcacggt tgcgccgctg ttcgctgtct gcccggccgg gtctgttggg
301 atcgtaggcg ggcgtattgg ccaaggcgag gatttcccc gtgcgggcat
351 ccaaaaccac caccgttcg gcttttgct gatggtattc gaccgccttg
401 ttcaactctt cataggccaa ggtctgaatc ctctgatcga gggaaaggat
451 gatgtctttg ccgttttgcg gtgctttatt gcgcggggag tccaagctgt
501 ccacaatatt cccctggcgg tcccgcaaaa caacttcgc gccgtcttcg
551 ccatacaggc tgtcttcaag cgaaagtcc aaaccttcct gacctttgcc
601 gtcaatatcg gtaaattcga tgacgtgtgc aaacagggtg cccatcgggg
651 aatggcggtt taa
```

This corresponds to the amino acid sequence <SEQ ID 900; ORF 240.ng>:

```
g240.pep
  1 MIEVIHFFGA ETRRQFACAD VGRFLHNAAH IQRGVNMGII AHGRRSDFIR
 51 LRIQPFVQIG FARIQCLRNH ERFDCRTRFD HIGYGTVAPL FAVCPAGSVG
101 IVGGRIGQGE DFPRAGIQNH HRSGFCLMVF DRLVQLFIGQ GLNPLIEGKD
151 DVFAVLRCFI ARGVQAVHNI ALPVPQNNFR AVFAIQAVFK RKFQTFLTFA
```

201 VNIGKSDDVC KQVAHRVMAF*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 901>:

```
m240.seq
1   ATGATAGAAG TCATACATTT CTTCCGCACC GAAACGCGCA GACAGTTTGC
51  TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATTT TATAAGGCTG
151 CGTATTCAGC CGTTCGTTCA AATCGGTTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
251 GCACGGTTGC GCCGCTGTTC GCTGTCTGCC CGGCCGGGCC TGTGSGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCCGTG CGGGCATCCA
351 AACCACCAC CGTTCCGGCT TTGCCTGAT GGTATTCGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTTCGGGG CTTTAKTGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGAAAACGA CTTCCGCGCC GTCTTCGCCA
551 TGCAAGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGGCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAA CAGGTTGCCC ATCGGGTAAT
651 GCGTTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 902; ORF 240>:

```
m240.pep
1   MIEVIHFFGT ETRRQFACAD VGRFLHDAAH IQRGVNMGIA HGRRSDFIRL
51  RIQPFVQIGF ARIQCLRNHK RFD CRTGFDH IGYGT VAPLF AVCPAGPVGI
101 VGGRIGQGED FPRAGIQXHH RSGFCLMVFD RLVQLFIGQG LNPLIEGKDD
151 VFAVFRGFXA RGVQAVHNIA LPVPQNDFRA VFAMQAVFKR KFQTFLTFAV
201 NIGKSDDVCK QVAHRVMAF*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 240 shows 94.5% identity over a 220 aa overlap with a predicted ORF (ORF 240.ng) from *N. gonorrhoeae*:

```
m240/g240

      10      20      30      40      50      59
m240.pep MIEVIHFFGTETRRQFACADVGRFLHDAAH IQRGVNMG I-AHGRRSDFIRLRIQPFVQIG
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g240      MIEVIHFFGAETRRQFACADVGRFLHNAAH IQRGVNMG IAHGRRSDFIRLRIQPFVQIG
          10      20      30      40      50      60

      60      70      80      90     100     110     119
m240.pep FARIQCLRNHKRFD CRTGFDH IGYGT VAPLF AVCPAGPVGIVGGRIGQGEDFPRAGIQXH
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g240      FARIQCLRNHERFD CRTGFDH IGYGT VAPLF AVCPAGSVGIVGGRIGQGEDFPRAGIQNH
          70      80      90     100     110     120

      120     130     140     150     160     170     179
m240.pep HRS GFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVFRGFXARGVQAVHNIALPVPQNDFR
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g240      HRS GFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVLRCFIARGVQAVHNIALPVPQNNFR
          130     140     150     160     170     180

      180     190     200     210     220
m240.pep AVFAMQAVFKRK FQTFLTFAVNIGKSDDVCKQVAHRVMAFX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g240      AVFAIQAVFKRK FQTFLTFAVNIGKSDDVCKQVAHRVMAF
          190     200     210     220
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 903>:

```
a240.seq
1   ATGATAGAAG TCATACATTT CTTCCGCACC GAAACGCGCA GACAGTTTGC
51  TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATTT TATAAGGCTG
151 CGTATTCAGC CGTTCGTTCA AATCGGTTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
```

```

251 GCACGGTTGC GCCGCTGTTT GCTGTCTGCC CGGCCGGGCC TGTGGGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCCGTG CGGGCATCCA
351 AAACCACCAC CGTTCCGGCT TTTGCCTGAT GGTATTCGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTTCGGGG CTTTATTGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAAACGA CTTCGCGGCC GTCTTCGCCA
551 TGCAGGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAAA CAGGTTGCCC ATCGGGTAAT
651 GGCGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 904; ORF 240.a>:

```

a240.pep
1 MIEVIHFFGT ETRRQFACAD VGRFLHDAAH IQRGVNMGIA HGRRSDFIRL
51 RIQPFVQIGF ARIQCLRNHK RFD CRTGFDH IGYGTVAPLF AVCPAGPVGI
101 VGGRIGQGED FPRAGIQNH RSGFCLMVFD RLVQLFIGQG LNPLIEGKDD
151 VFAVFRGFIA RGVQAVHNIA LPVPQND FRA VFAMQAVFKR KFQTFLTFAV
201 NIGKSDDVCK QVAHRVMAF*

```

m240/a240 99.1% identity in 219 aa overlap

m240.pep	10	20	30	40	50	60
	MIEVIHFFGTETRRQFACADVGRFLHDAAH IQRGVNMGIAHGRRSDFIRLRIQPFVQIGF					
a240	MIEVIHFFGTETRRQFACADVGRFLHDAAH IQRGVNMGIAHGRRSDFIRLRIQPFVQIGF					
	10	20	30	40	50	60
m240.pep	70	80	90	100	110	120
	ARIQCLRNHKRFDCRTGFDHIGYGTVAPLFAVCPAGPVGIVGGRIGQGEDFPRAGIQXHH					
a240	ARIQCLRNHKRFDCRTGFDHIGYGTVAPLFAVCPAGPVGIVGGRIGQGEDFPRAGIQNH					
	70	80	90	100	110	120
m240.pep	130	140	150	160	170	180
	RSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVFRGFXARGVQAVHNIALPVPQND FRA					
a240	RSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVFRGFIARGVQAVHNIALPVPQND FRA					
	130	140	150	160	170	180
m240.pep	190	200	210	220		
	VFAMQAVFKRKFQTFLTFAVNIGKSDDVCKQVAHRVMAFX					
a240	VFAMQAVFKRKFQTFLTFAVNIGKSDDVCKQVAHRVMAFX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 905>:

```

g241.seq
1 ATGATAGAAG TCATACATTT CTTCGGCACC GAAACGCGCA GACAGTTTGC
51 TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATTT TATAAGGCTG
151 CGTATTCAGC CGTTCGTTCA AATCGGTTTT GCCCGCATCC AATGCCCTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
251 GCACGGTTGC GCCGCTGTTT GCTGTCTGCC CGGCCGGGCC TGTGGGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCCGTG CGGGCATCCA
351 ArACCACCAC CGTTCCGGCT TTTGCCTGAT GGTATTCGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTTCGGGG CTTTATGTGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAAACGA CTTCGCGGCC GTCTTCGCCA
551 TGCAAGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAAA CAGGTTGCCC ATCGGGTAAT
651 GGCGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 906; ORF 241.ng>:

```

g241.pep
1 MPTRPTRAAN PPTPTTWLQT AYCPRPPYRP PSVQTHTPHE PASSTCAAKS

```

```

51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPS C RQSVVMTVR
101 TVDMTCVDFL IGCIAHAFNR SFKADFACQ RMVAVHHRLA VGNIGYTIDD
151 NIAGFRIVRF KHHTDLDFNR ERARIFNTDQ LRIMLTERIV GRKRHFDRIA
201 GILTVQRLFH QRENADVFN QIRNRFFGFI QKLIVGIIHL IMQRNHGIFC
251 NSHICPFRRS RLITAVF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 907>:

m241.seq (partial)

```

1      ..CGGCAATCAG TGGTGGTGAT GACCGTGCGG GCCGTGGACA TGACCGTGTG
51     CGATTTCTCT ATCGGATGCA TCGCGCACGC TTTCAACTGT AGCCTTAAAG
101    CGGATTTTCA TGCCTGCCAA AGGATGGTTG CCGTCCACCA CCGCCTTGCC
151    GTCGGCAACA TCGTTACAC GATAGACGAC AACATCGCGG GTTTCAGGAT
201    CGTCGGCTTC AAACATCATG CCGACTTCGA CTCAACAGG GAACACGCCC
251    GCATCTTCAG TACGGACCAA CTCCGGATCC TGCTCGCCGA ACGCATCGTC
301    GGGCGACAGC GCCACATGCA CCGTATCGCC GGCATCCTTA CCGTGCAACG
351    CCTCTTCCAC CAAAGGCGAA ATGCCGTCTG AACCGCCGTG CAGATACGCA
401    ATCGGTTCTT CGGTTTGTG CAAAGCTGTA TTGTTGGCAT CATACATCTC
451    ATAATGCAGC GAAACACCG AATTTTTCAC GATAGCCATA TTTGTCTTTT
501    CAGGAACAGC AGATTAATTA CAGGCGCATT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 908; ORF 241>:

m241.pep (partial)

```

1  ..RQSVVMTVR AVDMTVCDFL IGCIAHAFNC SLKADFHACQ RMVAVVHRLA
51  VGNIGYTIDD NIAGFRIVGF KHHADDFDNR EHARIFDTDQ LRILLAERIV
101 GRQRHIDRIA GILTQORLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL
151 IMQRNHGIFH DSHICPFRNS RLITGAF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 241 shows 91.5% identity over a 177 aa overlap with a predicted ORF (ORF 241.ng) from *N. gonorrhoeae*:

m241/g241

				10	20	30
m241.pep				RQSVVVM	TVRAVD	MTCDFLIGCIAHAFNC
					:	
g241	QPTYLLHPSNKM	PSETEQT	LFRRHQI	PPSCRQSVV	MTVRTVDM	TVCDFLIGCIAHAFNR
	70	80	90	100	110	120
	40	50	60	70	80	90
m241.pep	SLKADFACQRM	VAVHHRLA	VGNIGYTID	DNIAGFRI	VGFKHHAD	FDFNREHARIFD
	:				: :	: :
g241	SFKADFACQRM	VAVHHRLA	VGNIGYTID	DNIAGFRI	VRFKHHTD	LDFNRERARIFNT
	130	140	150	160	170	180
	100	110	120	130	140	150
m241.pep	LRILLAERIVG	RQRHIDRIA	GILTVQRLF	HQRENAAVT	AVQIRNRF	FGFVQKLIVGI
	: :	: :				:
g241	LRIMLTERIVG	RKRHFDRIA	GILTVQRLF	HQRENAAVT	AVQIRNRF	FGFIQKLIVGI
	190	200	210	220	230	240
	160	170				
m241.pep	IMQRNHGIFHD	SHICPFRNS	RRLITGA	FX		
		:				
g241	IMQRNHGIFCN	SHICPFRNS	RRLITGA	FX		
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 909>:

a241.seq

1	ATGCCAACAC	GTCCAACTCG	CGCCGCAAAG	CATCCAACCC	CGCCAACCTG
51	GCTTCAGACG	GCATACTGCC	CTCGTCCGCC	ATATCGTCCG	CCGTCCGTGC
101	AAACGCATAC	ACCGCATGAA	CCGGCTTCCT	CAACCTGCAC	GGCAAAATCA
151	CGCAAGCCAC	GGGAAAATTT	TCATAATGCC	CAACCGACAT	ACCTTCTCCA
201	TCCATCAAAC	AAAATGCCGT	CTGAAATGGA	ACAAACCCCT	TTCAACGGG

a241.pap

1	MPTRPTRA	AK	HPTPTWLQ	T	AYCPRPPY	RP	PSVQTHTP	HE	PASSTCAAKS
51	ANRRNFH	NA	QPTYLLH	PSN	KMPSEMEQ	TL	FRRHQIPP	SC	RQSVVMTVR
101	TVDMTVC	DFL	IGCIAHT	FNR	SLKADFH	ACQ	RMVAVHRL	T	QVNGYITDD
151	NIAGFR	IVGF	KHHADF	DFNR	EHARIF	NTDQ	LRILLA	ERIV	GRKRHIDRI
201	GILTQRL	HF	QRNAV	VTAV	QIRNR	FFGFV	QKLIVG	IIHL	IMQRNHGILH
251	DSHICP	FRNS	RLITGA	*					

				10	20	30
m241.pep				RQSVVVMTVRAVDMTVCDFLIGCIAHAFNC		
a241	QPTYLLHPSNKPMPSEMEQTLFRRHQIPPSCRQSVVVMTVRTVDMTVCDFLIGCIAHTFNR					
	70	80	90	100	110	120
	40	50	60	70	80	90
m241.pep	SLKADFHACQRMVAVHHRLAVGNIGYTIDDNIAGFRIVGFKHHADFDFNREHARIFD TDQ					
a241	SLKADFHACQRMVAVHHRLTVGNIGYTIDDNIAGFRIVGFKHHADFDFNREHARIFNTDQ					
	130	140	150	160	170	180
	100	110	120	130	140	150
m241.pep	LRILLAERIVGRQRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRRFFGFVQKLIVGIIHL					
a241	LRILLAERIVGRKRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRRFFGFVQKLIVGIIHL					
	190	200	210	220	230	240
	160	170				
m241.pep	IMQRNHGIFHDSHICPFRNSRLITGAFX					
a241	IMQRNHGILHDSHICPFRNSRLITGAFX					
	250	260				

g241-1.seq

1	ATGATAGAAG	TCATACATTT	CTTCGGCACC	GAAACGCGCA	GACAGTTTGC
51	TTGTGCCGAC	TTGGGACGAT	TCTCGCATGA	TGCCGCGCAC	ATCCAAGAG
101	GGGTAACAT	GGGTATCGCG	CACGGGAGAC	GGTCCGATTT	TATAAGGCTG
151	CGTATTGAG	CGTTCGTTC	AATCGGTTTT	GCCCGCATCC	AATGCCTTCG
201	CAATCACAAA	CGTTTGTATT	GCCGAACCGG	GCTCGATCAT	ATCGGTTACG
251	GCACGGTTGC	GCCGCTGTTC	GCTGTCTGCC	CGTCCGGGCC	TGTTGGGATC
301	GTAGCGGGG	GATTGGCCA	AGGCCAGTAT	TTCCCCCGTG	CGGGCATCCA
351	ArACACCAC	CGTTCGGGT	TTTGCGGTAT	GGTATTGCG	CGCCTTGTTT
401	AACTCTTCAT	AGGCCAAGGT	CTGAATCCTC	TGATCGAGGG	AAAGGATGAT
451	GTCCTTTGCC	TTTTTCCGGG	CTTTAATGCG	CGGGGAGTCC	AAGCTGTGCA
501	CAATATTGCC	CTGCCGGTCC	CGCAAAACGA	CGGCGGCC	GTCTTCGCCA
551	TGCAAGCTGT	CTTCAAGCGA	AAGTTCCAAA	CCTTCCGTAC	CTTGGCGTC
601	AATATCGGTA	AATCCGATGA	CGTGTGCAAA	CAGGTTGCCC	ATCGGGTAAT
651	GGCGTTTTAA				

BNSDOCID: <WO 8957280A2 | >

g241-1.pap

```

1  MPTRPTRAAN PPTPTTWLQT AYCPRPPYRP PSVQTHTPHE PASSTCAAKS
51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPSC RQSVVMTVR
101 TVDMTVCDLF IGCIHAFAFN SFKADFHACQ RMVAVHHRLA VGNIGYTIDD
151 NIAGFRIVRF KHHTDLDFNR ERARIFNTDQ LRIMLTERIV GRKRHFDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFI OKLIVGIIHL IMQRNHGIFC
251 NSHICPFRNS RLITGAF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 913>:

m241-1.seq

```

1  ATGCCAACAC GTCCAACCTCG CGCTGCAAAC CCTCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC
101 AAACGCGTAC ACCGCGTGAA CCGGCTTCTT CAACCTGCGC GGCAAAATCA
151 GCGAACCGAC GGGAAAATTC TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAC AAAATGCCGT CTGAAACGGA ACAAACCTTT TTCAGACGGC
251 ATCAGATACC TCCAAGCTGC CGGCAATCAG TGGTGGTGAT GACCGTGC GG
301 GCCGTGGACA TGACCGTGTG CGATTTCCTC ATCGGATGCA TCGCGCACGC
351 TTTCAACTGT AGCCTTAAAG CGGATTTTCA TGCCTGCCAA AGGATGGTTG
401 CCGTCCACCA CCGCCTTGCC GTCGGCAACA TCGGTACAC GATAGACGAC
451 AACATCGCCG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTTCAACAGG GAACACGCCC GCATCTTCGA TACGGACCAA CTCCGGATCC
551 TGCTGCCCGA ACGCATCGTC GGGCGACAGC GCCACATCGA CCGTATCGCC
601 GGCATCCTTA CCGTGCAACG CCTCTTCCAC CAAAGGGAAA ATGCCGTCGT
651 AACC GCCGTG CAGATACGCA ATCGGTTCTT CGGTTTGTG CAAAAGCTGA
701 TTGTTGGCAT CATACTCTC ATAATGCAGC GAAACCACGG AATTTTTCAC
751 GATAGCCATA TTTGTCTTT CAGGAACAGC AGATTAATTA CAGGCGCATT
801 CTA

```

This corresponds to the amino acid sequence <SEQ ID 914; ORF 241-1>:

m241-1.pap

```

1  MPTRPTRAAN PPTPTTWLQT AYCPRPPYRP PSVQTRTPRE PASSTCAAKS
51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPSC RQSVVMTVR
101 AVDMTVCDLF IGCIHAFAFN SLKADFHACQ RMVAVHHRLA VGNIGYTIDD
151 NIAGFRIVRF KHHTDLDFNR EHARIFDQDQ LRILLAERIV GRQRHIDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFV OKLIVGIIHL IMQRNHGIFH
251 DSHICPFRNS RLITGAF*

```

m241-1/g241-1 93.3% identity in 267 aa overlap

	10	20	30	40	50	60
m241-1.pap	MPTRPTRAANPPTPTTWLQTAYCPRPPYRPPSVQTRTPREPASSTCAAKSANRRENSHNA					
g241	MPTRPTRAANPPTPTTWLQTAYCPRPPYRPPSVQTHTPHEPASSTCAAKSANRRENSHNA					
	10	20	30	40	50	60
m241-1.pap	QPTYLLHPSNKMPSETEQLFRRHQIPPSCRQSVVMTVRVAVDMTVCDFLIGCIAHAFNC					
g241	QPTYLLHPSNKMPSETEQLFRRHQIPPSCRQSVVMTVRTVDMTVCDFLIGCIAHAFNR					
	70	80	90	100	110	120
m241-1.pap	SLKADFHACQRMVAVHHRLAVGNIGYTIDDNIAGFRIVGFKHHADDFNREHARIFDQDQ					
g241	SFKADFHACQRMVAVHHRLAVGNIGYTIDDNIAGFRIVRFKHHADDFNRRERARIFNTDQ					
	130	140	150	160	170	180
m241-1.pap	LRILLAERIVGRQRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL					
g241	LRIMLTERIVGRKRHFDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFIQKLIVGIIHL					
	190	200	210	220	230	240
m241-1.pap	IMQRNHGIFHDSHICPFRNSRLITGAF					
g241	IMQRNHGIFCNSHICPFRNSRLITGAF					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 915>:

a241-1.seq

```

1  ATGCCAACAC GTCCAACCTCG CGCCGCAAAG CATCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC

```

```

101 AAACGCATAC ACCGCATGAA CCGGCTTCCT CAACCTGCGC GGCAAAATCA
151 GCGAACCAGC GGGAAAATTT TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAC AAAATGCCGT CTGAAATGGA ACAAACCTT TTCAGACGGC
251 ATCAGATACC TCCAAGCTGC CGGCAATCAG TGGTGGTGAT GACCGTGCGG
301 ACCGTGGACA TGACCGTGTG CGATTTCTC ATCGGATGCA TCGCGCACAC
351 TTTCAACCGT AGCCTTAAAG CGGATTTTCA TGCCTGCCAA AGGATGGTTG
401 CCGTCCACCA CCGCCTTACC GTCGGCAACA TCGGTTACAC GATAGACGAC
451 AACATCGCCG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTTCAACAGG GAACACGCCC GCATCTTCAA TACGGACCAA CTCCGGATCC
551 TGCTCGCCGA ACGCATCGTC GGGCGAAAGC GCCACATCGA CCGTATCGCC
601 GGCATCCTTA CCGTGCAACG CCTCTTCCAC CAAAGGGAAA ATGCCGTCGT
651 AACC GCCGTG CAGATACGCA ATCGGTTCTT CGGTTTTGTC CAAAAGCTGA
701 TTGTTGGCAT CATACTCTC ATAATGCAGC GAAACCACGG AATTCTTCAC
751 GATAGCCATA TTTGTCTTT CAGGAACAGC AGATTAATTA CAGGCGCATT
801 CTAA

```

This corresponds to the amino acid sequence <SEQ ID 916; ORF 241-1.a>:

a241-1.pep

```

1  MPTRPTRAAK HPTPTWLQT AYCPRPYPYR PSVQTHPHE PASSTCAAKS
51  ANRRENFHNA QPTYLLHPSN KMPSEMEQTL FRRHQIPPSQ RQSVVMTVR
101 TVDMTVCDFL IGCIAHTFNR SLKADFHACQ RMVAVHRLT VGNIGYTIDD
151 NIAGFRIVGF KHHADFDENR EHARIFNTDQ LRILLAERIV GRKRHIDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL IMQRNHGILH
251 DSHICPFRNS RLITGAF*

```

m241-1/a241-1 95.1% identity in 267 aa overlap

	10	20	30	40	50	60
m241-1.pep	MPTRPTRAANPPTPPTWLQTAYCPRPPYRPPSVQTRTPREPASSTCAAKSANRRENSHNA					
a241	: : : : :					
	10	20	30	40	50	60
	70	80	90	100	110	120
m241-1.pep	QPTYLLHPSNKMPSETEQTLEFRRHQIPPSQSVVMTVRVAVDMTVCDFLIGCIAHAFNC					
a241	: : : : :					
	70	80	90	100	110	120
	130	140	150	160	170	180
m241-1.pep	SLKADFHACQRMVAVHRLAVGNIGYTIDDDNIAGFRIVGFKHHADFDENREHARIFDNTDQ					
a241	: : : : :					
	130	140	150	160	170	180
	190	200	210	220	230	240
m241-1.pep	LRILLAERIVGRQRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL					
a241	: : : : :					
	190	200	210	220	230	240
	250	260				
m241-1.pep	IMQRNHGIFHDSHICPFRNSRLITGAFX					
a241	: : :					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 917>:

g242.seq

```

1  atgatcggcg aacttggtgt tttgttcgtg atcgagcact tcaagcaacg
51  cgctggcggg atcgccccga aagtcgctgc ccaatttgtc gatttcgctg
101 agcaggaaca acgggtttct tacgcctgct tttgccatat tctgcaaaat
151 cttgccgggc atagagccga tataggtacg gcggtgcccc cggtattcgc
201 tttcgtcgcg cacgcgcccc aaggccatac ggacatatat ccgccccgtt
251 gctttggcga tggattcgcc caaagagggt ttgcccacgc ccggaggggc
301 gaccaaacac agaatcggac ctttgagctt gtccatacgt ttttgagcgg
351 cgaggatttc caaaatccgt tctttgactt tttccaggcc gtagtggtcg
401 gcatccagca ccagtcgggc tttggcgatg tctttgctga cgcgggattt
451 tttcttccac ggcagtcgga gcagggtgct gatgtagttg cgtacgacgg

```

501 tggattcggc agacatcggc ggcattcattt tgagtttttt cagttcggac
551 aggcattttt ctccgcttc tttggtcata cccgcctttt tgatgcctgc
601 ctccaaggca tccagtctgc cgttttcgtc ttcttcgccc aattctttgt
651 gtatcgcttt aatctgttcg ttcagataat attcgcggtg ggatttttcc
701 atttggcgtt tgacgcgtcc gcgtatgcgt ttttcggcct gcataatgtc
751 gagttcggat tccagctttg ccagcaggaa ttccatccgt ttgccgattt
801 cgggaattct caaaatctgt tggcgttgcg ccagtttcaa ctgcaaattgc
851 gctgcgaccg tatcggttag

This corresponds to the amino acid sequence <SEQ ID 918; ORF 242.ng>:

g242.pwp

1	MIGELVVLVF	IEHFKQRAGG	IAPKVAAQFV	DFVEQEQRVS	YACFCHILQN
51	LAGHRADIGT	AVPADFAFVA	HAAQGHDTIF	PPRCFGDGFA	QRGFAHARRA
101	DQTONRTFEL	VHTFLDGEVF	QNPFFDFFQA	VVVGIQHQSG	FGDVAFADAGF
151	FLPQRSEQGV	DVAAYDGGGF	RHRRHHEFFA	QFGQAFFFRF	FGHTRLFDAC
201	<u>LQGIQFAVEF</u>	<u>FFAQQVYVRF</u>	<u>NLRFVQIFAL</u>	<u>GGFHLAFDAS</u>	<u>AYAFFGLHNV</u>
251	EFGFQLCQQE	FHPFADFNGL	QNLLALRQFO	LQMRCDRIG*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 919>:

m242.seq

1	ATGATCGGCA	AACTTGTGT	TTTGTTCGGG	ATCGAGCACT	TCGAGCAACG
51	CGCTGGCGGG	ATCGCCTCGG	AAGTCGTTAC	CCAAATTGTC	GATTTCGTCG
101	AGCAGGAACA	AGGGGTTTTT	CACGCCGGCT	TTTGCCATAT	TCTGCAAAAT
151	CTTACCGGGG	ATAGAGCCGA	TATAGGTGCG	GCGGTGTCCC	CTGATTTTCGC
201	TTTCCTGCGC	CACGCGCCCC	AAAGCCATGC	GGACATATTT	CCGCCCCGGT
251	GCTTTGCGCA	TGGATTTCGC	CAAAAGAGTT	TGTCCACGC	CCGGAGGGCC
301	GACCAGGCAC	AGAATCGGGC	CTTTGAGTTT	GTCCATACGT	TTTTGGACGG
351	CGAGGTATTC	CAAAATCCGT	TCTTTGACTT	TTTCCAGGCC	GTAGTGGTCG
401	GCATCCAGCA	CCAGTCCGGC	TTTGGCGATG	TCTTTGCTGA	CGCGGGATTT
451	TTCTCTCCAC	GGCAGCTCGA	GCAAAGTGTC	GATGTAGTTG	CGTACGACGG
501	TGGATTCCGC	AGACATCGGT	GGCATCATTT	TCAGCTTTTT	CAGTTCGGAC
551	AGGCATTTTT	CTTCCGCTTC	TTTGTGTCATA	CGCGCTTTTT	TGATATCTGC
601	TTCCAAGGCA	TCCAGTTTCG	CGTTTTCGTC	TTCTTCGCCC	AGTTCTTTGT
651	GTATCGCTTT	AATCTGTTTC	TTCAGATAAT	ATTTCGCGCTG	GGATTTTTTCC
701	ATTTGCGGTT	TGACGCGTCC	GCGTATGCGT	TTTTCGGCCT	GCATAATGTC
751	GAGTTCCGAT	TCCAGCTGTG	CCAGCAGGAA	TTCCATCCGT	TTGCCGATTT
801	CGGGAATTTT	CAAAATCTGT	TGCGTTGCG	CCAGTTTCAA	CTGCAAATGC
851	GCTGCGACCG	TATCGGTAG			

This corresponds to the amino acid sequence <SEQ ID 920; ORF 242>:

m242 . pep

1	MIGKLVVLFG	IEHFEQRAGG	IASEVVQTFV	DFVEQEQGVF	HAGFCHILQN
51	LTGHRADIGA	AVSPDFAFVA	HAAQSHADIF	PPRCFGDGFA	QRGFAHARRA
101	DQAQNRAFEF	VHTFLDGEVF	QNPFFDFQFA	VVVGIQHQS	FGDVAFADAGF
151	FLPRQLEQSV	DVVAYDGGFR	RHRWHHFEL	QFGQAFFFRF	FGHTRLFDIC
201	FQGIQFAFVF	FFAQVDFVYR	NLFVQIIFAL	GFFHLAFDAS	AYAFFGLHNV
251	EFGFQLCQQE	FHPFADFNGF	QNLLALRQFO	LMQRCDRIG*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 242 shows 90.3% identity over a 289 aa overlap with a predicted ORF (ORF 242.ng) from *N. gonorrhoeae*:

m242/g24290.3% identity in 289 aa overlap

	10	20	30	40	50	60
m242.pep	MIGKLVVLFGLIEHFEQRAGGIASEVVTQFVDFVEQEQQGVFHAGFCHILQNLTGHRADIGA					
	: : : : : : :					
g242	MIGELVVLFVIEHFKQRAGGIAPKVAAQFVDFVEQEQRVSYACFCHILQNLAGHRADIGT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m242.pep	AVSPDFAFVAHAAQSHADIFPPRCFGDGFAQRGFAHARRADQAQNRAFEFVHTFLDGEVF					
	: : : : : : : : : : : : : : : :					
g242	AVPADFAFVAHAAQGHTDIFPPRCFGDGFAQRGFAHARRADQTQNRTFELVHTFLDGEVF					
	70	80	90	100	110	120

	130	140	150	160	170	180
m242 . pep	QNPFDFFFQAVVVGIIHQSGFGDVFDAGFFLPRQLEQSVDDVVAYDGGFRRHRWHHFELF					
g242	QNPFDFFFQAVVVGIIHQSGFGDVFDAGFFLPRQSEQGVDDVVAYDGGFRRHRWHHFELF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m242 . pep	QFGQAFFFRFFGHTRLFDICFOGIQFAVFVFFAQFFVYRNFNFVQIIFALGFFHLAFDAS					
g242	QFGQAFFFRFFGHTRLFDACLOGIQFAVFVFFAQFFVYRNFNFVQIIFALGFFHLAFDAS					
	190	200	210	220	230	240
	250	260	270	280	290	
m242 . pep	AYAFFGLHNVEFGFQLCQQEFHFPFADFGNLFQNLALRQFQLQMRCDRIGX					
g242	AYAFFGLHNVEFGFQLCQQEFHFPFADFGNLFQNLALRQFQLQMRCDRIGX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 921>:

a242 . seq	1	ATGATCGGCG	AACTTGTGT	TTTGCTCGGG	ATCAAGCACT	TCGAGCAACG
	51	CGCTGGCGGG	ATCGCCCGG	AAGTCGCTAN	CCAATTTGTC	GATTTTCGTCG
	101	AGCAGGAACA	ATGGGTTTT	TACGCCGGCT	TTTGCCATAT	TCTGCAAAAT
	151	CTTACCGGGC	ATGGAGCCGA	TATAGGTGCG	GCGGTGTCCC	CGGATTTTCGC
	201	TTTCGTGCGC	CACGCCGCC	AAAGCCATGC	GGACATATTT	CGCCCCCGTT
	251	GCTTTGGCGA	TGGATTCGCC	CAAAGAGGTT	TTGCCACGC	CTGGAGGGCC
	301	GACCAGGCAC	AGAATCGGGC	CTTTGAGTTT	GTCCATACGT	TTTTGGACGG
	351	CGAGGTATTC	CAAAATCCGT	TCTTTGACTT	TTTCCAGGCC	GTAGTGGTCG
	401	GTATCCAGCA	CCAATCCGGC	TTTGGCGATG	TCTTTGCTGA	CGCGGGATTT
	451	TTTCTTCCAC	GGCAGTTCGA	GCAGGGTGTC	GATGTAGTTG	CGTACGACGG
	501	TGGATTCGGC	AGACATCGGC	GGCATCATTT	TGAGCTTTTT	CAGTTCGGAC
	551	AGGCATTTTT	CTTCGCCTTC	TTTGGTCATA	CCCGCCTTTT	TGATATCTGC
	601	TTCCAAGGCA	TCCAGTTCGC	CGTTTTTCGC	TTCTTCGCCC	AGTTCTTTGT
	651	GTATCGCTTT	AATCTGTTCG	TTCAGATAAT	ATTCGCGCTG	GGATTTTTTCC
	701	ATTTGGCGTT	TGACGCGTCC	GCGTATGCGT	TTTTCGGCCT	GCATAATGTC
	751	GAGTTCGGAT	TCCAGCTGTG	CCAGCAGGAA	TTCCATCCGT	TTGCCGATTT
	801	CGGGAATTTT	CAAAATCTGT	TGGCGTTGCG	CCAGTTTCAA	CTGCAAATGC
	851	GCTGCGACCG	TATCGGTTAG			

This corresponds to the amino acid sequence <SEQ ID 922; ORF 242.a>:

a242 . pep	1	MIGELVVLG	IKHFEQRAGG	IAPEVAXQFV	DFVEQEQWVF	YAGFCHILQN
	51	LTGHGADIGA	AVSPDFAFVA	HAAQSHADIF	PPRCFGDGFA	QRGFVAHAWRA
	101	DQAQNRAFEF	VHTFLDGEVF	QNPFDFFFQA	VVVGIIHQSG	FGDVFDAGF
	151	FLPRQFEQGV	DVVAYDGGFG	RHRRHHFELF	QFGQAFFFRF	FGHTRLFDIC
	201	FOGIQFAVFV	FFAQFFVYRF	NLFVQIIFAL	GFFHLAFDAS	AYAFFGLHNV
	251	EFGFQLCQQE	FHPFADFGNF	QNLLALRQFQ	LQMRCDRIG*	

m242/a242 95.2% identity in 289 aa overlap

	10	20	30	40	50	60
m242 . pep	MIGKLVVLFGLIEHFEQRAGGIASEVVTQFVDFVEQEQGVFHAGFCHILQNLTGHRADIGA					
a242	MIGELVVLGIIKHFEQRAGGIAPEVAXQFVDFVEQEQWVFYAGFCHILQNLTGHGADIGA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m242 . pep	AVSPDFAFVAHAAQSHADIFPPRCFGDGFAQRGFVAHARRADQAQNRAFEFVHTFLDGEVF					
a242	AVSPDFAFVAHAAQSHADIFPPRCFGDGFAQRGFVAHAWRADQAQNRAFEFVHTFLDGEVF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m242 . pep	QNPFDFFFQAVVVGIIHQSGFGDVFDAGFFLPRQLEQSVDDVVAYDGGFRRHRWHHFELF					

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```

a242      QNPFFDFFQAVVVGIIHQSGFGDVFADAGFFLPRQFEQGVVDVVAYDGGGFRHRRHHFELF
           130      140      150      160      170      180
           190      200      210      220      230      240
m242.pep  QFGQAFFFRFFFGHTRLEFDICFQGIQFAVFVFFAQFFVYRFNLFVQIIFALGFFHLAFDAS
           |||||
a242      QFGQAFFFRFFFGHTRLEFDICFQGIQFAVFVFFAQFFVYRFNLFVQIIFALGFFHLAFDAS
           190      200      210      220      230      240
           250      260      270      280      290
m242.pep  AYAFFGLHNVEFGFQLCQQEFHFPFADFNGFNQNLALLRQFQLQMRCDRIGX
           |||||
a242      AYAFFGLHNVEFGFQLCQQEFHFPFADFNGFNQNLALLRQFQLQMRCDRIGX
           250      260      270      280      290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 923>:

```

g243.seq
1  ATGGTaatcg tctGGTTGcc cgAGTTaccg CCGATGCCGG CGACGATGGG
51 CATCAGCGCG GCGAGTGCGA CGATTTTTTC gatactgcCT TCAAACGCGC
101 CGATGACGCG GCTGGCGAGG AAGGCGGTGC AGAGGTTGAC GGCGAGCCAC
151 ATCCAGCGGT TTTTGACGGA ATCCAAGACG GGGGCGAACA GGTCTTCCTC
201 TTCCTGCAAA CCTGCCATGT TCAACATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATCTCGTCG ATGGTAATcc tgCCGATGAG CTTTTTGTTT
301 TCATCAACGA CGGCGCGCGT AACCAAGTCG TAG

```

This corresponds to the amino acid sequence <SEQ ID 924; ORF 243.ng>:

```

g243.pep
1  MVIVWLPELP PMPATMGISA ASATIFSILP SNAPMTRLAR KAVQRLTASH
51 IQRFLTESKT GANRSSSSCK PAMFNISASD SSRITSTISS MVILPMSFLF
101 SSTTGAVTKS *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 925>:

```

m243.seq
1  ATGGTAATCG TCTGGTTGCC CGAGTTACCG CCTATGCCGG CGACGATGGG
51 CATCAGCGCG GyGAGTGCGA CGATTTTTTC GATGCTGCCT TCAAACGCGC
101 CGATAACACG GyTGGCGAGG AAGGCGGTGC AGAGGTTGAC GGCGAGCCAC
151 ATCCAGyGGT TTTTCACCGA ATCCACACG GGGGCGAAyA GGTCTTCCTC
201 TTCCTGCAAA CCCGCCATAT TCAGCATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATCTCGTCG ATGGTAATCC TGCCGATGAG CTTTTTGTTT
301 TCATCGACGA CGGCGCGCGT AACCAAGTCG TAG

```

This corresponds to the amino acid sequence <SEQ ID 926; ORF 243>:

```

m243.pep
1  MVIVWLPELP PMPATMGISA XSATIFSMLP SNAPITRLAR KAVQRLTASH
51 IQXFFTESHT GANRSSSSCK PAIFSISASD SSRITSTISS MVILPMSFLF
101 SSTTGAVTKS *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 243 shows 92.7% identity over a 110 aa overlap with a predicted ORF (ORF 243.ng) from *N. gonorrhoeae*:

```

m243/g243
           10      20      30      40      50      60
m243.pep  MVIVWLPELPMPATMGISAXSATIFSMLPSNAPITRLARKAVQRLTASHIQXFFTESHT
           |||||
g243      MVIVWLPELPMPATMGISAASATIFSILPSNAPMTRLARKAVQRLTASHIQRFLTESKT
           10      20      30      40      50      60
           70      80      90      100     110
m243.pep  GANRSSSSCKPAIFSISASDSSRITSTISSMVILPMSFLFSSTTGAVTKSX
           |||||
g243      GANRSSSSCKPAMFNISASDSSRITSTISSMVILPMSFLFSSTTGAVTKSX

```

70 80 90 100 110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 927>:

```
a243.seq
1  ATGGTAATCG TCTGGTTGCC CGAGTTACCG CCTATGCCGG CGACGATGGG
51  CATCAGCGCG GCGAGTGCGA CGATTTTTC GATGCTGCCT TCAAACGCGC
101 CGATAACACG GCTGGCGAGG AAGGCGGTGC AGAGGTTGAC GGCGAGCCAC
151 ATCCAGCGGT TTTTGACGGA ATCCAAGACG GGGGCGAATA AGTCTTCCTC
201 TTCTTGCAAA CCCGCCATAT TCAACATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATTTCTGTC ACGGTCACCC TGCCGATGAG CTTTTTGTTT
301 TCATCGACGA CGGGCGCGGT AACCAAGTCA TAG
```

This corresponds to the amino acid sequence <SEQ ID 928; ORF 243.a>:

```
a243.pep
1  MVIVWLPELP PMPATMGISA ASATIFSMLP SNAPITRLAR KAVQRLTASH
51  IQRFLTESKT GANKSSSSCK PAIFNISASD SSRITSTISS TVTLPMSEFLF
101 SSTTGAVTKS *
```

m243/a243 92.7% identity in 110 aa overlap

	10	20	30	40	50	60
m243.pep	MVIVWLPELPMPMPATMGISAXSATIFSMLPSNAPITRLARKAVQRLTASHIQXFFTESHT					
a243	MVIVWLPELPMPMPATMGISAASATIFSMLPSNAPITRLARKAVQRLTASHIQRFLTESKT					
	10	20	30	40	50	60
	70	80	90	100	110	
m243.pep	GANRSSSSCKPAIFNISASDSSRITSTISSMVILPMSFLFSSTTGAVTKSX					
a243	GANKSSSSCKPAIFNISASDSSRITSTISSTVTLPMSEFLFSSTTGAVTKSX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 929>:

```
g244.seq
1  atgccgcctg aagcccggcc ggccgggttca gacggcattg ccgctttact
51  tcgatcggtt tatacgcaaa acgcgcttca ggaaataaat cagattattc
101 cccagacgcc ttcaggcttc cttccgtgcc accgtaacca tagccgggcg
151 caacacacgg tcggacaggg tataaccctt cttcatcaca ccaaccacgg
201 tattgggttc ctgctcactg gccaccgcct gcatcgccctg atggatattc
251 ggatcgagct tatcgccgcg tttaggattg atttccttga tttcggtggc
301 atcaaacgcc ttctgcaact cattcaaagt catctgcaca cccattttca
351 gcgcatcgaa attaccgctc tgatccaaaa gcgccatttc cagataatcc
401 ttgaccggca acattttccac ggcaaaacttc tgtccggcga acttgtgctg
451 atcggcaatt tcctgctggt ggccggcgccg caggttttgc tcgtttgccg
501 aagcgcgag ttgttcgtct ttcaactgcg cttccagctc ggcaatccgc
551 gcctgcaaat cctcataagc cggctcggcg gcagcctggt cctgtacacc
601 gtccgcattt cctactgtct cgacgggttc caccgcctcc acattttcaa
651 ccgcttcttc actgttttgc tgctgtgtct gttcgctcat atcgatccc
701 tcaaaacaaa ttggaaatca aaatccggtt attaccgag caagataagg
751 acattttcaa gaaacttcaa gcaaaggcag gaaatttcac atccgccgcc
801 gaatacccta ccgcaaaaac catataaacg gtaa
```

This corresponds to the amino acid sequence <SEQ ID 930; ORF 244.ng>:

```
g244.pep
1  MPPEARPAGS DGIAALLRSV YTQNALQEIN QIIPQTPSGF LPCHRNHSRA
51  QHTVGQGITL LHHTNHGIGF LLTGHLRLHRL MDIRIELIAR FRIDFLDLRG
101 IKRLQLIQS HLHTHFQRIE ITALIQKRHF QIILDRQHFH GKLLSGELVR
151 IGNFLLVAAA QVLLVCQSAQ LFVFQLRFQL GNPRLQILIS RLGGSLFLYT
201 VRISYCLDGF HRLHIFNRF TVLLCLFAH IVSLKTNWKS KSGYPSKIR
251 TFSRNFQRQ EISHPPPNTL PQKPYKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 931>:

m244.seq

```

1  ATGCCGTCTG AAGCCCGACA GGC GG GTTCA GACGGCATTG CCGCTTTACT
51  TCGATCGGTT TATACGCAAA ACGCGCTTCA GGAAATAAAT CAGATTATTC
101 CCCAGACGCC TTCAGGCTTC CTTCTGCGCC ACCGTAACCA TAGCCGGGCG
151 CAACACGCGG TCGGACAGCG TATAACCCCT CTTTCATCACA CCCACCACGG
201 TATTCGGCTC CTGTTGCTT GCCACCGCCT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATCGCCCGC TTTAGGGTTG ATTTCCCTGA TTTGCGTAGC
301 ATCAAATGCT TTCTGCAACT CGTTCAAAGT CATCTGCACG CCCATTTTCA
351 GCGCATCGAA ATTGCCGCTC TGATCCAAAA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTTCCAC GGCAAACTTC TGTCCGGCGA ACTTGTGCGT
451 ATCCGCAATT TyCTGCTGGT GGCGGCGGCG CAGGTTTTGC TCGTTTGCCA
501 AAGCGCGCTG CTCGTCTTTC AACTGCGTTT CCAGCTCGGC AATCCGCGCC
551 TGCAAATCCT CATAAGCCGG CTCTGCGGCA GCCTGTTTCT GCACACCGTC
601 CGCATTTTCT ACTGTTTTCGA CGGTTTCCAC CGCCTCCACA TTTTCAACCG
651 CTTCTTCACT GTTTTGCTGC TGTGTCTGTT CGCTCATATC GTATCCCTTA
701 AAACAAATTG GAAATCAAAA TCCAGTTATT ACCCGCGCAA GATAAGGACA
751 TTTTCAAGAA ACTTCAAKCA AAakCAGAGA ATTTCAAAT CATTTCAAAA
801 TCCCCTACCG AAAAAATAAT ATAGACGGTA A

```

This corresponds to the amino acid sequence <SEQ ID 932; ORF 244>:

m244.pep

```

1  MPSEARQAGS DGIAALLRSV YTONALQEIN QIIPQTPSGF LLRHRNHSRA
51  QHAVGQRITL LHHTHHGIRL LFACHRLHRL MDIRIELIAR FRVDFDLRS
101 IKCFLQLVQS HLHAHFQRIE IAALIQRHF QIILDRQHFH GKLLSGELVR
151 IRNFLVAAA QVLLVCQSAL LVFQLRFQLG NPRLQILISR LCGSLFLHTV
201 RISYCFDGFH RLHIFNRFFT VLLLCFLFAHI VSLKTNWWSK SSYYPRKIRT
251 FSRNFXQXQR ISNSFSNPLP KXYRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 244 shows 86.3% identity over a 277 aa overlap with a predicted ORF (ORF 244.ng) from *N. gonorrhoeae*:

M244/G244

m244.pep	10	20	30	40	50	60
	MPSEARQAGSDGIAALLRSVYTONALQEINQIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
g244	MPPEARPAGSDGIAALLRSVYTONALQEINQIIPQTPSGFLPCHRNHSRAQHTVGGQITL					
	10	20	30	40	50	60
m244.pep	70	80	90	100	110	120
	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRSIKCFLQLVQSHLHAHFQRIE					
g244	LHHTNHGIGFLLTGHRHLRLMDIRIELIARFRIDFLDLRGIKRLQLIQSHLHTHFQRIE					
	70	80	90	100	110	120
m244.pep	130	140	150	160	170	180
	IAALIQRHFQIILDRQHFHKGKLLSGELVRIRNFLVAAAQVLLVCQSAALLVFQLRFQL					
g244	ITALIQRHFQIILDRQHFHKGKLLSGELVRIGNFLVAAAQVLLVCQSAQLFVQLRFQL					
	130	140	150	160	170	180
m244.pep	190	200	210	220	230	240
	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFT VLLLCFLFAHIVSLKTNWKS					
g244	GNPRLQILISRLGSLFLYTVRISYCLDGFHRLHIFNRFFT VLLLCFLFAHIVSLKTNWKS					
	190	200	210	220	230	240
m244.pep	250	260	270			
	KSSYYPRKIRTFSRNFXQXQRISNSFSNPLPKXYRRX					
g244	KSGYYPSKIRTFSRNFKQREISHPPNTLPQKPYKRX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 933>:

```
a244.seq
1   ATGCCGCTCTG AAGCCCCGACA GCGGGGTTCA GACGGCATTG CCGCTTTACT
51  TCGATCGGTT  TATACGCAAA  ACGCGCTTCA GGAAATAAAT CAGATTATTC
101 CCCAGACGCC  TTCAGGCTTC  CTTCTGTGCC ACCGTAACCA TAGCCGGGCG
151 CAACACGCGG  TCGGACAGCG  TATAACCCTT CTCATCACG  CCCACCACGG
201 TATTGGGTTC  CTGTTGCTT  GCCACCGCCT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT  TATCGCCCGC  TTTAGGATTG ATTCCTTGA  TTTGCGTAGC
301 ATCAAATGCT  TTCTGCAACT  CGTTCAAAGT CATCTGCACG CCCATTTTCA
351 GCGCATCGAA  ATTGCCGCTC  TGATCCAAA  GCGCCATTTC CAGATAATCC
401 TTGACCGGCA  GCATTTCCAC  GGCAAACCTC TGTCCGGCGA ACTTGTGCGT
451 ATCCGCAATT  TCCTGCTGGT  GCGGCGGGCG CAGGTTTTGC TCGTTTGCCA
501 AAGCGCGCAG  CTGCTCGTCT  TTCAACTGCG CTTCCAGCTC GGCAATCCGC
551 GCCTGCAAAT  CCTCATAAGC  CGGCTCTGCG GCAGCCTGTT CCTGCACACC
601 GTCCGCATTT  CCTACTGTCT  CGACGGTTTC CACCGCCTCC ACATTTTCAA
651 CCGCTTCTTC  ACTGTTTTGC  TGCTGTGTCT GTTCGCTCAT ATCGTATCCC
701 TTAAACAAA  TTGGAATCA  AAATCCAGTT ATTACCCGCG CAAGATAAGG
751 ACATTTTCAA  GAAACTTCAA  GCAAAGGCAG AGAATTTCAA ATTCATTTTC
801 AAATCCCTA  CCGAAAAAT  AATATAGACG GTAA
```

This corresponds to the amino acid sequence <SEQ ID 934; ORF 244.a>:

```
a244.pep
1   MPSEARQAGS DGIAALLRSV YTONALQEIN QIIPQTPSGF LLCHRNHSRA
51  QHAVGQRITL LHHAHHGIGF LFACHRLHRL MDIRIELIAR FRIDFLDLRS
101 IKCFLQLVQS HLHAFQRIE IAALIQKRHF QIILDRQHFH GKLLSGELVR
151 IRNFLLVAAA QVLLVCQSAQ LLVFQLRFQL GNPRQLILIS RLCGSLFLHT
201 VRISYCLDGF HRLHIFNRFF TVLLLCFLFAH IVSLKTNWKS KSSYYPRKIR
251 TFSRNFQQRQ RISNSFSNPL PKK*YRR*
```

m244/a244 96.8% identity in 277 aa overlap

m244.pep	10	20	30	40	50	60
	MPSEARQAGSDGIAALLRSVYTONALQEINQIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
a244	MPSEARQAGSDGIAALLRSVYTONALQEINQIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
	10	20	30	40	50	60
m244.pep	70	80	90	100	110	120
	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFLDLRSIKCFLQLVQSHLHAFQRIE					
a244	LHHAHHGIGFLFACHRLHRLMDIRIELIARFRIDFLDLRSIKCFLQLVQSHLHAFQRIE					
	70	80	90	100	110	120
m244.pep	130	140	150	160	170	179
	IAALIQKRHFQIILDRQHFH GKLLSGELVRIRNFLLVAAAQVLLVCQSA-LLVFQLRFQL					
a244	IAALIQKRHFQIILDRQHFH GKLLSGELVRIRNFLLVAAAQVLLVCQSAQLLVFQLRFQL					
	130	140	150	160	170	180
m244.pep	180	190	200	210	220	230
	GNPRQLILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFTLLCLFAHIVSLKTNWKS					
a244	GNPRQLILISRLCGSLFLHTVRISYCLDGFHRLHIFNRFFTLLCLFAHIVSLKTNWKS					
	190	200	210	220	230	240
m244.pep	240	250	260	270		
	KSSYYPRKIRTFSRNFXQXQRISNSFSNPLPKKXYRRX					
a244	KSSYYPRKIRTFSRNFKQRQRISNSFSNPLPKKXYRRX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 935>:

```
g244-1.seq
1   atgccgcctg aagccccggc ggccgggttca gacggcattg cgcgtttact
```

51	togatcggtt	tatacgcaaa	acgcgcttca	ggaaataaat	cagattatcc
101	cccagacgcc	ttcaggcttc	cttcgcgtgc	accgtaacca	tagccggggc
151	caacacacgg	tcggacaggg	tataaacctt	cttcatcaca	ccaaccacgg
201	tattgggttc	ctgtctcactg	gccaccgcct	gcactgcctg	atggatattc
251	ggatcgagct	tatcgccgcg	tttaggattg	atttccttga	tttgcgtggc
301	atcaaacgcc	ttctgcgaat	cattcaaaagt	catctgcaca	cccattttca
351	gcgcatcgaa	attaccgctc	tgatccaaaa	gcgcattttc	cagataatcc
401	ttgaccggca	acatttccac	ggcaaacctt	tgtccggcga	acttgtgcgt
451	atcggcaatt	tcttgcgtgt	ggcggcgggc	cagggtttgc	tcgtttgccg
501	aagcgcgcag	ttgttcgtct	ttcaactgcg	cttcacagct	ggcaatccgc
551	gcttcgcaat	cctcataagc	cggctcggcg	gcagcctgtt	cttgtacacc
601	gtccgcattt	cctactgtct	cgacgggttt	caccgcctcc	acattttcaa
651	ccgcttcttc	actgttttgc	tgctgtgtct	gttcgctcat	atcgatatcc
701	tcaaaacaaa	tgggaatcaa	aaatccggtt	attacccgag	caagataagg
751	acattttcaa	gaaactttcaa	gcataaggcag	gaaattttcac	atccgcgcgc
801	gaataaccta	ccgcaaaaaac	catataaacg	gtaa	

This corresponds to the amino acid sequence <SEQ ID 936; ORF 244-1.ng>:

g244-1.pep

1	MPPEARPAGS	DGIAALLRSV	YTQNALQEIN	QIIPQTPSGF	LPCHRNHSRA
51	QRTVGGQITL	LLHTNHNIGF	LLTGHNLHRL	MDRIELRIAL	FRIDFLDLRG
101	IHKTLQGIQS	HLHTEFQRIE	ITALGKRFH	QIILDRQHFF	KGLLSGELVR
151	<u>IGNFLLVAAA</u>	<u>QVLLVCQSAQ</u>	<u>LFVFQLRFQL</u>	<u>GNPRLQILIS</u>	<u>RLGGSFLYLT</u>
201	VRISYCLDGF	HLRHTFNRF	<u>TVLLLCFLAH</u>	IVSLKTNWKS	KSGYYPKSKIR
251	TFSRNFKFO	EISHPPEPNTL	POPKYK*		

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 937>:

m244-1.seq

1	ATGCCGCTGTG	AAGCCCCGACA	GGCGGGTTTCA	GACGGCATTG	CCGCTTTTACT
51	TCGATCGGTT	TATACGCAAA	ACGCGCTTCA	GGAAATAAAT	CAGATTATTC
101	CCCAGACGCC	TTCAGGCTTC	CTTCTGCGCC	ACCGTAACCA	TAGCCGGGGC
151	CAACACGCGG	TCGGACAGCG	TATAACCCCT	CTTCATCACA	CCCAACACGG
201	TATTGCGCTC	CTGTGTCGTT	GCCACCGCCT	GCATCGCCTG	ATGGATATTC
251	GGATCGAGCT	TATCGCCCGC	TTTAGGGTTG	ATTTCCTTTA	TTTGGCTAGC
301	ATCAAAATGCT	TTCTGCAACT	CGTTCAAAGT	CATCTGCACG	CCCATTTTCA
351	GCGCATCGAA	ATTGCCGCTC	TGATCCAAAA	GCGCCATTTC	CAGATAATCC
401	TTGACCGGCA	GCATTTCCAC	GGCAAACTTC	TGTCGGGCGA	ACTTGTGGCT
451	ATCCGCAATT	TyCTGCTGGT	GGCGGCGCGC	CAGGTTTTGC	TCGTTTGCCA
501	AAGCGCGCTG	CTCGCTTTTC	AACCTGCGTT	CCAGCTCGCA	AATCCGCGCC
551	TGCAAAATCCT	CATAGCCCGG	CTCTGCGGCA	GCCTGTTTCT	GCACACCGCT
601	CGCATTTTCT	ACTGTTTTCA	CGCTTTCCAC	CGCCTCCACA	TTTTCACCGC
651	CTCTTTCAC	GTTTGTCTGC	TGTGTCTGTT	CGCTCATATC	GATACCTTTA
701	AAACAAATTG	GAAATCAAAA	TCCAGTTATT	ACCCGCGCAA	GATAAGGACA
751	TTTTCAAGAA	ACTTCAAKCA	AAAKCAGAGA	ATTTCAAATT	CATTTTCAAA
801	TCCCCTACCG	AAAAATAAA			

This corresponds to the amino acid sequence <SEQ ID 938; ORF 244-1>:

m244-1.pcp

```

1  MPSEARQAGS  DGIAALLRSV  YTQNALQEIN  QIIPQTPSGF  LLRHRNHSRA
51  QHAVQGRITL  LHHTHMGIRL  LFACHRHLRH  MDRIELIAR  FRVDFLDLRS
101 IKCFLQLQVS  HLHAHFQRIE  IAAIKLKHFF  QIILDRQHFH  KGLLSGELVR
151 IRNFWLLVAAA QVLLVCQSAL LVFQLRFQLG  NPNRLQILIS  RLCSSLFHTV
201 RISYCFDGFX  RLHIPIRNFET  VLLLCLFAHI  VSLKTNWKSX  SSYYPKIRT
251 FSRNFXOGXR  ISNSFNSDLP  KK*

```

m244-1/G244-1 86.3% identity in 277 aa overlap

	10	20	30	40	50	60
m244-1.pep	MPSEARQAGSDGIAALLRSVYTQNALQEINQIIPQT	PSGFLLRHNRHSRAQHAVGQRITL				
g244-1	MPPEARPAGSDGIAALLRSVYTQNALQEINQIIPQT	PSGFLPCHNRHSRAQHTVGGQITL				
	10	20	30	40	50	60
	70	80	90	100	110	120
m244-1.pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDF	LDLSIKCFLQLVQSHLHAHFQRIE				
g244-1	LHHTNHGIFLLTGHRHLHRLMDIRIELIARFRIDF	LDLGRLLQLIQSHLHTHFQRIE				
	70	80	90	100	110	120

	130	140	150	160	170	180
m244-1.pep	IAALIQRHFIQIILDRQHFGKLLSGELVRI	RNFLLVAAQVLLVCQSAALLVFQLR	FQ			
	:					:
g244-1	ITALIQRHFIQIILDRQHFGKLLSGELVRI	GNFLLVAAQVLLVCQSAQLFVFQLR	FQ			
	130	140	150	160	170	180
	190	200	210	220	230	240
m244-1.pep	GNPRLQILISRLCGSLFLHTVRI	SYCFDGFHRLHIFNRF	FTVLLCLFAHIVSLK	TN	W	K
			:	:		
g244-1	GNPRLQILISRLGGSFLFYTVRI	SYCLDGFHRLHIFNRF	FTVLLCLFAHIVSLK	TN	W	K
	190	200	210	220	230	240
	250	260	270			
m244-1.pep	KSSYYPRKIRTF	SRNFXQXQRISN	SFSNPLPKKX			
	:		:	: :		
g244-1	KSGYYP	SKIRTF	SRNFKQRQEIS	HPPTLPQKPYKRX		
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 939>:

a244-1.seq

```
1 ATGCCGCTCTG AAGCCCCGACA GGCGGGTTTCA GACGGCATTG CCGCTTTACT
51 TCGATCGGTT TATACGCAAA AC CGCTGTCCA GGAATAAATC CAGATTATTC
101 CCCAGACGCC TCCAGGCTTC CTTCTGTGCC ACGGTAACCA TAGCCGGGGC
151 CAACACGCGG TCGGACAGCG TATAACCCTT CTTCATCAGC CCCACCACGG
201 TATTGGGTTT CTGTTCGCTT GCCACCGCCT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATGCCCGCG TTTAGGATTG ATTTCTTGA TTTGCGTAGC
301 ATCAAATGCT TTCTGCAACT CGTTCAAAGT CATCTGCACG CCCATTTTCA
351 GCGCATCGAA ATTGCCGCTC TGATCAA AAA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTCTCCAC GGCAAACTTC TGTCCGGCGA ACTTGTGCGT
451 ATCCGCAATT TCTCTGTGGT GCGCGCGGCG CAGGTTTTGC TCGTTTGCCA
501 AAGCGCGCAG CTGCTCGTCT TTCAACTGCG CTTCCAGCTC GGCAATCCGC
551 GCCTCGAAAT CCTCATAGC CGGCTGTGCG GCAGCCTGTT CCTGCACACC
601 GTCCGCAATT CCTACTGTCT GCAGGTTTTC CACCGCTCC ACATTTTCAA
651 CCGCTTCTTC ACTGTTTTGC TGCTGTGTCT GTTCGCTCAT ATCGTATCCC
701 TTA AAACAAA TTGGAATCA AAATCCAGT ATTACCGCG CAAGATAAGG
751 ACATTTTCAA GAACTTCAA GCAAAGGCAG AGAATTTCAA ATTCATTTTC
801 AAATCCCCTA CCGAAAAAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 940; ORF 244-1.a>:

a244-1.pep

1	MPSEARQAGS	DGIAALLRSV	YTONALQEIN	QIIPOTPSGF	LLCHRNHSRA
51	QHAVGQRITL	LHNAHHGIGF	LFACHRLHRL	MDIRIELIAR	FRIDFLDLSR
101	IKCFLQLVQS	HLHAHFQRIE	IAALIQKRHF	QIILDRQHEH	GKLLSGELVR
151	IRNFLVAAA	QVLLVCQSAQ	LLVFQLRFQL	GNPRLQILIS	RLCGSLFLHT
201	VRISYCLDGF	HLRHIFNRF	TVLLCLLFAH	IVSLKTNWKS	KSSYYPRKIR
251	TFSRNFKQGR	RISNFSNPL	PKK*		

m244-1/a244-1 96.8% identity in 274 aa overlap

		10	20	30	40	50	60
m244-1.pep		MPSEARQAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
a244-1		MPSEARQAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLLCHRNHSRAQHAVGQRITL					
		10	20	30	40	50	60
		70	80	90	100	110	120
m244-1.pep		LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRSIKCFQLVQSHLHAHFQRIE					
		: :					
a244-1		LHHAHHGIGFLFACHRLHRLMDIRIELIARFRIDFLDLRSIKCFQLVQSHLHAHFQRIE					
		70	80	90	100	110	120
		130	140	150	160	170	179
m244-1.pep		IAALIQRHFQIILDRQHFHGKLLSGELVIRIRNFFLVAAQVLLVCQSA-LLVFQLRFQL					
a244-1		IAALIQRHFQIILDRQHFHGKLLSGELVIRIRNFFLVAAQVLLVCQSAQLLVFQLRFQL					
		130	140	150	160	170	180
	180	190	200	210	220	230	239
m244-1.pep		GNPRLQILISRLCGSLFLHTVRIISYCFDGFHRLHIFNRFFTVLLCLFAHIVSLKTNWKS					
a244-1		GNPRLQILISRLCGSLFLHTVRIISYCLDGFHRLHIFNRFFTVLLCLFAHIVSLKTNWKS					
		190	200	210	220	230	240

240 250 260 270
 m244-1.pep KSSYYPRKIRTFSRNFXQXQRISNSFSNPLPKXX
 |||||
 a244-1 KSSYYPRKIRTFSRNFKQRQRISNSFSNPLPKXX
 250 260 270

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 941>:

```
g246.seq
1  atgtacgggc ggaacggtag tactcaagcg gccgttgccct tcggttttcga
51  ccagacacag cgtgcccggt tcggcaacgg cgaagtttac gccgctcaag
101 ccgacatcgg cagtgcgtgta aatatcgcgc agggcttttgc gggcgaatcc
151 ggtcagttgg tccacgtcgt ctgtaagcgg tgtgcccagg ttttggatgga
201 acagttcgct gacctgtctt ttggttttat ggattgcggg catcacgata
251 tgggtcggtt tttcgccctgc catttggaag ataaactcgc ccaagtcgct
301 ttccaccgcc ttaatgcctt ttgcttcaag ataatgggtt agctcgattt
351 cttcgctgac catggatttg cctttgacca tcagcttgcc gtttttggct
401 gtgatgatgt cgtggataat ttggcaggct tcggcagggg tttccgccca
451 gtgtactttc acgcccact tagtcagggt ttcttccaac tgctccagca
501 gcgcgggttaa
```

This corresponds to the amino acid sequence <SEQ ID 942; ORF 246.ng>:

g246.pep

1	MYGRNGSTQA	AVAFVFDQTQ	RARFGNGEVY	AAQADIGSAV	NIAQGFAGES
51	GQLVHVVCKR	CAEVLVEQFA	DLFFGFMDCG	HHDMGRFFAC	HLDDKLAQVA
101	FHRLNAFCFK	IMVQLDFFAD	HGFAFDHQLA	VFGCDDVVND	LAGFGRGFRP
151	VYFHAQLSQV	FFQLLQQRG*			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 943>:

```
m246.seq (partial)
      1  ATGCACGGGC  GGTACGGTGG  TACTCAAGCG  ACCGTTgCTT  CGTTTTCCAC
     51  CAGACACAGC  GTACCTGTTT  CAGCAACGGC  AAAGTTTACG  CCACTCAAAC
    101  CGACATCGGC  AGTGCTGTAA  ATATCGCGCA  GTGCTTTACG  GGCGAAGCCG
    151  GTCAGTTGGT  CTACATCGTC  TGTCAGCGGC  GTACCAGGT  TTTGGTGGAA
    201  CAGTTCGCTA  ACCTGTTCTT  TGGTTTTGTG  GATAGCAGGC  ATCACGATAT
    251  GGGTCGGTTT  TTCGCTGCCC  ATTTGGACGA  TGAACTCGCC  CAAGTCGCTT
    301  TCTACCGCTT  TAATGcyTTT  TGCTTCAAGA  TAATGrTTCA  GCTCGATTTC
    351  CTCGCTGACC  ATCGATTGCG  CTTTGACCAT  CAGCTTGCCG  TTTTTGGCTG
    401  TGATGATGTC  GTGGATAATT  TGGCAGGCTT  CGGTCGGGGT  TTCTGCCCG...
```

This corresponds to the amino acid sequence <SEQ ID 944; ORF 246>:

```
m246.pep (partial)
      1 MHGRYGGTQA TVAFVFHQQT RTCFSNGKVY ATQTDIGSAV NIAQCFTGEA
     51 GQLVYIVCQR RTEVLVEQFA NLFFGFVDSR HHDMMGRFFAC HLDDELAQVA
    101 FYRFNAFCFK IMXQLDFLAD HRFAFDHOLA VFGCDDVVDN LAGFGRGFCE...
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 246 shows 80.0% identity over a 150 aa overlap with a predicted ORF (ORF 246.ng) from *N. gonorrhoeae*:

m246/g246

```

                10          20          30          40          50          60
m246.pep      MHGRYGGTQATVAFVFHQTRQTCFSNGKVYATQTDIGSAVNIAQCFTGEAGQLVYIVCQR
                |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
g246          MYGRNGSTQAAVAFVFDQTRARFRNGEVYAAQADIGSAVNIAQGFAGESGQLVHVVCKR
                10          20          30          40          50          60

                70          80          90          100         110         120
m246.pep      RTEVLVEQFANLFFGFVDSRHHDMGRFFACHLDDELAQVAFYRFNAFCFKIMXQLDFLAD
                :|||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
g246          CAEVLVEQFADLFFGFMDCGHHDMGRFFACHLDDKLAQVAFHRLNAFCFKIMVOLFDFAL

```


565

	70	80	90	100	110	120
	130	140	150			
m246.pep	HRFAFDHQLAVFGCDDVVDNLAGFGRGFCP					
g246	HGFAFDHQLAVFGCDDVVDNLAGFGRGFRPVYFHAQLSQVFFQLLQQRGX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 945>:

a246.seq (partial)

```

1   ATGCACGGGC GGAACGGTGG TACTCAAGCG ACCGTTGCCT TCGTTTCCA
51  CCAGACACAG CGTACCTGTT TCAGCAACGG CGAAGTTCAC GCCACTCAA
101 CCGACATCGG CAGTGCTGTA AATATCGCGC AGTGCTTTAC GGGCGAAGCC
151 GGTCAAGTGG TCTACGTCGT CCGTTAACGG TGTGCCGAGG TTTTGGTGGA
201 ACAGTTCGCT AACCTGTTCT TTGGTTTAT GGATTGCGGG CATCACGATA
251 TGGGTCGGTT TTTCACCTGC CATTGGACG ATGAACTCGC CCAAGTCGCT
301 TTCCACCGCT TTAATGCCTT TTGCTTCAAG ATAATGGTTC AGCTCGATTT
351 CCTCGCTGAC CATCGATTG CCTTTGACCA TCAGCTTGCC GTTTTGGCT
401 GTGATGATGT CGTGGATGAT TTCGCAGGCT TCGGCCGGTG TTTCCGCCCA
451 TGTACTTTT ACGCCCACT TGGTCAGGTT TTCTCCAGC TGCTCCAGCA
501 G

```

This corresponds to the amino acid sequence <SEQ ID 946; ORF 246.a>:

a246.pep (partial)

```

1   MHGRNGGTQA TVAFVFHQTO RTCFSNGEVH ATQTDIGSAV NIAQCFTGEA
51  GQLVYVVR*R CAEVLVEQFA NLFFGFMDCG HHDMGRFFTC HLDDELAQVA
101 FHRENAFCFK IMVQLDFLAD HRFAFDHQLA VFGCDDVVD FAFGRGCRFP
151 VYFYAQLGQV FFQLLQ

```

m246/a246 88.0% identity in 150 aa overlap

	10	20	30	40	50	60
m246.pep	MHGRYGGTQATVAFVFHQTRTCFSNGKVYATQTDIGSAVNIAQCFTGEAGQLVYIVCQR					
a246	MHGRNGGTQATVAFVFHQTRTCFSNGEVHATQTDIGSAVNIAQCFTGEAGQLVYVVRXR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m246.pep	RTEVLVEQFANLFFGFVDSRHHDMGRFFACHLDELAQVAFYRFNAFCFKIMXQLDFLAD					
	:					
a246	CAEVLVEQFANLFFGFMDCGHHDMGRFFTCHLDELAQVAFHRENAFCFKIMVQLDFLAD					
	70	80	90	100	110	120
	130	140	150			
m246.pep	HRFAFDHQLAVFGCDDVVDNLAGFGRGFCP					
a246	HRFAFDHQLAVFGCDDVVDFAFGGRGFRPVYFYAQLGQVFFQLLQ					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 947>:

g247.seq

```

1   atgaaacgta aaatgctaaa cgtaccaaag ggcggttatg atggtatgaa
51  gggttttacc attgttgaat ttctggttgc gggcctgctc agtataattg
101 tcctgatagc ggtcgtatcg agttacttta catcccggaa attaaatgat
151 gtggcaaacg agcgtcttgc cattcaacag gatttgcgga atgcggcaac
201 attaatgtgc cgcgatgcaa gaatggcggg gagcttcggt tgtttcaata
251 tgtccgagca tactaaagac gatattgttg attcaagtaa tcaaactcaa
301 tctaaccctg caaaacccgg tgccaaacaa gaaaatcccc ttttttccct
351 aaaaaggagc ggcattggata aacaactgat tcccgttgct gaatccatag
401 atattaaata tccgggtttt atccagcgcc ttaacgcatt ggttttccaa
451 tacggtatcg atgatcttga tgcgagtgtg gagactgttg tagtcagcag
501 ctgttccaaa atagcaaaac cgggtaagaa aatatctacc ttgcaagaag
551 caaagagtgc attacagatt actaatgatg ataaacaaaa tggaaatatc

```

```

601 acccgctcaga aacatgtggt caatgcctat gcggtcggca ggtttggcaa
651 taatgaggaa agtttgttcc gcttccaatt ggatgataag ggcaagtggg
701 gtaatcctca gttgctcgtg aaaaagggtta aacgtatgga tgtgcggtat
751 atttatgttt ccggttgctc tgaagatgaa gatgccggca aagaggaaaa
801 attcagatat acgaataaat tcgacaaatc caaaaatgct gttacgcctg
851 ccgggggtgga ggttttattg gatagcggcc ttaatgcaa gattgccgct
901 tcttcagaca atagtattta tgcttaccgt atcaatgcga caatacgcg
951 gggaaatgta tgcgcaaaca gaacactttg a

```

This corresponds to the amino acid sequence <SEQ ID 948; ORF 247.ng>:

g247.pep

```

1 MKRKMLNVPK GGYDGMKGFT IVEFLVAGLL SIIVLIIVVS SYFTSRKLND
51 VANERLAIQQ DLRNAATLIV RDARMAGSFG CFNMSEHTKD DIVDSSNQTS
101 SNLAKPGAKQ ENPLFSLKRS GMDKQLIPVA ESIDIKYPGF IQRLNALVFO
151 YGIDDLASA ETVVSSCSK IAKPGKKIST LQEAQSALQI TNDDKQNGNI
201 TRQKHVVNAY AVGRFGNNEE SLFRFQLDDK GKWGNPQLLV KKVKRMDVRY
251 IYVSGCPEDE DAGKEEFKRY TNKFDSKNA VTPAGVEVLL DSGLNAKIAA
301 SSDNSIYAYR INATIRGGNV CANRTL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 949>:

m247.seq (partial)

```

1 ATsAGACGTA AAATGCTAAA CGTwsyArAA GGCAGTTATG ATGGTATGAA
51 AGGTTTTTACC ATTATTGAAT TTTTGGTTGC GGGCCTGCTC AGTATGATTG
101 TCCTGATGGC GGTCGGATCG AGTTACTTCA CATCCCGGAA ATTAAATGAT
151 GCGGCAAACG AGCGTCTTGC CGCGCAACAG GATTTCGCGA ATGCGGCAAC
201 ATTGATTGTC CGCGATGCGA GAATGGCAGG CGGCTTCGGT TGTTTCAATA
251 TGTCCGAGCA TCCTGCAACT GATGTTATTC CCGATACGAC GCAACAAAAT
301 TCTCCTTTTT CCTTAAAAAG GAACGCTATA GATAAACTTA TTCCCATAGC
351 GGAATCTTCA AATATCAATT ATCAGAATTT TTTCCAGGTT GGTAGCGCAT
401 TGATTTTTTCA ATACGGAATC GATGATGTTA ATGCAAGCAC CGCGACTACC
451 GTCGTACGCA GCTGTGCCGC AATATCGAAA CCGGGCAAGC AAATCCCTAC
501 TTTAGAAGAT GCAAAAAAAG AATTGAAGAT TCCGGATCAG GATAAGGAGC
551 AAAATGGCAA TATAGCGCGT CAAAGGCATG TGGTCAATGC CTATGCGGTC
601 GGCAGGATTG CCGATGAGGA AAGTTTGTTC CGCTTCCAAT TGGATGATAA
651 GGGCAAGTGG GGTAATCCTC AGTTGC...

```

This corresponds to the amino acid sequence <SEQ ID 950; ORF 247>:

m247.pep (partial)

```

1 XRRKMLNVXX GSYDGMKGFT IIEFLVAGLL SMIVLMAVGS SYFTSRKLND
51 AANERLAAQQ DLRNAATLIV RDARMAGGFG CFNMSEHPAT DVIPDTTQQN
101 SPFSLKRNGI DKLIPIAESS NINYQNFFQV GSALIFQYGI DDVNASTATT
151 VVSSCAAISK PGKQIPTLED AKKELKIPDQ DKEQNGNIAR QRHVVNAYAV
201 GRIADEESLF RFQLDDKGKW GNPQL...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 247 shows 69.3% identity over a 238 aa overlap with a predicted ORF (ORF 247.ng) from *N. gonorrhoeae*:

m247/g247

```

              10      20      30      40      50      60
m247.pep  XRRKMLNVXXGSYDGMKGFTIIEFLVAGLLSMIVLMAVGSSYFTSRKLND AANERLAAQQ
          : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
g247      MKRKMLNVPKGGYDGMKGFTIVEFLVAGLLSIIVLIIVVSSYFTSRKLNDVANERLAIQQ
              10      20      30      40      50      60

              70      80      90      100
m247.pep  DLRNAATLIVRDARMAGGFGCFNMSEHPATDVI-----PD TTQQNSPFSLKRN
          ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
g247      DLRNAATLIVRDARMAGSFGCFNMSEHTKDDIVDSSNQTSNLAKPGAKQENPLFSLKRS
              70      80      90      100      110      120

110      120      130      140      150      160
m247.pep  GIDK-LIPIAESSNINYQNFFQVGSALIFQYGI DDVNASTATT VVSSCAAISKPGKQIPT
          || : || : || : || : || : || : || : || : || : || : || : || : || : ||

```

567

```

g247      GMDKQLIPVAESIDIKYPGFIQRLNALVFQYGIDDLASAETVVVSSCSKIAKPGKKIST
           130      140      150      160      170      180

           170      180      190      200      210      220
m247.pep  LEDAKKELKIPDQDKEQNGNIARQHRVFNAYAVGRIAD-EESLFRFQLDDKGKGNPQL
           |::||: |::|::| |::|::| |::|::| |::|::| |::|::| |::|::|
g247      LQEAKSALQITNDDK-QNGNITRQKHVVFNAYAVGRFGNNEESLFRFQLDDKGKGNPQLL
           190      200      210      220      230

           240      250      260      270      280      290
g247      VKKVKRMDVRYIYVSGCPEDEDAGKEEFKFRYTNKFDKSKNAVTPAGVEVLLDSGLNAKIA

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 951>:

```

a247.seq
1  ATGAGACGTA AAATGCTAAA CGTACCAAAA GGCAATTATG ATGGTATGAA
51  GGGTTTTACC ATTATTGAAT TTTTGGTTGC GGGCATGCTC AGTATGATTG
101 TCCTGATGGC GGTCGGATCG AGTTACTTCA CATCCCGGAA ATTAAATGAT
151 GCGGCAAACG AGCGTCTTTC CGCGCAACAG GATTGCGGA ATGCGGCAAC
201 ATTGATTGTC CGCGATGCAA GAATGGCAGG GGGCTTCGGT TGTTTCAATA
251 TGTCCGAGCA TACTAAAAAT GATATTATTG TTGATCCAAG TAAGCAAAC
301 CAACATGTCC CTGTAAAACC CGGTGCCAAA CAAGAAAATC CCCTTTTTC
351 TTTAGAGTGG GCTAATACTA ATAATACTAA TAATAATACA GCTAAATTGA
401 TTCCTATTGC TGAATCCACA GATATTAAAT ATCCGGGTTT TGCCCAGGCT
451 CGTCCGGCAT TGATTTTCCA ATACGGCATC GATGATCTTG ATGCGAGTGC
501 TGAGACTGTT GTAGTCAGCA GCTGTTCCAA AATAGCAAAA CCGGGTAAGA
551 AAATATCTAC CTTGCAAGAA GCAAAGAGTG CATTACAGAT TACTAATGAT
601 GATAACAAA ATGGAAATAT CACCCGTCAA AGGCATGTGG TCAATGCCA
651 TGCGGTCGGC AGGATTGCCG GTGAGGAAGG TTTGTTCCGC TTCCAATTGG
701 ATGATAAGGG CAAGTGGGGT AATCCTCAGT TGCTCGTGAA AAAGATTAGA
751 CATATGAAAG TCGGTATAT CTATGTTTCC GACTGTCTTG AAGATGACGA
801 TGCCGGCAAA GAGGAAAAAT TCAAAATATC GGGTACATTC GACAGCTCCA
851 CAAATGCTGT TACGCCCCGC GGGGTGGAGG TTTTATTGAG TACCGGTACT
901 GATACCAAGA TTGCCGCTTC TTCAGACAAT CATATTTATG CTTACCGTAT
951 CGATGCGACA ATACGCGGGG GAAATGTATG CGAAACAGA ACACTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 952; ORF 247.a>:

```

a247.pep
1  MRRKMLNVPK GNYDGMKGFT IIEFLVAGML SMIVLMAVGS SYFTSRKLND
51  AANERLSAQO DLRNAATLIV RDARMAGGFG CFNMSEHTKN DIIVDPSKQT
101 QHVPVPGAK QENPLFSLEW ANTNTNTNNT AKLIPIAEST DIKYPGFAQA
151 RPALIFQYGI DDLASAETV VVSSCSKIAK PGKKISTLQE AKSALQITND
201 DKQNGNITRQ RHVVFNAYAVG RIAGEEGLFR FQLDDKGKWG NPQLLVKKIR
251 HMKVRYIYVS DCPEDDDAGK EEKFKYTGTF DSSTNAVTPA GVEVLLSXGT
301 DTKIAASSDN HIYAYRIDAT IRGNVCANR TL*

```

m247/a247 70.9% identity in 244 aa overlap

```

m247.pep  XRRKMLNVXXGSYDGMKGFTIIEFLVAGLLSMIVLMAVGSSYFTSRKLND AANERLAAQQ
           |::|::| |::|::| |::|::| |::|::| |::|::| |::|::| |::|::|
a247      MRRKMLNVPKGNYDGMKGFTIIEFLVAGMLSMIVLMAVGSSYFTSRKLND AANERLSAQO
           10      20      30      40      50      60

           70      80      90      100
m247.pep  DLRNAATLIVRDARMAGGFGCFNMSEHPATDVI-----PDTTQONSPFSLK-
           |::|::| |::|::| |::|::| |::|::| |::|::| |::|::| |::|::|
a247      DLRNAATLIVRDARMAGGFGCFNMSEHTKNDIIVDPSKQTHVPVPGAKQENPLFSLEW
           70      80      90      100      110      120

           130      140      150      160      170      180
m247.pep  -----RNGIDKLIPIAESSNINYQNFFQVGSALIFQYGIDDVNASTATTVVSSCAAISK
           |::|::| |::|::| |::|::| |::|::| |::|::| |::|::| |::|::|
a247      ANTNTNTNTAKLIPIAESTDIKYPGFAQARPALIFQYGIDDLASAETVVVSSCSKIAK
           130      140      150      160      170      180

```

	170	180	190	200	210	220
m247.pep	PGKQIPTLED	AKKELKIPDQ	KEQNGNIARQ	RHVVNAYAVG	RIADEESLFR	FQLDDKGKW
a247	PGKKISTLQEA	KSALQITNDDK	-QNGNITRQ	RHVVNAYAVG	RIAGEEGLFR	FQLDDKGKW
	190	200	210	220	230	
m247.pep	GNPQL					
a247	GNPQLLVKKIR	HMKVRYIYV	SDCPEDDDAG	KEEKFKYTGT	FDSSTNAVTP	PAGVEVLLSXG
	240	250	260	270	280	290

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 953>:

g247-1.seq (partial) ..

```

1   CCCGGTGCCA AACAAGAAAA TCCCCTTTTT TCCTTAAAAA GGAGCGGCAT
51  GGATAAACAA CTGATTCCCG TTGCTGAATC CATAGATATT AAATATCCGG
101 GTTTTATCCA GCGCCTTAAC GCATTGGTTT TCCAATACGG TATCGATGAT
151 CTTGATGCGA GTGCTGAGAC TGTGTAGTTC AGCAGCTGTT CCAAAATAGC
201 AAAACCGGGT AAGAAAATAT CTACCTTGCA AGAAGCAAAG AGTGCATTAC
251 AGATTACTAA TGATGATAAA CAAAATGGAA ATATCACCCG TCAGAAACAT
301 GTGGTCAATG CCTATGCGGT CGGCAGGTTT GGCAATAATG AGGAAAGTTT
351 GTTCCGCTTC CAATTGGATG ATAAGGGCAA GTGGGGTAAT CCTCAGTTGC
401 TCGTGAAAAA GGTAAACGTT ATGGATGTGC GGTATATTTA TGTTCGCGGT
451 TGTCTGAAG ATGAAGATGC CGGCAAAGAG GAAAAATTCA GATATACGAA
501 TAAATTCGAC AAATCCAAAA ATGCTGTAC GCCTGCCGGG GTGGAGGTTT
551 TATTGGATAG CGGCCTTAAT GCCAAGATTG CCGCTTCTTC AGACAATAGT
601 ATTTATGCTT ACCGTATCAA TCGACAATA CGCGGGGGAA ATGTATGCGC
651 AAACAGAACA CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 954; ORF 247-1.ng>:

g247-1.pep (partial) ..

```

1   P GAKQENPLF SLKRSMDKQ LIPVAESIDI KYPGFIQRLN ALVFQYQIDD
51  L DASAETVVV SSSSKIAPKG KKISTLQEAQ SALQITNDDK QNGNITRQKH
101 V VNAYAVGRF GNNEESLFRF QLDDKGKWN PQLLVKKVKR MDVRYIYVSG
151 C PPEDEAGKE EKFRYTNKFD KSKNAVTPAG VEVLLDSGLN AKIAASSDNS
201 I YAYRINATI RGNVNCANRT L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 955>:

m247-1.seq

```

1   ATGAGACGTA AAATGCTAAA CGTACCAAAA GGCAGTTATG ATGGTATGAA
51  AGGTTTTACC ATTATTGAAT TTTTGGTTGC GGGCCTGCTC AGTATGATTG
101 TCCTGATGGC GGTCCGATCG AGTTACTTCA CATCCCGGAA ATTAAATGAT
151 GCGGCAACAG AGCGTCTTGC CGCGCAACAG GATTTGCGGA ATGCGGCAAC
201 ATTGATTGTC CGCGATGCGA GAATGGCAGG CGGCTTCGGT TGTTCCTAATA
251 TGTCCGAGCA TCCTGCAACT GATGTTATTC CCGATACGAC GCAACAAAAT
301 TCTCCTTTT CTTTAAAAAG GAACGGTATA GATAAACTTA TTCCCATAGC
351 GGAATCTTCA AATATCAATT ATCAGAATTT TTTCCAGGTT GGTAGCGCAT
401 TGATTTTTC ATACGGAATC GATGATGTTA ATGCAAGCAC CGCGACTACC
451 GTCGTCAGCA GCTGTGCCGC AATATCGAAA CCGGGCAAGC AAATCCCTAC
501 TTTAGAAGAT GCAAAAAAAG AATTGAAGAT TCCGGATCAG GATAAGGAGC
551 AAAATGGCAA TATAGCGCGT CAAAGGCATG TGGTCAATGC CTATGCGGTC
601 GGCAGGATTG CCGATGAGGA AGGTTTGTTT CGCTTCCAAT TGGATGATAA
651 GGGCAAGTGG GGTAACTCTC AGTTGCTCGT GAAAAAGGTT AGACATATGA
701 AAGTGCAGTA TATCTATGTT TCCGGCTGTC CTGAAGATGA CGATGCCGGC
751 AAAGAGGAAA CATTCAAATA TACGGATAAA TTGCACAGCG CCCAAAATGC
801 GTTTACGCCG GCCGGGGTGG AGGTTTTATT GAGTAGCGGT ACTGATACCA
851 AGATTGCCGC TTCTTCAGAC AATCATATTT ATGCTTACCG TATCGATGCG
901 ACAATACCGG GGGGAAATGT ATGCGCAAAC AGAACACTTT GA

```

This corresponds to the amino acid sequence <SEQ ID 956; ORF 247-1>:

m247-1.pep

```

1   MRRKMLNVPK GSYDGMKGFT IIEFLVAGLL SMIVLMAVGS SYFTSRKLND
51  AANERLAAQQ DLRNAATLIV RDARMAGGFG CFNMSEHPAT DVIPDTTQON
101 SPFSLKRRGI DKLPIAESS NINYQNFFQV GSALIFQYGI DDVNASTATT
151 VVSSCAAISK PGKQIPTLED AKKELKIPDQ DKEQNGNIAR QRHVVNAYAV
201 GRIADEEGLF RFQLDDKGKW GNPQLLVKKV RHMKVRYIYV SDCPEDDDAG
251 KEETFKYTDK FDSAQNAVTP AGVEVLLSSG TDTKIAASSD NHIYAYRIDA
301 TIRGGNVCAN RTL*

```

m247-1 / g247-1 72.1% identity in 222 aa overlap

```

              70      80      90      100      110      120
m247-1.pep    NAATLIVRDARMAGGFGCFNMSEHPATDVIPDTTQONSPPFSLKRNGIDK-LIPIAESSNI
              | : | : | | | | | : | : | | | | | : |
g247-1        PGAKQENPLFSLKRSGMDKQLIPVAESIDI
              10      20      30

              130      140      150      160      170      180
m247-1.pep    NYQNFFQVGSALIFQYGIDDVNASTATTVVSSCAAISKPGKQIPTLEDAKKELKIPDQDK
              : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
g247-1        KYPGFIQRLNALVFQYGIDDLASAETVVVSSCSKIAPGKKISTLQEAQSALQITNDDK
              40      50      60      70      80      90

              190      200      210      220      230      240
m247-1.pep    EQNGNIARQRHVVNAYAVGRIAD-EEGLFRFQDDKKGWGNPQLLVKKVRHMKVRYIYVS
              | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
g247-1        -QNGNITRQKHVVNAYAVGRFGNNEESLFRFQDDKKGWGNPQLLVKKVRMDVRYIYVS
              100      110      120      130      140

              250      260      270      280      290      300
m247-1.pep    GCPEDDDAGKEETFKYTDKFDSDAQNNAVTPAGVEVLLSSGTDTKIAASSDNHIYAYRIDAT
              | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
g247-1        GCPEDDDAGKEEFKRYTNKFDKSKNAVTPAGVEVLLDSSLNAKIAASSDNSIYAYRINAT
              150      160      170      180      190      200

              310
m247-1.pep    IRGGNVCANRTLX
              | | | | |
g247-1        IRGGNVCANRTLX
              210      220

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 957>:

a247-1.seq (partial)

```

1  AATAATACAG CTAATTGAT TCCTATTGCT GAATCCACAG ATATTAAATA
51 TCCGGGTTTT GCCCAGGCTC GTCCGGCATT GATTTTCCAA TACGGCATCG
101 ATGATCTTGA TGCGAGTGCT GAGACTGTTG TAGTCAGCAG CTGTTCCAAA
151 ATAGCAAAAC CGGGTAAGAA AATATCTACC TTGCAAGAAG CAAAGAGTGC
201 ATTACAGATT ACTAATGATG ATAAACAAA TGGAAATATC ACCCGTCAA
251 GGCATGTGGT CAATGCCTAT GCGGTCGGCA GGATTGCCGG TGAGGAAGGT
301 TTGTTCCGCT TCCAATTGGA TGATAAGGGC AAGTGGGGTA ATCCTCAGTT
351 GCTCGTGAAA AAGATTAGAC ATATGAAAGT GCGGTATATC TATGTTCCG
401 ACTGTCTTGA AGATGACGAT GCCGGCAAAG AGGAAAAATT CAAATATACG
451 GGTACATTCG ACAGCTCCAC AAATGCTGTT ACGCCCGCCG GGGTGGAGGT
501 TTTATTGAGT AGCGGTACTG ATACCAAGAT TGCCGCTTCT TCAGACAATC
551 ATATTATATG TTACCGTATC GATGCGACAA TACGCGGGGG AAATGTATGC
601 GCAAACAGAA CACTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 958; ORF 247-1.a>:

a247-1.pep (partial)..

```

1  NNTAKLIPIA ESTDIKYPGF AQARPALIFQ YGIDDLASA ETVVVSSCSK
51  IAKPGKKIST LQEAQSALQI TNDDKQNGNI TRQRHVVNAY AVGRIAGEEG
101 LFRFQDDKG KGNPQLLVK KIRHMKVRYI YVSDCPEDDD AGKEEFKYT
151 GTFDSSTNAV TPAGVEVLLS SGTDTKIAAS SDNHIYAYRI DATIRGGNVC
201 ANRTL*

```

m247-1 / a247-1 80.6% identity in 206 aa overlap

```

              10      20      30
a247-1.pep    NNTAKLIPIAESTDIKYPGFAQARPALIFQ
              | : | | | | | : | : | : | : | : |
m247-1        GFGCFNMSEHPATDVIPDTTQONSPPFSLKRNGIDKLIPIAESSNINYNQNFFQVGSALIFQ
              80      90      100      110      120      130

              40      50      60      70      80      89
a247-1.pep    YGIDDLASAETVVVSSCSKIAPGKKISTLQEAQSALQITNDDK-QNGNITRQRHVVNA
              | | | | | : | | | | | : | | | | | : | : | | | | |
m247-1        YGIDDVNASTATTVVSSCAAISKPGKQIPTLEDAKKELKIPDQDKEQNGNIARQRHVVNA
              140      150      160      170      180      190

              90      100      110      120      130      140      149
a247-1.pep    YAVGRIAGEEGLFRFQDDKKGWGNPQLLVKKIRHMKVRYIYVSDCPEDDDAGKEEFKY
              | | | | | | | | | | | | | | | : | | | | | | | | | | |

```

```

m247-1      YAVGRIADEEGLFRFQDDKGKGNPQLLVKKVRHMKVRYIYVSGCPEDDDAGKEETFKY
            200      210      220      230      240      250

a247-1.pep  150      160      170      180      190      200
            TGTFDSSSTNAVTPAGVEVLLSSGTDTKIAASSDNHIYAYRIDATIRGGNVCANRTLX
            | |||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m247-1      260      270      280      290      300      310
            TDKFDSAQNAVTPAGVEVLLSSGTDTKIAASSDNHIYAYRIDATIRGGNVCANRTLX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 959>:

```

g248.seq
1   atgcgcaaac agaacacttt gacaggaatc ccgacttctg acggacagag
51  ggggtccgca ctgtttatcg tgctgatggt gatgatagtc gtggcctttt
101 tggttgtaac tgccgcccag tcctacaata ccgaacagag gatcagtgcc
151 aacgaatcag acaggaaatt ggctttgtct ttagccgagg cggctttgcg
201 ggagggcgaa tttcagggtt tggatttgga atatgctgcg gacagtaagg
251 ttacgtttag cgaaaactgt gaaaaaggct tgtgtaccgc agtgaatgtg
301 cggacaaaata ataattggtag tgaagaggct tttggcaata tcgtggtgca
351 aggcaagccc gccgttgagg cggtgaaacg ttcttgccct gcaaagtctg
401 gcaaaaattc taccgacctg tgcattgaca ataaagggat ggaatataat
451 aaaggcgcgg caggcgctag caaatgccg cgctatatta tcgaatattt
501 aggcgtgaag aacggacaaa atgtttatcg gggtactgcc aaggcttggg
551 gtaagaatgc caataccgtg gtcgtccttc aatcttatgt aggcaataat
601 gatgagcaat aa

```

This corresponds to the amino acid sequence <SEQ ID 960; ORF 248.ng>:

```

g248.pep
1   MRKQNTLTGI PTSDGQRGSA LFIVLMVMIV VAFLVVTAAQ SYNTEQRISA
51  NESDRKLALS LAEALREGE FQVLDLEYAA DSKVTFSENC EKGLCTAVNV
101 RTNNGSEEA FGNIVVQKP AVEAVKRSCP AKSGKNSTDL CIDNKGMEYN
151 KGAAGVSKMP RYIIIEYLGVK NGQNVYRVTA KAWGKNANTV VVLQSYVGN
201 DEQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 961>:

```

m248.seq (partial)
1   ..GGGTTTGCAC TGTTAATCGT GCTGATGGTG ATrATCGTCG TGGCT.TyWT
51  gGwTGTAAC T GCCGCGCAGT CTTACAATAC cGAGCAGCGk ATCAGTkCCA
101 ACGAATCAGA CAGGAAATTG GCTwTGTCTT TGGCCGAGkC GkCTwTGCGG
151 GAAGGCGAAC TTCAGGTTTT GGATTtTGAA TATGATACGG ACAGTAAGGT
201 TACATTTAGC GAAAACTGTG GAAAAGGTCT GTsTGCCGCA GTGAATGTGC
251 GGACAAATAA TGATAATGAA GAGGCTTTTG ACAATATCGT GGTGCAAGGC
301 AAGCCCACCG TTGAGGCGGT GAAGCGTTCT TGCCCTGCAA ATTCTACCGA
351 CCTGTGCATT GACAAGAAAG GGwTGGAATA TAAGAAAGGC ACGAGAAGCG
401 TCac.AAAAT GCCACGTTAT ATTATCGAAT ATTTGGGCGT GwAGAACGGA
451 GAAAATGTTT ATCGGGTTAC TGCCAAGGCT TGGGGtAAGA ATGCCAATAC
501 CGTGGTCGTC CTTCAATCTT ATGTAAGCAA TAATGATGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 962; ORF 248>:

```

m248.pep (partial)
1   ..GFALLIVLMV XIVVAFXXVT AAQSYNTEQR ISXNESDRKL AXSLAEXXXR
51  EGELQVLDLE YDTSKVTFS ENCGKGLXAA VNVRTNNDNE EAFDNIVVQG
101 KPTVEAVKRS CPANSTDLCI DKKGXEYKKG TRSVTKMPRY IIEYLGvXNG
151 ENVYRVTAKE WKKNANTVVV LQSYVSNND *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 248 shows 81.1% identity over a 185 aa overlap with a predicted ORF (ORF 248.ng) from *N. gonorrhoeae*:

m248/g248

```

m248.pep      10      20      30      40
               GFALLIVLMVXIVVAFXXVTAAQSYNTEQRISXNESDRKLAXS
               | ||: |||| |||| | ||||| ||||| ||||| ||||| |||||

```

571

```

g248      MRKQNTLTGIPTSDGQRGSAFIVLMVMIVVAFVVTAAQSYNTEQRISANESDRKLALS
           10      20      30      40      50      60

           50      60      70      80      90      100
m248.pep  LAEXXXREGELQVLDLEYDTSKVTFSENCGKGLXAAVNVRTNND-NEEAFDNIVVQGKP
           |||  |||:||||| :||||||| || :|||||: :||| |||||
g248      LAEAAALREGEFQVLDLEYAADS KVTFSENCEKGLCTAVNVRTNNGSEEAFGNIVVQGKP
           70      80      90      100      110      120

           110      120      130      140      150
m248.pep  TVEAVKRSCPA---NSTDLCKKGXEYKKGTRSVTKMPRYII EYLGXNGENVYRVTA
           :||||||| |||||:| ||:|: :|:||||||| ||:|||||
g248      AVEAVKRSCPAKSGKNSTDLCKDKGMEYKNGAAGVSKMPRYII EYLGXNGQNVYRVTA
           130      140      150      160      170      180

           160      170      180
m248.pep  KAWGKNANTVVVLQSYVSNNDEX
           ||||| |||||:||||
g248      KAWGKNANTVVVLQSYVGNNDEQX
           190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 963>:

```

a248.seq
1  ATGCGCAAAC AGAACACTTT GACGGGAATC CCGACTTCTG ACGGACAGAG
51  GGGGTTTGCA CTGTTTATCG TGCTGATGGT GATGATCGTC GTGGCTTTT
101 TGGTTGTAAC TGCCGCGCAG TCTTACAATA CCGAGCAGCG GATCAGTGCC
151 AACGAATCAG ACAGGAAATT GGCTTTGTCT TTGCCCAGAG CGGCTTTGCG
201 GGAAGGCGAA CTTCAGGTTT TGGATTGGA ATATGATACG GACAGTAAGG
251 TTACATTTAG CGAAACTGT GGAAAAGGTC TGTGTACCGC AGTGAATGTG
301 CGGACAAATA ATGATAATGA AGAGGCTTTT GACAATATCG TGGTGCAAGG
351 CAAGCCCACC GTTGAGGCGG TGAAGCGTTC TTGCACTGCA AAATCTACAG
401 GCCTGTGCAT TGACAATAAA GGGATGGAAT ATAAGAAAGG CACGCAAAGC
451 GTCAGCAAAA TGCCACGTTA TATTATCGAA TATTGGGCG TGAAGAACGG
501 AGAAAATGTT TATCGGGTTA CTGCCAAGGC TTGGGGTAAG AATGCCAATA
551 CCGTGGTCGT CCTTCAATCT TATGTAAGCA ATAATGATGA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 964; ORF 248.a>:

```

a248.pep
1  MRKQNTLTGI PTSDGQRGFA LFIVLMVMIV VAFVVTAAQ SYNTEQRISA
51  NESDRKLALS LAEAAALREGE LQVLDLEYDT DSKVTFSENC GKGLCTAVNV
101 RTNNDNEEAF DNIVVQGKPT VEAVKRSC TA KSTGLCIDNK GMEYKKGTS
151 VSKMPRYIE YLGXNGENV YRVTA KAWGK NANTVVVLQS YVSNNDE*

```

m248/a248 89.4% identity in 180 aa overlap

```

m248.pep      GFALLIVLMVXIVVAFXXVTAAQSYNTEQRISXNESDRKLAXS
               10      20      30      40
a248          MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFVVTAAQSYNTEQRISANESDRKLALS
               10      20      30      40      50      60

           50      60      70      80      90      100
m248.pep  LAEXXXREGELQVLDLEYDTSKVTFSENCGKGLXAAVNVRTNNDNEEAFDNIVVQGKPT
           |||  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a248      LAEAAALREGEFQVLDLEYDTSKVTFSENCGKGLCTAVNVRTNNDNEEAFDNIVVQGKPT
           70      80      90      100      110      120

           110      120      130      140      150      160
m248.pep  VEAVKRSCPANSTDLCIDKKGXEYKKGTRSVTKMPRYII EYLGXNGENVYRVTA KAWGK
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a248      VEAVKRSC TAKSTGLCIDNK GMEYKKGTS VSKMPRYII EYLGXNGENVYRVTA KAWGK
           130      140      150      160      170      180

           170      180
m248.pep  NANTVVVLQSYVSNNDEX

```

a248

|||||
NANTVVVLQSYVSNNDEX
190

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 965>:

m248-1.seq

```

1  ATGCGCAAAC AGAACACTTT GACGGGAATC CCGACTTCTG ACGGACAGAG
51  GGGGTTTGCA CTGTTTATCG TGCTGATGGT GATGATCGTC GTGGCTTTT
101 TGGTTGTAAC TGCCGCGCAG TCTTACAATA CCGAGCAGCG GATCAGTGCC
151 AACGAATCAG ACAGGAAATT GGCTTTGTCT TTGGCCGAGG CGGCTTTGCG
201 GGAAGGCGAA CTTCAGGTTT TGGATTGGA ATATGATACG GACAGTAAGG
251 TTACATTAG CGAAACTGT GGAAAAGGTC TGTGTGCCGC AGTGAATGTG
301 CGGACAAATA ATGATAATGA AGAGGCTTTT GACAATATCG TGGTGCAAGG
351 CAAGCCCACC GTTGAGGCGG TGAAGCGTTC TTGCCCTGCA AATTCTACCG
401 ACCTGTGCAT TGACAAGAAA GGGATGGAAT ATAAGAAAGG CACGAGAAGC
451 GTCAGCAAAA TGCCACGTTA TATTATCGAA TATTGCGGCG TGAAGAACGG
501 AGAAAAATGTT TATCGGGTTA CTGCCAAGGC TTGGGGTAAG AATGCCAATA
551 CCGTGGTCGT CCTTCAATCT TATGTAAGCA ATAATGATGA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 966; ORF 248-1>:

m248-1.pep

```

1  MRKQNTLTGI PTSDGQRGFA LFIVLMVMIV VAFLVVTAAQ SYNTEQRISA
51  NESDRKLALS LAEALREGE LQVLDLEYDT DSKVTFSENC GKGLCAAVNV
101 RTNNDNEEAF DNIVVQGKPT VEAVKRSCPA NSTDLCDKK GMEYKKGTRS
151 VSKMPRYIIE YLGKNGENV YRVTAKAWGK NANTVVVLQS YVSNNDE*

```

m248-1/g248 89.1% identity in 202 aa overlap

	10	20	30	40	50	60
m248-1.pep	MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFLVVTAAQSYNTEQRISANESDRKLALS					
g248	MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFLVVTAAQSYNTEQRISANESDRKLALS					
	10	20	30	40	50	60
m248-1.pep	LAEALREGE LQVLDLEYDTDSKVTFSENC GKGLCAAVNVRTNND-NEEAFDNIVVQGKPT					
g248	LAEALREGE FQVLDLEYAADSKVTFSENCEKGLCTAVNVRTNNDNEEAFDNIVVQGKPT					
	70	80	90	100	110	119
m248-1.pep						
g248						
	120	130	140	150	160	170
m248-1.pep	TVEAVKRSCPA-----NSTDLCDKKGMEYKKGTRSVSKMPRYIIEYLGKNGENVYRVT					
g248	AVEAVKRSCPAKSGKNSTDLCDKNKMEYKGAAGVSKMPRYIIEYLGKNGQNVYRVT					
	130	140	150	160	170	180
m248-1.pep						
g248						
	180	190				
m248-1.pep	KAWGKNANTVVVLQSYVSNNDEX					
g248	KAWGKNANTVVVLQSYVGNNDQX					
	190	200				

m248-1/a248 97.0% identity in 197 aa overlap

	10	20	30	40	50	60
m248-1.pep	MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFLVVTAAQSYNTEQRISANESDRKLALS					
a248	MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFLVVTAAQSYNTEQRISANESDRKLALS					
	10	20	30	40	50	60
m248-1.pep	LAEALREGE LQVLDLEYDTDSKVTFSENC GKGLCAAVNVRTNNDNEEAFDNIVVQGKPT					
a248	LAEALREGE LQVLDLEYDTDSKVTFSENC GKGLCTAVNVRTNNDNEEAFDNIVVQGKPT					
	70	80	90	100	110	120
m248-1.pep						
a248						
	130	140	150	160	170	180
m248-1.pep	VEAVKRSCPANSTDLCDKKGMEYKKGTRSVSKMPRYIIEYLGKNGENVYRVTAKAWGK					
a248	VEAVKRSCAKSTGLCDKNKMEYKKGTSVSKMPRYIIEYLGKNGENVYRVTAKAWGK					
	130	140	150	160	170	180


```

                                190
m248-1.pep  NANTVVVLQSYVSNNDX
              |||||
a248         NANTVVVLQSYVSNNDX
                                190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 967>:

```
g249.seq
1  atgaagaata atgattgctt ggcctgaaa aatccccagt ccggtatggc
51  gttgatagaa gtcttggtcg ctatgctcgt tctgaccatc ggtattttgg
101 cattgctgtc cgtacagtta cggacagtcg cttccgtcag ggaggcggaa
151 acgcaaacca tcgtcagcca aatcacgcaa aacctgatag aaggaaatgtt
201 gatgaatccg aactatgatt tggacagcaa caagaaaaac tatgctcttt
251 acatgggaaa acagacacta tcagctgtgg atggtgagtt tatgcttgat
301 gccgagaaaa gtaaggcgca gttggcagag gaacaattga agagatttag
351 tcatgagctg aaaaatgcct tgccggatgc ggtagctatt cattacgccg
401 tctgcaagga ttcgtcgggt gacgcgccga cattgtccga cagcggtgct
451 ttttcttcaa attgcgacaa taaggcaaac ggggatactt tgattaaagt
501 attgtgggta aatgattcgg caggggattc ggatatttcc cgtacgaatc
551 ttgaagtgag cggcgacaat atcgtatata cctatcaggc aagggtcggg
601 ggtcgtgaat ga
```

This corresponds to the amino acid sequence <SEQ ID 968; ORF 249.ng>:

```
g249.pep
  1  MKNNDCLRLK  NPQSGMALIE  VLVAMLVLTI  GILALLSVQL  RTVASVREAE
51  TQTIVSQITQ  NLMEGMLMNP  TIDLDSNKK  N  YSLYMGKQTL  SAVDGEFMLD
101 AEKSKAQLAE  EQLKRFSHEL  KNALPDAVA  I  HYAVCKDSSG  DAPTLSDSGA
151 FSSNCDNKAN  GDTLIKVLWV  NDSAGDSDI  S  RTNLEVSGDN  IVVYQARVG
201 GRE*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 969>:

```
m249.seq
1 ATGAAGAATA ATGATTGCTT CCGCCTGAAA GATTCCCAGT CCGGTATGGC
51 GCTGATAGAA GTCTTGGTTG CTATGCTCGT TCTGACCATC GGTATTTTGG
101 CACTATTGTC GTGACAGTTG CCGGACAGCT NNNNNNNNNN NNNNNNNNNN
151 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNTTGATGG AGGGAATGTT
201 GATGAATCCG ACCATTGATT CGGACAGCAA CAAGAAAAAC TATAATCTTT
251 ACATGGGAAA CCATACACTA TCAGCTGTGG ATGGCGATTT TGCGATTGAT
301 GCCATGAAAA CTAAGGGGCA ATTGGCAGAG GCACAATTGA AGAGATTTAG
351 TTATGAGCTG AAAAAATGCC TGCCGGATGC GGCAGCCATC CATTACGCCG
401 TCTGCAAGGA TTCGTCGGGT AACGCGCCGA CATTGTCCGG CAATGCTTTT
451 TCTTCAAATT GCGACAATAA GGCAAACGGG GATACTTTAA TTAAAGTATT
501 GTGGGTAAAT GATTCGGCAG GGGATTCCGA TATTTCCCGT ACGAATCTTG
551 AGGTGAGCGG CGACAATATC GTATATACTT ATCAGGCAAG GGTCGGAGGT
601 CGGGAATGA
```

This corresponds to the amino acid sequence <SEQ ID 970; ORF 249>:

```
m249 . pep
      1  MKNNDCFR LK  DSQSGMALIE  VLVAMLV LTI  GILALLSVQL  RTVXXXXXXXX
     51  XXXXXXXXXXXX  XLM EGM L MNP  TIDSDSNKKN  YNLYMGNHTL  SAVDGDFAID
    101  AMKTKGQLAE  AQLKRFSYEL  KNALPDAAI  HYAVCKDSSG  NAPTLSGNAF
    151  SSNC DNKANG  DTLIKVLWVN  DSAGDS DISR  TNLEVSGDNI  VYTYQARVGG
    201  RE*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 249 shows 81.3% identity over a 203 aa overlap with a predicted ORF (ORF 249.ng) from *N. gonorrhoeae*:

m249/g249

m249.pep MKQND¹⁰CFLKDS²⁰QS³⁰GMALEI⁴⁰VLVAMLVITIGILALLSVQLRTVXXXXXXXXXXXXXXXXXXXXX
| | | : | : | | | | | | | | | | | | | | | | | | | | | | | : | : | :

574

```

g249      MKNNDCLRLKNPQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAETQTIVSQITQ
           10      20      30      40      50      60
m249.pep  XLMEGMLMNPTIDSDSNKKNYNLYMGNH-TLSAVDGDFAIDAMKTKQLAEALKRFSYEL
           70      80      90      100     110     120
g249      NLMEGMLMNPTIDLDSNKKNYSLYMGKQTLTSAVDGEFMLDAEKSKAQLAEELKRFSHEL
           70      80      90      100     110     120
m249.pep  KNALPDAAAIHYAVCKDSSGNAPTLSGN-AFSSNCDNKANGDTLIKVLWVNDSDAGSDSI
           130     140     150     160     170     179
g249      KNALPDAAAIHYAVCKDSSGDAPTLSDSGAFSSNCDNKANGDTLIKVLWVNDSDAGSDSI
           130     140     150     160     170     180
m249.pep  RTNLEVSGDNIVYTYQARVGGREX
           180     190     200
g249      RTNLEVSGDNIVYTYQARVGGREX
           190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 971>:

```

a249.seq
1   ATGAAGAATA ATGATTGCTT CCGCCTGAAA AACCCCCAGT CCGGTATGGC
51  GCTGATAGAA GTCTTGGTCG CTATGCTCGT TCTGACCATC GGTATTTTGG
101 CACTATTGTC TGTTCACTTG CGGACAGTCG CTTCCGTCAG GGAGGCAGAG
151 ACGCAAACCA TCGTCAGTCA AATCACGCAA AACCTGATGG AAGGAATGTT
201 GATGAATCCG ACCATTGATT CGGACAGCAA CAAGAAAAAC TATAATCTTT
251 ACATGGGAAA CCATCATGCA CTATCAGTTG TGGATGGCGA TTTTCAGGTT
301 GATGCCATAA AAATAAGAC GCAGTTGGCA GAGGCACAAT TGAAGAGATT
351 TAGTTATGAG CTGAAAAATG CCTTGCCGGA TCGGCCAGCC ATCCATTACG
401 CCGTCTGCAA GGATTCGTCG GGTGTTGCGC CGACATTGTC CGCCGGCAGT
451 ACTTTTCTT CAAATTGCGA TGGTAGTGCA AATGGGGATA CTTTGATTAA
501 AGTATTGTGG GTAAATGATT CGGCAGGGGA TTCGGATATC GCCCGTACGA
551 ATCTTGAGAC GAACGGCAAC AATATCGTAT ATACCTATCA GGCAAGGGTC
601 GGAGGTCGGG AATGA

```

This corresponds to the amino acid sequence <SEQ ID 972; ORF 249.a>:

```

a249.pep
1   MKNNDCFRLK NPQSGMALIE VLVAMLVLT I GILALLSVQL RTVASVREAE
51  TQTIVSQITQ NLMEGMLMNP TIDSDSNKKN YNLYMGNHHA LSVVDGDFQV
101 DAIKTKTQLA EAQLKRFSYE LKNALPDAAA IHYAVCKDSS GVAPTLSAGS
151 TFSSNCDGSA NGDTLIKVLW VNDSDAGSDI ARTNLETNGN NIVYTYQARV
201 GGRE*

```

m249/a249 81.9% identity in 204 aa overlap

```

m249.pep  MKNNDCFRLKDSQSGMALIEVLVAMLVLTIGILALLSVQLRTVXXXXXXXXXXXXXXXXXXXX
           10      20      30      40      50      60
a249      MKNNDCFRLKNPQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAETQTIVSQITQ
           10      20      30      40      50      60
m249.pep  XLMEGMLMNPTIDSDSNKKNYNLYMGNH-TLSAVDGDFAIDAMKTKQLAEALKRFSYE
           70      80      90      100     110     119
a249      NLMEGMLMNPTIDSDSNKKNYNLYMGNH-HALSVDGDFQVDAIKTKTQLAEALKRFSYE
           70      80      90      100     110     120
m249.pep  LKNALPDAAAIHYAVCKDSSGNAPTLS-GNAFSSNCDNKANGDTLIKVLWVNDSDAGSDSI
           120     130     140     150     160     170
a249      LKNALPDAAAIHYAVCKDSSGVAPTLSAGSTFSSNCDGSANGDTLIKVLWVNDSDAGSDSI
           130     140     150     160     170     180

```

575

```

          180      190      200
m249.pep  SRTNLEVSGDNIVYTYQARVGGREX
          :|||||:|:|||||
a249      ARTNLETNGNNIVYTYQARVGGREX
          190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 973>:

m249-1.seq

```

1  ATGAAGAATA ATGATTGCTT CCGCTGAAA GATTCCCAGT CCGGTATGGC
51  GCTGATAGAA GTCTTGGTTG CTATGCTCGT TCTGACCATC GGTATTTTGG
101 CACTATTGTC TGTACAGTTG CGGACAGTCG CTTCCGTCAG GGAGGCGGAG
151 ACACAAACCA TCGTCAGCCA AATCACGCAA AACCTGATGG AGGGAATGTT
201 GATGAATCCG ACCATTGATT CCGACAGCAA CAAGAAAAAC TATAATCTTT
251 ACATGGGAAA CCATACACTA TCAGCTGTGG ATGGCGATTT TGCGATTGAT
301 GCCATGAAAA CTAAGGGGCA ATTGGCAGAG GCACAATTGA AGAGATTTAG
351 TTATGAGCTG AAAAATGCCT TGCCGGATGC GGCAGCCATC CATTACGCCG
401 TCTGCAAGGA TTCGTCGGGT AACGCGCCGA CATTGTCCGG CAATGCTTTT
451 TCTTCAAATT GCGACAATAA GGCAAACGGG GATACTTTAA TTAAAGTATT
501 GTGGGTAAAT GATTTCGGCAG GGGATTCCGA TATTTCCCGT ACGAATCTTG
551 AGGTGAGCGG GCACAATATC GTATATACTT ATCAGGCAAG GGTCGGAGGT
601 CGGGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 974; ORF 249-1>:

m249-1.pep

```

1  MKNNDCFRLK DSQSGMALIE VLVAMLVLT I GILALLSVQL RTVASVREAE
51  TQITVSQITQ NLMEGMLMNP TIDSDSNKK N YNLYMGNH TL SAVDGDFAID
101 AMKTKGQLAE AQLKRFSYEL KNALPDAAI HYAVCKDSSG NAPTLSGNAP
151 SSNCDNKANG DTLIKVLWVN DSAGDSDISR TNLEVSGDNI VITYQARVGG
201 RE*

```

m249-1/g249 90.1% identity in 203 aa overlap

```

          10      20      30      40      50      60
m249-1.pep  MKNNDCFRLKDSQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAEQTIVSQITQ
          |||||:|:|||||
g249        MKNNDCLRLKNPQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAEQTIVSQITQ
          10      20      30      40      50      60

          70      80      90      100     110     120
m249-1.pep  NLMEGMLMNP TIDSDSNKK N YNLYMGNH TL SAVDGDFAIDAMKTKGQLAE AQLKRFSYEL
          |||||:|:|||||:|:|||||:|:|||||:|:|||||
g249        NLMEGMLMNP TIDSDSNKK N YNLYMGK Q T L SAVDGEFMLDAEKSQAQLAE EQLKRFSHEL
          70      80      90      100     110     120

          130     140     150     160     170     179
m249-1.pep  KNALPDAAIHYAVCKDSSGNAPTLSGN-AFSSNCDNKANGDTLIKVLWVND SAGDSDIS
          |||||:|:|||||:|:|||||:|:|||||:|:|||||
g249        KNALPDAAIHYAVCKDSSGDAPTLSDSGAFSSNCDNKANGDTLIKVLWVND SAGDSDIS
          130     140     150     160     170     180

          180     190     200
m249-1.pep  RTNLEVSGDNIVYTYQARVGGREX
          |||||:|:|||||
g249        RTNLEVSGDNIVYTYQARVGGREX
          190     200

```

a249/ L36117

gi|643582 (L36117) prepilin leader sequence requires cleavage to be active [Pseudomonas aeruginosa]
 >gi|1161222 (L48934) involved in type 4 fimbrial biogenesis; contains pre-pilin like leader sequence [Pseudomonas aeruginosa]
 >gi|1246299 (L76605) reference L36117, L48934 [Pseudomonas aeruginosa] Length = 185
 Score = 50.4 bits (118), Expect = 9e-06
 Identities = 45/183 (24%), Positives = 84/183 (45%), Gaps = 26/183 (14%)

```

Query: 13  QSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAEQTIVSQITQNLMEGMLMNP T 72
          QSG ++IEVLVA+L+++IG+L ++++Q +T+ ++ + + + NL+E M +P
Sbjct: 12  QSGFSMIEVLVALLISIGVLGMIAMQGKTIQYTADSVERNKAAMLGSLNLES MRASPKA 71

Query: 73  DSDSNKKNYNLYMGNHHSVVDGDFQVDAIKTKTQLAEA---QLKRFSYELKNALPDAA 129

```

Sbjct: 72 D + M G A + T L +A +L ++ ++KN LP A
 LYDVKDQ-----MATQSDFFKAKGSAFPTAPSSCTPLPDIAIKDRLGCVAEQVKNELPGAG 126

Query: 130 AI---HYAVCKDSSGVAPTLSAGSTFSSNCDGSAANGDTL-IKVLWVNDSSAGDSIDIARTNL 185
 + Y +C+ S +CDG G L I++ W + A ++

Sbjct: 127 DLLKSDYYICRSSK-----PGDCDG--KGSMLERLAWRGKQACVNAADSSA 172

Query: 186 ETN 188
 +T+

Sbjct: 173 DTS 175

m249-1/a249 90.7% identity in 204 aa overlap

	10	20	30	40	50	60
m249-1.pep	MKNND	CFRLKDSQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAE	TQTIVSQITQ			
a249	MKNND	CFRLKNPQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAE	TQTIVSQITQ			
	10	20	30	40	50	60
	70	80	90	100	110	119
m249-1.pep	NLM	EGMLMNPTIDSDSNKKNYNLYMGNH-TLSAVDGDFAIDAMKTGQLAE	AQLKRFSYE			
a249	NLM	EGMLMNPTIDSDSNKKNYNLYMGNHHSVVDGDFQVDAIKTKQLAE	AQLKRFSYE			
	70	80	90	100	110	120
	120	130	140	150	160	170
m249-1.pep	LKNALPDAAAIHYAVCKDSSGNAPTLS-GNAFSSNCDNKANGDTLIKVLWVNDSSAGDS	DI				
a249	LKNALPDAAAIHYAVCKDSSGVAPTLSAGSTFSSNCDGSAANGDTLIKVLWVNDSSAGDS	DI				
	130	140	150	160	170	180
	180	190	200			
m249-1.pep	SRTNLEVSGDNIVYTYQARVGGREX					
a249	ARTNLETNGNNIVYTYQARVGGREX					
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 975>:

g250.seq

```

1   atgacgcaca cagcctctcc acgtgatgaa ttcatacgcg gcataaaaga
51  aagttcgccc atgctgattg ggcttttgcc ttgggcattg atactcggtg
101 tgcagggcgg gcaaaaaggt atgggcccggc tggaaatgct gctgatgacg
151 gggatgaact ttgccggcgg ctccgaattt gccacgggtca acctgtgggc
201 ggaacctctg ccgatactgc ttatcgccac cataaccttt atgattaatt
251 cgcgccatat cctgatgggg ggcggcgctt gccacgcaca tgaagaaat
301 accgctgaaa aaagccgcgc ccgcgctgtt ttttatgtgt ga

```

This corresponds to the amino acid sequence <SEQ ID 976; ORF 250.ng>:

g250.pep

```

1   MHTASPRDE FIRIKESSP MLIGLLPWAL ILGMQGGQKG MGRLEMLLMT
51  GMNFAGGSEF ATVNLWAEPL PILLIATITF MINSRHILMG GGACHAHERN
101 TAEKSRARAV FYV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 977>:

m250.seq

```

1   ATGCACACCT TCCCCGCATA ACGAATTTAT ACGCGGCATC AAAGAAAGTT
51  CGCCTATGCT GATTGGGCTG CTGCCTTGGG CATTAAATACT CGGTATGCAG
101 GCGGACAAA AAGGCATGAG CTGGCTGGAA ATGTTGTTGA TGACCAAGTAT
151 GAACTTCGCC GCGGCTCCG AGTTTGCCAC GGTCACCTG TGGGCsGAAC
201 CTCTGCCGAT ACTGCTTATC GCCACCGTAA CCTTTATGAT TAATTCCTCG
251 CATATCCTGA T.GGGGGCGG CGCTTGCCCC GCACCTGAAA GGAaTACCGC
301 TGAAAAAGC CGTGCCCGCA CTGTTTTTTA TGTGTGA

```

This corresponds to the amino acid sequence <SEQ ID 978; ORF 250>:

m250.pep

```

1   MHTPSPHNEF IRGIKESPM LIGLLPWALI LGMQGGQKGM SWLEMLLMTS
51  MNFAGGSEFA TVNLWAEPLP ILLIATVTFM INSRHILMGG GACPAPERNT
101 AEKSRARTVF YV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 250 shows 91.0% identity over a 111 aa overlap with a predicted ORF (ORF 250.ng) from *N. gonorrhoeae*:

m250/g250

	10	20	30	40	50	59
m250 . pep	MHTPSPHNEFIRGIKESSPMLIGLLPWALILGMQGGQKGMWSWLEMLLMTSMNFAGGSEF					
	: :					
g250	MHTASPRDEFIRGIKESSPMLIGLLPWALILGMQGGQKGMGRLEMLLMTGMNFAGGSEF					
	10	20	30	40	50	60
	60	70	80	90	100	110
m250 . pep	ATVNLWAEPLPILLIATVTFMINSRHILMGGGACAPAPERNTAEKSRARTVIFYVX					
	:					
g250	ATVNLWAEPLPILLIATITFMINSRHILMGGGACHAHERNTAEKSRARAVFYV					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 979>:

a250 . seq

1	ATGACACACA	TAAGCTCGCC	CCGTAACGAA	TTTATACGCG	GCATCAAAGA
51	AAGTTCGCCC	ATGCTGATCG	GGCTTTTGCC	TTGGGCATTA	ATACTCGGTA
101	TGCAGGGTGG	ACAAAAAGGC	ATGAGCTGGC	TGGAATGTT	GTTGATGACC
151	GGTATGAACT	TCGCCGGCGG	CTCCGAGTTT	GCCACGGTCA	ACCTGTGGGC
201	GGAACCTCTG	CCGATACTGC	TTATCGCCAC	CGTAACCTTT	ATGATTAATT
251	CTCGGCATAT	CCTGATGGGG	G.CGGCACTT	GCCCCGACC	TGAAAGAAAT
301	ACCGCTGAAA	AAAGCCGTGC	CCGCACTGTT	TTTTATGTGT	GA

This corresponds to the amino acid sequence <SEQ ID 980; ORF 250.a>:

a250 . pep

1	MTHISSPRNE	FIRGIKESSP	MLIGLLPWAL	ILGMQGGQKG	MSWLEMLLMT
51	GMNFAGGSEF	ATVNLWAEPL	PILLIATVTF	MINSRHILMG	XGTCPAPERNTAEKSRARTV
101	FYV*				

m250/a250 94.6% identity in 111 aa overlap

	10	20	30	40	50	
59						
m250 . pep	MHTPSPHNEFIRGIKESSPMLIGLLPWALILGMQGGQKGMWSWLEMLLMTSMNFAGGSEF					
	: :					
a250	MTHISSPRNEFIRGIKESSPMLIGLLPWALILGMQGGQKGMWSWLEMLLMTGMNFAGGSEF					
	10	20	30	40	50	
60						
	60	70	80	90	100	110
m250 . pep	ATVNLWAEPLPILLIATVTFMINSRHILMGGGACAPAPERNTAEKSRARTVIFYVX					
	:					
a250	ATVNLWAEPLPILLIATVTFMINSRHILMGXGTCPAPERNTAEKSRARTVIFYVX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 981>:

g251 . seq

1	atgcctgacc	caatagggat	tcttttcgct	gccgtcgggg	ttgatttttt
51	tgccgttgtt	ttgagggggc	gttttcaacg	aataggcgcg	gttgcatgt
101	tgataataat	aatcctgatg	gcggagggtcg	gaacacaaac	ggtcgtaacc

151	gaggttgacg	ctcaggttgt	ggcggatttt	ggcggtatcg	aaggattttt
201	tgaatgccgc	ctgcaagagc	ctgtggcttt	ccccgtaa	cacgcggtcg
251	gatttgtagt	aggaagacgg	cttgctcgga	ctcgggcggc	aatatttgtc
301	cgaaccgtcg	gcggaacagt	gcgtctgctg	aaaatgattg	tccaaaccga
351	tgccctgcg	gtcgtaagag	aggcggcat	aatccgcccc	agtgtcttta
401	tcggcatctg	tatagacata	tccaaaccg	tagcgctctt	tgggtgtgcgt
451	ctcgtcgtaa	aacacgcccc	taccgtatcc	cgcgcccacc	tccgcacgct
501	tttcaccgtt	ggtaatcagc	ccgctgtatt	tgcggccgcc	cgcgtatttg
551	ccgtagcctc	ttatcgatcc	gtatttttta	tttcatcaa	aaaccgcctt
601	ggtcaggaat	gccggaaccg	tcatatcgcg	cgtgtcgaaa	gtttgtgctg
651	tgcgttcgag	tatgcgcgcg	atgtagtgcg	gtttgttttc	aaaacgaaaa
701	ccggggcgga	acagccacga	ccggttttcg	tatga	

This corresponds to the amino acid sequence <SEQ ID 982; ORF 251.ng>:

g251.pwp

1	<u>MPDP</u> <u>IGILFA</u>	<u>AVGVDFFAV</u>	<u>LRGRFORIGA</u>	<u>VGMLIIIIILM</u>	<u>AEVGTKTVVT</u>
51	<u>EVDAQGVADF</u>	<u>GGIEGFECR</u>	<u>LQEPVAFPN</u>	<u>HAVGFVVGR</u>	<u>LVGTRAAIFV</u>
101	<u>RTVGQTVTRL</u>	<u>KMIVQTDALP</u>	<u>VNREAGIIRP</u>	<u>SVFIGIGIDI</u>	<u>FQTVAAFGVR</u>
151	<u>LVVKHARTVF</u>	<u>RAHLRTVFTV</u>	<u>GNQPAVFAAA</u>	<u>RVFAVASYSR</u>	<u>VFFVFIKNRL</u>
201	<u>GQECRNRHIA</u>	<u>RVESLLRAFE</u>	<u>YAADVVPFVF</u>	<u>KTKTRAQQR</u>	<u>PAFV*</u>

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 983>:

m251.seq

1	ATGCGTGTCTG	CGGTAGTCGT	AGCGCAAGCC	CGCGCCGACA	TCCGCCACC
51	TGCCCAAACG	GACATTGTCC	CGAACTGCCG	CGTAATAGCT	TTTACCGTTG
101	ATGCTGCGCG	GCGTGCAATC	CGTATAAGTA	TTGTTGCCCA	AGCGGCAGAT
151	TTGCCCCGTA	ACGCAATTC	CCCTGCCTAT	GGTGACCCAA	TAGGGGCTGG
201	TTTCACTGTC	GTTGGGGCTG	ATTTTTTTTC	CGTTGTTTTG	AGGGGGCGTG
251	TTTCAGCAAT	AGGCGCGGTT	GGCATTTTGA	TAATAATAAT	CCTGATGCGC
301	GAGATTAGAG	CCAAAGCGGT	CAAACCCGAG	ATTCACGCTC	AGGTGTGTGC
351	GGATTTTGGC	GGTATCGAAG	GATTTTGTGA	ATGCCGCTCG	CAAGAGCCTG
401	TGGCTTTCCC	CGTAAATCAC	GCGATCGGAT	TTGTAATAGG	AAAACGGCTT
451	GTCGGCACTC	GGGCGGCAAT	ATTTGTCCGA	ACCGTCGGCA	GAACAGTGCG
501	TCTGGCTAAA	ATGATTATCC	AAACCGATCG	CCTGCCGGTG	GTAAAGAGAGG
551	CGGGCATAAT	CCGCCCAAGT	GTCTTTATCG	GCATTGGTAT	AGACATATTC
601	CAAACCGTAG	CGGCTTTTGG	TGTGCGTCTC	TCGTGTA AAC	ACGCCGTAC
651	CGTATTCGCG	GCCCACCAGC	GCACCGTTTT	CGCCGTTGGT	AAACAGTCCG
701	CCGTATTGT	GGTTGCCCGC	GTATTTGCCG	TTACCGGGCA	AAGAACCCGC
751	CTGTTTTTTA	TTTGATCAAA	AAACCGCCTT	GGTCAGGAAT	GCCGGAACCG
801	TCATATCGCG	CGTGTGCAAA	GTTTGTTCG	TGTGTTTCGAG	TATGCCGCCG
851	ATGTAGTGCC	GCTTATTCTC	AAAACGAAA	CCCGGGCGGA	ACAGCCACGA
901	CCGGCTTTTCG	TATGA			

This corresponds to the amino acid sequence <SEQ ID 984; ORF 251>:

m251.ppt

```

1  MRAAVVVAQA RADIRPPAQT DIVPNCRVIA FTVDAARRAV RISIVAQAAD
51  LPRNDISPAY GDPIGAGFTA VGADFFAVVL RGRVRRIGAV GMLIIILMA
101 EIRAKAVKPE IHAQVVADFG GIEGFFECRL QEPVAFPVNH AIGFVIGKRL
151 VGTRAAIFVR TVGRTVRLLK MIIQTDALPV VREAGIIRPS VFIGIGIDIF
201 QTVAAFGVRL VVKHARTVFR AHQRTVFVAVG KQSAVFVVAR VFAVTGQRTTR
251 LFFCIKIKNRL GQECRNRIHA RVESLLRVFE YAADVPLIL KTKTRAEQPR
301 PAFV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 251 shows 85.2% identity over a 243 aa overlap with a predicted ORF (ORF 251.ng) from *N. gonorrhoeae*:

m251/g251

```

      40          50          60          70          80          90
m251.pep  TVDAARRAVRISIVAQAADLPRNDISPAYGDPIGAGFTAVGADFFAVVLRGRVRRIGAVG
           |||||  |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
g251      MPDPIGILFAAVGVDFFAVVLRGRFQRIGAVG
           10          20          30

```

579

	100	110	120	130	140	150
m251.pep	MLIIILMAEIRAKAVKPEIHAQVVADFGGIEGFFECRLQEPVAFPNHAI GFVIGKRLV					
g251	MLIIILMAEVGKT VVTEVDAQVVADFGGIEGFFECRLQEPVAFPNH AVGFVVGRRLV					
	40	50	60	70	80	90
	160	170	180	190	200	210
m251.pep	GTRAAIFVRTVGR TVRLLKMI IQTDALPVVREAGIIRPSVFIGIGIDIFQTVA AFGVRLV					
g251	GTRAAIFVRTVGGTVRLLKMIVQTDALPVVREAGIIRPSVFIGIGIDIFQTVA AFGVRLV					
	100	110	120	130	140	150
	220	230	240	250	260	270
m251.pep	VKHARTVFRAHQRTVFAVGKQSAVFVVARVFAVTGQTRLFFCIKNRLGQECRNRHIAR					
g251	VKHARTVFRAHLRTVFTVGNQPAVFAAARVFAVASYRS-VFFIFIKNRLGQECRNRHIAR					
	160	170	180	190	200	210
	280	290	300			
m251.pep	VESLLRVFEYAADVPLILKTKTRAEQPRPAFVX					
g251	VESLLRAFEYAADVVPFVKTKTRAEQPRPAFVX					
	220	230	240			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 985>:

```

a251.seq
1   ATGCGTGCTG CGGTAGTCGT AGCGCAACCC CGCGCCGACA TCCGCCACAC
51  TGCCCAAACG GACATTGTCC CGAACTGCCG CGTAATAGCT TTTGCCGTTG
101 ATGCTGCGCG GCGTGCAGTC CGTATAAGTA TTGTTGCCCA AGCGGCAGAT
151 TTGCCCCGTA ACCACATTTC CCCTGCCTAT GCTGACCCAA TAGGGTTGGT
201 CCTTGCCGCC GTTGGGGTTG GCGGTTTTAG GGGGCGTTTT CGACGAATAG
251 GCGCGGTTGG CATGTTGATA ATAATAATCC TGATGGCGGA GATTAGAGTC
301 AAAGCGGTCA AAACCGAGAT TCACGCTCAG GTTGTGGCGG ATTTTGGCGG
351 TATCGAAGGA TTTTGTGAAT GCCGCTGCA AGAGCCTGTG GCTTTCCTCG
401 TAAATCACGC GGTCCGATTT GTAGTAGGAA AACGGCTTGT CGGCACTCGG
451 GCGGCAATAT TTGTCCGAAC CGTCGGCAGA ACAGTGCCTC TGCTGAAAT
501 GATTGTCCAA ACCGATGCCC TGCCGGTCGT AAGAGAGGCG GGCATAATCC
551 ACCCAAGTGT CTTTATCGGC ATTGGTATAG ACATATTCCA AACCCTAGCG
601 GCTTTTGGTG TGCGTCTCGT CGTAAACAC GCCCGTACCG TATTCCGCGC
651 CCACCAGCGC ACCGTTTTCG CCGTTGGTAA ACAGACCGCC GTATTTGTGG
701 TCGCCCGCGT ATTTGCCGTT GCCTCTTATC GGTCCGTATT TTCTATTTTC
751 ATCAAAAACC GCCTTGGTCA GGAATGCCGG AACCCTCATA TCGCGCGTGT
801 CGAAAGTTTG TTGCGTGTGT TCGAGTATGC CGCCGATGTA GTGCCGTTTG
851 TTTTCAAAC GAAAACCCGG GCGGAACAGC CACGATCGGC TTTCGTATGA

```

This corresponds to the amino acid sequence <SEQ ID 986; ORF 251.a>:

```

a251.pep
1   MRAAVVVAQP RADIRPPAQT DIVPNCRVIA FAVDAARRAV RISIVAQAAD
51  LPRNHISPAY ADPIGLVLAA VGVGGFRGRF RRIGAVGMLI IILMAEIRV
101 KAVKTEIHAQ VVADFGGIEG FFECRLQEPV AFFPNHAVGF VVGKRLVGR
151 AAIFVRTVGR TVRLLKMIVQ TDALPVVREA GIIHPSVFIG IGIDIFQTV
201 AFGVRLVVKH ARTVFRAHQRT VFAVGKQTA VFVVARVFAV ASYRSVFSIF
251 IKNRLGQECR NRHIARVESL LRVFEYAADV VPFVFKTKTR AEQPRSAFV*

```

m251/a251 88.5% identity in 304 aa overlap

	10	20	30	40	50	60
m251.pep	MRAAVVVAQARADIRPPAQT DIVPNCRVIAFTVDAARRAVRISIVAQAADLPRNDISPAY					
a251	MRAAVVVAQPRADIRPPAQT DIVPNCRVIAFAVDAARRAVRISIVAQAADLPRNHISPAY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m251.pep	GDPIGAGFTAVGADFFAVVLRGRVRRIGAVGMLIIILMAEIRAKAVKPEIHAQVVADFG					
	: : : :					

580

```

a251      ADPIGLVLAAGVGGF----RGRFRRIGAVGMLIIIIILMAEIRVKAVKTEIHAQVVADFG
              70          80          90          100          110

              130          140          150          160          170          180
m251.pep  GIEGFFECRLQEPVAFPVNHAIGFVIGKRLVGTAAIFVRTVGRTVRLLKMIQTALPV
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a251      GIEGFFECRLQEPVAFPVNHAVGVVGKRLVGTAAIFVRTVGRTVRLLKMIQTALPV
              120          130          140          150          160          170

              190          200          210          220          230          240
m251.pep  VREAGIIRPSVFIGIGIDIFQTVAAFGVRLVVKHARTVFAHQRTVFAVGKQSAVFVVAR
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a251      VREAGIIRPSVFIGIGIDIFQTVAAFGVRLVVKHARTVFAHQRTVFAVGKQSAVFVVAR
              180          190          200          210          220          230

              250          260          270          280          290          300
m251.pep  VFAVTGQRTLFFICIKNRLGQECNRNRIARVESLLRVFEYAADVPLIKTKTRAEQPR
              |||::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
a251      VFAVASYRS-VFSIFIKNRLGQECNRNRIARVESLLRVFEYAADVPFVKTKTRAEQPR
              240          250          260          270          280          290

m251.pep  PAFVX
              |||
a251      SAFVX
              300

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 987>:

```

g253.seq
1  atgatcgaca gggaccgtat gttgcgggac acgttggaac gtgtgctgac
51  ggggtcgttc tggttatggg tgggtggtggc atcgatgatg tttaccgccg
101 gattttcagg cacttatctt ctgatggaca atcaggggct gaatttcctt
151 ttagttttgg cgggagtgtt gggcatgaat acgctgatgc tggcagtatg
201 gttggcaacg ttgttcctgc gcgtgaaagt gggacgggtt ttcagcagtc
251 cggcgacgtg gtttcggggc aaaggccctg taaatcaggc ggtgttgctg
301 ctgtatgcgg accagtggcg gcaaccttcg gtacgatgga aaataggcgc
351 aacggcgcac agcttgtggc tctgcacgct gctcggaatg ctggtgtcgg
401 tattgctgct gcttttgggt cggcaatata cgttcaactg ggaaagcacg
451 ctgttgagca atgcccgttc ggtacgcgcg gtggaaatgt tggcatggct
501 gccgtcgaaa ctcggtttcc ctgtccccga tgcgcgggcg gtcacgaaag
551 gtcgtctgaa cggcaatatt gccgatgcgc gggcttggtc ggggctgctg
601 gtcggcagta tcgtctgcta cggcatcctg ccgcgcctct tggcttggtt
651 agtgtgtaaa atccttttga aaacaagcga aaacggattg gatttggaag
701 aaacctatta tcaggcggtc atccgccgct ggcagaacaa aatcacgat
751 gcggatacgc gtcgggaaac cgtgtccgcc gtttcgccga aaatcgtctt
801 gaacgatgcg ccgaaatggg cgtcatgctt ggagaccgag tggcaggacg
851 gccaatggtt cgagggcagg ctggcgagcg aatggctgga taagggcggt
901 gccgccaatc ggggaacagg tgccgcgctg gagacagagc tgaagcagaa
951 accggcgcaa ctgcttatcg gcgtacgcgc ccaaactgtg ccggaccggg
1001 gcgtgctgcg gcagattgtg cggctttcgg aagcggcgca gggcggcgcg
1051 gtggtgcagc ttttggcgga acaggggctt tcagacgacc tttcggaaaa
1101 gctggaacat tggcgtaacg cgctgaccga atgcggcgcg gcgtggcttg
1151 agcctgacag ggtggcgagc gaaggccgtt tgaaagacca ataa

```

This corresponds to the amino acid sequence <SEQ ID 988; ORF 253.ng>:

```

g253.pep
1  MIDRDRMLRD TLERVRAGSF WLWVVVASMM FTAGFSGYL LMDNQGLNFF
51  LVLAVGLGMN TLMIAVLAT LFLRVKGRF FSSPATWFRG KGPVNQAVLR
101 LYADQWRQPS VRWKIGATAH SLWLCTLLGM LVSLLLLLV RQYTFNWEST
151 LLSNAASVRA VEMLAWLPK LGFPVPDARA VIEGRNLGNI ADARAWSGLL
201 VGSIVCYGIL PRLLAWVCK ILLKTSENGL DLEKTYQAV IRRWQNKITD
251 ADTRRETUSA VSPKIVLNDK PKWALMLETE WQDGQWFEGR LAQEWLDKGV

```


m253.seq
1 ATGATTGACA GGAACCGTAT GCTGCGGGAG ACGTTGGAAC GTGTGCGTGC

51	GGGGTCGTTT	TGTTGTGGG	TGGTGGCGGC	GACGTTTGCA	TTTTTTACCG
101	GTTTTTCAGT	CACTTATCTT	CTAATGGACA	ATCAGGGTCT	GAATTTCTTT
151	TTGGTTTGG	CGGGCGTGT	GGGCATGAAT	ACGCTGATGC	TGGCAGTATG
201	GTTGGCAATG	TTGTTCCCTG	GTGTGAAAGT	GGGGCGTTTT	TTCAGCAGTC
251	CGGCGACGTG	GTTTCGGGGC	AAAGACCCCT	TAAATCAGGC	GGTGTTCGCG
301	CTGTATGCGG	ACGAGTGGCG	GCAACCTTCG	GTACGTTGGA	AAATAGGCGC
351	AACGTCGCAC	AGCCTGTGGC	TCTGCACGCT	GCTCGGAATG	CTGGTGTGCG
401	TATTGTTGCT	GCTTTTGGTG	CGGCAATATA	CGTTCAACTG	GGAAAGCACG
451	CTGTTGAGCA	ATGCCGCTTC	GGTACGCGCG	GTGGAAATGT	TGGCATGGCT
501	GCCGTCGAAA	CTCGGTTTCC	CTGTCCCCGA	TGCGCGGGCG	GTCATCGAAG
551	GCCGTCGAAA	CGGCAATATT	GCCGATCGCG	GGGCTTGGTC	GGGGCTGCTG
601	GTCGCGAGTA	TCGCCTGCTA	CGGCATCCTG	CCGCGCCTGC	TGGCTTGGGT
651	AGTGTGTAAA	ATCCTTTTGA	AAACAAGCGA	AAACGGATTG	GATTTGGAAA
701	AGCCCTATTA	TCAGGCGGTC	ATCCGCCGCT	GGCAGAACAA	AATCACCGAT
751	GCGGATACGC	GTCGGGAAAC	CGTGTCCGCG	GTTTCACCGA	AAATCATATT
801	GAACGATGCG	CCGAAATGGG	CGGTCAATCT	GGAGACCGAG	TAGGACGACG
851	GCGAATGGTT	CCGAGGCGAG	TGGCGCGAGG	ATAAGCTGGA	TGAAGGCGTT
901	GCCACCAATC	GGGAACAGGT	TGCCGCGCTG	GAGACAGAGC	TGAAGCAGAA
951	ACCGGCGCAA	CTGCTTATCG	GCGTGC CGCG	CCAAACTGTG	CCGGACCGCG
1001	GCGTGTGCG	GCAGATTGTC	CGACTCTCGG	AAGCGGCGCA	GGGCGGCGCG
1051	GTGGTGCAGC	TTTTGGCGGA	ACAGGGGCTT	TCAGCAGCAC	TTTCGGAAAA
1101	GCTGGAACAT	TGGCGTAAAG	CGCTGGCCGA	ATGCGGCGCG	CGGTGGCTTG
1151	AGCCTGACAG	GGCGGCGCAG	GAAGGGCGTT	TGAAAGACCA	ATAA

```
m253.pep
  1  MIDNRNRLRE  TLERVRAGSF  WLWVVAATFA  FFTGFSVTYL  LMDNQGLNFF
51  LVLAGVLGMN  TLMLAVWLAM  LFLRVKVGRF  FSSPATWFRG  KDPVNQAVLR
101 LYADEWRQPS  VRWKIGATSH  SLWLCTLLGM  LVSVLLLLLV  RQYTFNWEST
151 LLSNAASVRA  VEMLAWLPSP  LGFPVPDARA  VIEGRLNGNI  ADARAWSGLL
201 VGSIACYGIL  PRLLAWVVCK  ILLKTSENGLE  DLEKPPYQAV  IRRWQNKITD
251 ADTRRETVSA  VSPKILNDA  PKWAVMLETE  WQDGWEFGR  LAQEWLKDGV
301 ATNREQVAAL  ETELKQKPAQ  LLIQVRAQTV  PDRGVLQIV  RLSEAAQGGA
351 VVQLLAEQGL  SDDLSEKLEH  WRNALAECGA  AWLEPDRAAQ  EGRLKQD*
```

Homology with a predicted ORF from *N. gonorrhoeae*

	10	20	30	40	50	60
m253.pep	MIDRNRMLRETLEVRVAGSFVLWVVAAATFAFFTGFVSVTYLLMDNQGLNFFLVLVLAGVLGMN					
	: :					
g253	MIDRDRMLRDTLERVRAGSFVLWVVVASMMFTAGFSGTYYLLMDNQGLNFFLVLVLAGVLGMN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m253.pep	TLMLAVWLAMLFLRVKVGRRFSSPATWFRGKDPVNQAVLRRLYADEWRQPSVRWKIGATSH					
g253	TLMLAVWLATLFLRVKVGRRFSSPATWFRGKGPNQAVLRRLYADQWRQPSVRWKIGATAH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m253.pep	SLWLCTLLGMLVSVLLLLLVQRQYTFNWESTLLSNAASVRAVEMLAWLP SKLGFPVPDARA					
g253	SLWLCTLLGMLVSVLLLLLVQRQYTFNWESTLLSNAASVRAVEMLAWLP SKLGFPVPDARA					
	130	140	150	160	170	180

	190	200	210	220	230	240
m253.pep	VIEGRLNGNIADARAWSGLLVGSIACYGILPRLLAWVVKILLKTSENGLDLEKPPYQAV					
	:					
g253	VIEGRLNGNIADARAWSGLLVGSIVCYGILPRLLAWVVKILLKTSENGLDLEKTYQAV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m253.pep	IRRWQNKITDADTRRETVSASP K I I LNDAPKWAVMLETEWQDGEWFEGRLAQEWLDKGV					
	:					
g253	IRRWQNKITDADTRRETVSASP K I V LNDAPKWALMLETEWQDQWFEGR LAQEWLDKGV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m253.pep	ATNREQVAALETELKQKPAQLLIGVRAQTV PDRGVLRQIVRLSEAAQGGAVVQLLAEQGL					
	:					
g253	AANREQVAALETELKQKPAQLLIGVRAQTV PDRGVLRQIVRLSEAAQGGAVVQLLAEQGL					
	310	320	330	340	350	360
	370	380	390			
m253.pep	SDDLSEKLEHWRNALAECGAAWLEPDRAAQEGRLKDQX					
	:					
g253	SDDLSEKLEHWRNALTECGAAWLEPDRAVAQEGRLKDQX					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 991>:

```

a253.seq
1  ATGATCGACA GGAACCGTAT GCTGCGGGAG ACGTTGGAAC GTGTGCGTGC
51  GGGGTCGTTT TGGTTGTGGG TGGCGGCGGC GACGTTTGCG TTTTATACCG
101 GTTTTTCAGT TACTTATCTT CTAATGGACA ATCAGGGTCT GAATTTCTTT
151 TTGGTTTGG CGGGCGTGTG GGGCATGAAT ACGCTGATGC TGGCAGTATG
201 GTTGGCAATG TTGTTCTCTG GCGTGAAGT GGGGCGTTT TTCAGCAGTC
251 CGGCGACGTG GTTTCGGGGC AAAGACCTG TCAATCAGGC GGTGTTGCGG
301 CTGTATGCGG ACGAGTGGCG GCAACCTTCG GTACGTTGGA AAATAGGCGC
351 AACGTGCGAC AGCCTGTGGC TCTGCACGCT GCTCGGAATG CTGGTGTCCG
401 TATTGTTGCT GCTTTTGGTG CGGCAATATA CGTCAACTG GGAAAGCAGC
451 CTGTTGGGCG ATTCGTCTTC GGTACGGCTG GTGGAAATGT TGGCATGGCT
501 GCCTGCGAAA CTGGGTTTTT CCGTGCCTGA TCGCGGGCG GTCATCGAAG
551 GTCGTCTGAA CGGCAATATT GCCGATGCGC GGGCTTGCTC GGGGCTGCTG
601 GTCGGCAGTA TCGCCTGCTA CGGCATCCTG CCGCGCCTCT TGGCTTGGGC
651 GGTATGCAAA ATCCTTTTGA AAACAAGCGA AAACGGCTTG GATTGGAAGA
701 AGCCCTATTA TCAGGCGGTC ATCCGCCGCT GGCAGAACAA AATCACCAGT
751 GCGGATACGC GTCGGGAAAC CGTGTCGCC GTTTCGCCGA AAATCGTCTT
801 GAACGATGCG CCGAAATGGG CGGTCATGCT GGAGACCGAA TGGCAGGACG
851 GCGAATGGTT CGAGGGCAGG CTGGCGCAGG AATGGCTGGA TAAGGGCGTT
901 GCCGCCAATC GGAACAGGT TGCCGCGCTG GAGACAGAGC TGAAGCAGAA
951 ACCGGCGCAA CTGCTTATCG GCGTGC GCGC CCAACTGTG CCCGACCGCG
1001 GCGTGTTCG GCAGATCGTC CGACTTTCG AAGCGGCGCA GGGCGGCGCG
1051 GTGGTGCAGC TTTTGGCGGA ACAGGGGCTT TCAGACGACC TTTCGGAAGA
1101 GCTGGAACAT TGGCGTAACG CGCTGACCGA ATGCGGCGCG CGGTGGCTGG
1151 AACCCGACAG AGCGGCGCAG GAAGGCCGTC TGAAAACCAA CGACCGCACT
1201 TGA

```

This corresponds to the amino acid sequence <SEQ ID 992; ORF 253.a>:

```

a253.pep
1  MIDRNRMLRE TLERVRAGSF WLWVAATFA FFTGFSVTYL LMDNQGLNFF
51  LVLAVGLGMN TLMLAVWLAM LFLRVKVGRF FSSPATWFRG KDPVNQAVLR
101 LYADEWRQPS VRWKIGATSH SLWLCTLLGM LSVLLLLLLV RQYTFNWEST
151 LLGDSSSVRL VEMLAWLPAK LGFPVPDARA VIEGRLNGNI ADARAWSGLL
201 VGSIACTYGL PRLLAWAVCK ILLKTSENGL DLEKPPYQAV IRRWQNKITD
251 ADTRRETUSA VSPKIVLNDK PKWAVMLETE WQDGEWFEGR LAQEWLDKGV
301 AANREQVAAL ETELKQKPAQ LLIGVRAQTV PDRGVLRQIV RLSEAAQGGG
351 VVQLLAEQGL SDDLSEKLEH WRNALTECGA AWLEPDRAAQ EGRLKTNDR
401 *

```

m253/a253 97.2% identity in 395 aa overlap

	10	20	30	40	50	60
m253.pep	MIDRNRMLRETLERVAGSFWLWVVAATFAFFTGFVSVTYLLMDNQGLNFFLVLAGVLMGN					
a253	MIDRNRMLRETLERVAGSFWLWVVAATFAFFTGFVSVTYLLMDNQGLNFFLVLAGVLMGN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m253.pep	TLMLAVWLAMLFRLVKVGRFFSSPATWFRGKDPVNQAVLRRLYADEWRQPSVRWKIGATSH					
a253	TLMLAVWLAMLFRLVKVGRFFSSPATWFRGKDPVNQAVLRRLYADEWRQPSVRWKIGATSH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m253.pep	SLWLCTLLGMLVSVLLLLLVQRQYTFNWESTLLSNAASVRVEMLAWLPSKLGFPVPDARA					
a253	SLWLCTLLGMLVSVLLLLLVQRQYTFNWESTLLGSSSVRLVEMLAWLPAKLGFPVPDARA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m253.pep	VIEGRNLNGNIADARAWSGLLVGSIACYGILPRLAWVVKILLKTSENGLDLEKPYQAV					
a253	VIEGRNLNGNIADARAWSGLLVGSIACYGILPRLAWAVCKILLKTSENGLDLEKPYQAV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m253.pep	IRRWQNKITDADTRRETSAVSPKIILNDAPKWAVMLETEWQDGEWFEGRLAQEWLDKGV					
a253	IRRWQNKITDADTRRETSAVSPKIVLNDAPKWAVMLETEWQDGEWFEGRLAQEWLDKGV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m253.pep	ATNREQVAALETELKQKPAQLLIGVRAQTPDRGVLRQIVRLSEAAQGGAUVQLLAEQGL					
a253	AANREQVAALETELKQKPAQLLIGVRAQTPDRGVLRQIVRLSEAAQGGAUVQLLAEQGL					
	310	320	330	340	350	360
	370	380	390			
m253.pep	SDDLSEKLEHWRNALAECGAAWLEPDRAAQEGRLKDQX					
a253	SDDLSEKLEHWRNALTECGAAWLEPDRAAQEGRLKTNDRTX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 993>:

g254.seq

```

1  atgtatgcag gcgaacgctt caatacttac agccatttga gcggtttgat
51  tctggcggcg gcaggtttga tgctgatgct gctgaaaacc ataggacacg
101 gggacggata ccgtatcttc agcgtatcgg tttacggcat cagccttctt
151 ctgctctatt tgagttcctc gctgtaccac ggaattgcag ccggaaaact
201 gaaaagcatt ttgaaaaaaa ccgaccactg catgatttat gtgctgattg
251 ccggaagcta cacaccgttt gcactgggtt ctttgagaaa cgggcccgggc
301 tggacgggat tttcactgtc ctggctgctg gcggctgcag gaatcgcaca
351 agaactcacc atcggacgga aaagcgaaaa acgtctgctg tctattgcga
401 tttatatcgt aatgggctgg atggtcttgg cggtaatgaa atccctgaca
451 gcctcactcc cgccggcagg actggcttgg ctggcggcag gcggtatgct
501 gtacagcgtc ggcatttact ggtttgtaaa cgatgaaaaa atccgacacg
551 ggcacggaat ctggcatctg ttcgtattgg gcggcagcat aacccaattt
601 gtcagcgtgt acggttatgt aatctga

```

This corresponds to the amino acid sequence <SEQ ID 994; ORF 254.ng>:

g254.pep

```

1  MYAGERFNTY SHLSGLILAA AGLMLMLLKT IGHGDGYRIF SVSVYGISLL

```

51 LLYLSSSLYH GIAAGKLKSI LKKTDHCMYI VLIAGSYTPF ALVSLRNGPG
 101 WTVFSLSWLL AAAGIAQELT IGRKSEKRLI SIAIYIVMGW MVLAVMKSLT
 151 ASLPPAGLAW LAAGGMLYSV GIYWFVNDEK IRHGHGIWHL FVLGGSITQF
 201 VSVYGYVI*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 995>:

m254.seq (partial)
 1 ..GTATCGGTTT ACGGCATCAG CCTTCTTCTG CTCTATTTGA GTTCCTGGCT
 51 GTACCACGGA ATTGCAGCCG GAAAACCTGAA AAGCATTTTG AAAAAACCG
 101 ACCACTGCAT GATTATATGTG CTGATTGCCG GAAGCTACAC ACCGTTTGCA
 151 CTGGTTTCTT TGAGAAACGG GCCGGGCTGG ACGGTATTTT CACTGTCCTG
 201 GCTGCTGGCG GCTGCAGGAA TCGCACAAGA ACTCACCATC GGACGGAAAA
 251 GCGAAAAACG TCTGCTGTCT ATTGTGATT ATGTCGTCAT GGGTTGGATG
 301 GTCTTGGCGG TAATGAAATC CCTGACAGCC TCACTCCCGT CGGCAGGACT
 351 GGCTTGGCTG GCGGCAGGCG GTATGCTGTA CAGTGTGGCG ATTTACTGGT
 401 TTGTAAACGA TGAAAAATC CGACACGGGC ACGGAATCTG GCATCTGTTC
 451 GTATTGGGCG GCAGCATCAC CCAATTGTG AGCGTGTACG GTTACGTAAT
 501 CTGA

This corresponds to the amino acid sequence <SEQ ID 996; ORF 254>:

m254.pep (partial)
 1 ..VSVYGISLLL LYLSSWLYHG IAAGKLKSI KKTDHCMYI VLIAGSYTPFA
 51 LVSLRNGPGW TVFSLSWLLA AAGIAQELTI GRKSEKRLLS IYIYVVMGWM
 101 VLAVMKSLTA SLPSAGLAWL AAGGMLYSVG IYWFVNDEKI RHGHGIWHLF
 151 VLGGSITQFV SVYGYVI*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 254 shows 97.6% identity over a 167 aa overlap with a predicted ORF (ORF 254.ng) from *N. gonorrhoeae*:

m254/g254

m254.pep				10	20	30
				VSVYGISLLL	LYLSSWLYHG	IAAGKLKSI
g254	HLSGLILAAAGLMLMLLKTIGHGDYRIFSVSVYGISLLL	LYLSSSLYHG	IAAGKLKSI			
	20	30	40	50	60	70
m254.pep		40	50	60	70	80
		KKTDHCMYI	VLIAGSYTPF	ALVSLRNGPGW	TVFSLSWLLA	AAGIAQELTI
g254		KKTDHCMYI	VLIAGSYTPF	ALVSLRNGPGW	TVFSLSWLLA	AAGIAQELTI
	80	90	100	110	120	130
m254.pep		100	110	120	130	140
		IVIYVVMGWM	MVLAVMKSLT	ASLPSAGLAW	LAAGGMLYSV	GIYWFVNDEK
g254		IAIYIVMGWM	MVLAVMKSLT	ASLPPAGLAW	LAAGGMLYSV	GIYWFVNDEK
	140	150	160	170	180	190
m254.pep		160				
		VLGGSITQFV	SVYGYVIX			
g254		VLGGSITQFV	SVYGYVIX			
	200					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 997>:

a254.seq
 1 ATGTATACAG GCGAACGCTT CAATACTTAC AGCCATTTGA GCGGTTTGAT
 51 TCTGGCGGCG GCAGGTTTGG CGCTGATGCT GCTGAAAACC ATAGGACACG
 101 GGGACGGCTA CCGTATCTTC AGCGTATCGG TTTACGGCAT CAGCCTTCTT
 151 CTGCTCTATT TGAGTTCCTC GCTGTACCAC GGAATTGCAT CCGGAAAACCT
 201 GAAAAGCATT TTGAAAAAAA CCGACCACTG CATGATTTAT GTGCTGATTG
 251 CCGGAAGCTA CACACCGTTT GCACTGGTTT CTTTGAGAAA CGGGCCGGGC

1	MYTGERFNTY	SHLSGLILAA	AGLALMLLKT	IGHGDGYRIF	SVSVYGISLL
51	LLYLSSSLYH	GIAAGKLKSI	LKKTDHCMYI	VLIAGSYTPF	ALVSLRNGPG
101	WTVFSLSWLL	AAAGIAQELT	IGRKSEKRL	SLAIYIVMGW	MVLAVMKSLT
151	ASLPPAGLAW	LAAGGMLYSV	GIYWFVNDEK	IRHGHWIHL	FVLGGSITQF
201	VSVYGYVI*				

[illegible]

BNSDOCID: <WO_9957280A2_1>

1	atggttggtgac	aggaagcctt	gcggggtcag	ttcgtgcgcg	gttgcgtgc
51	cgcgttgctg	tacgctgtca	aaacctgcgc	cgatttccac	gcctttgacg
101	gcgttgatgc	ccatcatcgc	gtaggcgatt	tcggcatcga	ggcggtcgaa
151	aacgggttcg	cccaaaccga	cggggacggt	ggcgcgttcg	atatgcagtt
201	tcgcgcgcga	ggaatccaag	gatttgcgca	caccgtccat	atagtgttcc
251	agttcgcgca	tttgcttttg	gttggcggca	aaaaaggat	tttgggaaat
301	gtgttcgctg	ccttcaaacc	ggattttttt	ttcgcgcact	ttggtaacgt
351	aggcgtgat	ttcgtgcgcg	aattttttct	tcagccattt	tttggaacg
401	gtccgcgcgg	caacgcgggc	tcgcggttcg	cgggcggaac	tcctgccgcc
451	gccccggtag	tcgcgcgtac	cgtattttgt	ccaataggta	tagtcggcgt
501	gtccggggcg	gaaggcgggt	gcgatgtcgc	cgtagtcttc	gctgcgcgtg
551	tcggttgtgc	ggattcgt			

g255 . pep

```

1  MVGQEALRQ FVAVFAAALR YAVKTCADFH AFDGVDahr VGDFGIEAVE
51 NGFAQTGDGV GGFDmFRAD GIQGFaHTVH IVFQFGDLAL VGGKKRILGN
101 VFAAFKpDFF FADLGNvGGD FRAEFFQPF FGNGSGGNAG CGFAGGTPAA
151 APVVARTVfV PIGIVGvSGA EGGGDvAVfV AALVGvAD*

```

m255.seq

1	GTGGTTGGAC	AGGAAGCCTT	GCGGGGTCAG	TTCGTCGCCG	TGTTGCTGCG
51	CGCGTTGCGT	TACGCTGTCA	AAACCTGCGC	CGATTTCAC	GCCTTTGACG
101	GCGTTGATGC	CCATCATCGC	GTAGGCATT	TCGGCATCGA	GGCGGTCAAA
151	AACAGGTTTC	CCCAAGCCGA	CAGGGACATT	GGCTGCTTCG	ATATGCAGCT
201	TCGCGCCGAC	GGAAATCCAAG	GATTTGCGCA	CGCTGTCCAT	ATAGTTTTC
251	AGCTCGGCAA	TTTGCGCTATG	GTTGCGGCGA	AAAAAAGGAT	TTTGGGAAAT
301	GTGTTGCGAG	CCTTCAAACC	GGATTTCTTT	TTGCGCGACT	TTGGTAACGT
351	AGGCGGTGAT	TTCCGTGCCG	AATTTTTCTT	TCAACCATT	TTTGGCAACG
401	GCTCCGGCAG	CAACGCGGGC	GGCGGTTTCA	CGGGCGGAGC	TCCTGCCGCC
451	GCCGCGGTAG	TCGCGCGTGC	CGTATTGTG	CCAAATAGGTA	TAGTCGGCGT
501	GCCGCGGGCG	GAGCTGGGTG	GCGATGTTGC	CGTAGTCTTT	GCTGCGCTGG
551	TCGGTATTGC	GGATTAA			

m255 . pep

```

1  VVGQEALRGQ FVAVFAAALR YAVKTCADFH AFDGVDAAHR VGDFGIEAVK
51 NRFAQADIRI GCFCMQLRAD GIQGFHAHAVH IVFQLGNLAM VGKKRILGN
101 VFAAFKPDFF FADLGNVGGD FRAEFFFQPF FGNGSGSNAG GGFTGGAPAA
151 AAVVARAVFV PIGIVGVAGA EAGGDVAVVF AALVGIAD*

```

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 255 shows 88.8% identity over a 188 aa overlap with a predicted ORF (ORF 255.ng) from *N. gonorrhoeae*:

m255/q255

	10	20	30	40	50	60
m255.pep	VVGQEALRGQFVAVFAAALRYAVKTCADFHAFDGVDAHHRVGD	DFGIEAVKNRFAQAD	RI			
	:					
g255	MVGQEALRGQFVAVFAAALRYAVKTCADFHAFDGVDAHHRVGD	DFGIEAVENGFAQT	DGDV			
	:					
	10	20	30	40	50	60
	70	80	90	100	110	120
m255.pep	GCFDMQLRADGIQGF	FAHAVHIVFQLGNL	LAMVGGKKRILGNV	FAAFKP	DDFF	FADLGNVGGD
g255	GGFDMQFRADGIQGF	AHTVHIVFQFGL	LALVGGKKRILGNV	FAAFKP	DDFF	FADLGNVGGD
	70	80	90	100	110	120
	130	140	150	160	170	180
m255.pep	FRAEFFFQPF	FGNGSGSNAGGG	TGGAPAAA	AVVARAVFVPI	GIVGVAGAE	AGGDVAVVF
g255	FRAEFFFQPF	FGNGSGGNAGCG	FAGGTPAAAP	PVVARTVFVPI	GIVGVSGAE	GGGDVAVVF

587

	130	140	150	160	170	180
		189				
m255.pep	AALVGIADX					
	:					
g255	AALVGVADX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1003>:

```

a255.seq
1   GTGGTTGGAC AGGAAGCCTT GCGGGGTGAG TTCGTCGCCG TGTTGCGCTGC
51  CGCGTTGCGT TACGCTGTCA AAACCTGCGC CGATTTCACG GCCTTTGACG
101 GCGTTGATGC CCATCATGGC GTAGGCGATT TCGGCATCGA GGCGGTCGAA
151 TACGGGTTTCG CCCAAGCCGA CGGGGACGTT GGCGGCTTCA ATATGCAGCT
201 TCGCGCCGAC GGAATCCAAG GATTTGCGCA CGCTGTCCAT ATAGTTTCC
251 AGCTCGGCAA TTTGGCTATG GTTGGCGGCA AAAAAAGGAT TTTGGGAAAT
301 GTGTTTCGCAG CCTTCAAACC GGATTTCTTT TTCGCCGACT TGGGTAACTG
351 AGGCGGTGAT TTCCGTGCCG AATTTTCTT TCAACCATT TTTGGCAACG
401 GCTCCGGCGG CAACGCGGGC GCGGTTTCG CGGGCGGAAC TCCTGCCGCC
451 GCCCCGGTAG TCGCGCGTGC CGTATTTGTG CCAATAGGTA TAGTCGGCGT
501 GGCCGGGGCG GAAGCTGGTG GCGATGTTGC CGTAGTCTTT GCTGCGCTGG
551 TCGGTATTGC GGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1004; ORF 255.a>:

```

a255.pep
1   VVGQEALRGE FVAVFAAALR YAVKTCADFH AFDGVDAAHG VGDFGIEAVE
51  YGFAQADGDV GGFNMQLRAD GIQGFHAVH IVFQLGNLAM VGGKKRILGN
101 VFAAFKPDFF FADLGNVGGD FRAEFFFQPF FGNGSGGNAG GGFAGGTPAA
151 APVVARAVFV FIGIVGVAGA EAGGDVAVVF AALVGIAD*

```

m255/a255 93.1% identity in 188 aa overlap

	10	20	30	40	50	60
m255.pep	VVGQEALRGQFVAVFAAALRYAVKTCADFHAFDGVDAHHRVGD	FDGIEAVKNRFAQAD	RDI			
a255	VVGQEALRGEFVAVFAAALRYAVKTCADFHAFDGVDAHHRVGD	FDGIEAVEYGFAQAD	GDV			
	70	80	90	100	110	120
m255.pep	GCFDMQLRADGIQGFHAVHIVFQLGNLAMVGGKKRILGNVFAAFKPDF	FFADLGNVGGD				
a255	GGFNMQLRADGIQGFHAVHIVFQLGNLAMVGGKKRILGNVFAAFKPDF	FFADLGNVGGD				
	130	140	150	160	170	180
m255.pep	FRAEFFFQPF	FGNGSGSNAGGGFTGGAPAAA	AVVARAVFVPIGIVGVAGAEAGGDVAVVF			
a255	FRAEFFFQPF	FGNGSGSNAGGGFAGGTPAA	APVVARAVFVPIGIVGVAGAEAGGDVAVVF			
	130	140	150	160	170	180
		189				
m255.pep	AALVGIADX					
a255	AALVGIADX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1005>:

```

g256.seq
1   atgctcgcgg tacgcaatcg gggttggcac ggcgcagtcg tccatttcgg
51  cagctgcggc ggcgtagcga acaccgcccc ggtgttctac cacttggggtg
101 ataccgccga aatcgctttt gctttggaca cgctcaccgc gcgttaccgt
151 gaaatatacg ccgtcggcgt atcgctgggc ggcaacgcgc cggcaaaata
201 tttgggcgaa cagggcaaaa aggcattgcc gcacgcctcg gccgccgtat
251 ccgccccgtg tgatgcagag gcggcaggca gccgcttcga cagcggcatc
301 acgcggtgcg tctacacgcg ctacttcctc cgcacactga tacccaaagc

```

g256.pcp

```

1  MLAVNRNRGWH  GAVVHFRSCG  GVANTAPVVFY  HLGDTAEIAF  ALDTLTARYR
51  EIYAVGVSLG  GNAPACKYLGE  QGKKALPHAS  AAVSAPVDAE  AAGSRFDSGI
1  TRLLYTRYFL  RTLIPKARSL  QGFQTAFAAG  CKTLGEFDDR  FTAPLHGFD
151 RHDYYRQTSK  KPLLKHVAKP  LLLLNANDP  FLPEALPRA  DEASEAVTLF
201 QPAHGHHAGF  VSSTGGRHLH  QWLPQTVLSY  FDSFRTNRR*

```

m256.seq

1	ATGCTTGCGG	TACGCGATCG	GGGTTGGCAC	GGCGTAGTCG	TCCATTTCGG
51	CAGCTGCGGC	GGCATTGCCA	ACACCGCTCC	GGTGTCTAC	CA. CTGGGC
101	ATACCGACCA	AATCGCCTTT	ACTTTGGACA	CGTTCGCGC	GC GTTACCGT
151	GAAAATACG	CCGTGCGCGT	ATCGCTGGGC	GGCAACGCGC	TGGCAAATA
201	TTTGGGCGAA	CAGGGCAAAA	AGGCATTGCC	GCAAGCCGCT	GCCGT CATCT
251	CCGCCCCCGT	CGATGCAGAG	CGCGCAGGCA	CAGCGTTCGA	CACCGGCATC
301	ACGCGGCTGC	TCTACACGCG	CTACTTCCTC	CGCACCCTGA	TACCCAAAGC
351	AAAATCGCTC	CAAGGTTTTC	AGACGGCATT	TGCCCGAGGG	TGCAAAACAC
401	TGGCGCAGTT	TGACGACCCG	TTCACCGCGC	CGCTGCAACG	CTTTGCCGAC
451	GGGCACAGT	ACTACGCCCA	AACTTCTCTC	AAACCGCTGC	TCAAACACGT
501	TGCCAAACCG	CTGTCTCTGC	TCAATGCCGT	CAACGACCCC	TTCTGCGCGC
551	CCGAAGCCCT	GCCCCGCGCA	GACGAAGTAT	CCGAAGCCGT	TACCTGT TTC
601	CAGCCGGCAT	ATGGTGGTCA	TGTCTGGCTTT	GTCAGCAGCA	CCGGCGGCAG
651	GCTGCACCTG	CAATGGCTGC	CGCAGACCGT	CCTGTCCTAT	TTCGACAGCT
701	TCCGCACAAA	CAGGCGTTAA			

m256 . pep

```

1  MLAVRDRGWG  GVVVHFRSCG  GIANTAPVFY  XLGDTAEIAF  TLDTFAARYR
51  EIYAVGVSLG  GNALAKYLVE  QGKKALPQAA  AVISAPVDAE  AAGRFRDSGI
101  TRLLYTRYFL  RTLIPKAKSL  QGFQTAFAAG  CKTLGEFDDR  FTAPLHGFAD
151  RHDYYRQTSK  KPLLKHVAKP  LLLLNAVNDP  FLPEALPRA  DEVSEAVTLF
201  QPAYGGHVGF  VSSTGGRHLH  QWLQPTVLSY  FDSFRTNRR*

```

Homology with a predicted ORF from *N. gonorrhoeae*

m256/g256

```

m256.pep      10      20      30      40      50      60
               MLAVRD1RGW2HGVV3HFR4SCGG5IANTAPV6FYHL7GDTAE8IAFT9LD10TFAA11RYRE12IYAV13GVSL14G
g256          10      20      30      40      50      60
               MLAVRN1RGW2HGAV3VHFR4SCGG5VANTAPV6FYHL7GDTAE8IAFALD9TLTARY10RE11IYAV12GVSL13G

m256.pep      70      80      90      100     110     120
               GNALAKYLGEQGKKALPQAAAVISAPVDAEAAAGRRFD1SGITRL2LYTRY3FLRT4LIPKA5KS6L
g256          70      80      90      100     110     120
               GNAPAKYLGEQGKKALPHASA1AVSAPVDAEAAAGSRFD2SGITRL3LYTRY4FLRT5LIPKA6RS7L

m256.pep      130     140     150     160     170     180
               QGFQTAFAAGCKTLGEFDD1RFTAPLHGFA2DRHDY3YRQTSC4KPLLKH5VAKPL6LLLLNA7VND8P
g256          130     140     150     160     170     180
               QGFQTAFAAGCKTLGEFDD1RFTAPLHGFA2DRHDY3YRQTSC4KPLLKH5VAKPL6LLLLNA7AND8P

```


589

	130	140	150	160	170	180
	190	200	210	220	230	240
m256.pep	FLPPEALPRADEVSEAVTLFQPAYGGHVGFSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	: : : : :					
g256	FLPPEALPRADEASEAVTLFQPAHGGHAGFVSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1009>:

```

a256.seq
1   ATGCTCGCGG TACGCGATCG GGGTTGGAAC GCGTAGTCG TCCATTTCCG
51  CAGCTGCGGC GCGTAGCGA ACACCGCCCC GGTGTTCTAC CACTTGGGCG
101 ATACCGCCGA AATTGCCTTT ACTTTGGACA CGCTCGCCGC GCGTTACCGT
151 GAAATATACG CCGTCGGCGT ATCGCTGGGC GGCAACCGCG TGGCAAATA
201 TTTGGGCGAA CAGGGCGAAA ACGCGCTGCC GCAAGCCGCC GCCGTCATCT
251 CCGCACCCGT CGATGCAGAG GCGGCAGGCA ACCGCTTCGA CAGCGGCATC
301 ACACGGCTGC TCTACACGCG CTACTTCCTC CGCACACTGA TACCCAAAGC
351 ACGGTCGCTC CAAGGTTTTT AGACGGCATT TGCCGCAGGG TGCAAAACAC
401 TGGGCGAGTT TGACGACCGT TTCACCGCAC CGCTGCACGG CTTTGCCGAT
451 CGGCACGACT ACTACGCCA AACTTCCTGC AAACCGCTGC TCAAACACGT
501 TGCCAAACCG CTGCTCCTGC TCAATGCCGT CAACGACCCC TTCCTGCCGC
551 CCGAAGCGCT GCCCGCGCA GACGAAGTGT CCGAAGCCGT TACCTGTTC
601 CAGCCGACAC ACGGTGGTCA TGTGGGCTTT GTCGGCAGCA CCGGCGCAG
651 GCTGCACCTG CAATGGTTGC CGCAGACCGT CCTGTCTAT TTCGACAGCT
701 TCCGCACAAA CAGGCGTTAA
  
```

This corresponds to the amino acid sequence <SEQ ID 1010; ORF 256.a>:

```

a256.pep
1   MLAVRDRGWN GVVVHFRSCG GVANTAPVfy HLGDTAEIAF TLDTLAARYR
51  EIIYAVGVS LG NALAKYLGE QGENALPQAA AVISAPVDAE AAGNRFDSGI
101 TRLLYTRYFL RTLIPKARSL QGFQTAFAAG CKTLGEFDDR FTAPLHGFAD
151 RHDYYRQTSC KPLLKHVAKP LLLNNAVNDP FLPPEALPRA DEVSEAVTLF
201 QPTHGGHVG F VGSTGGRLHL QWLPQTVLSY FDSFRTNRR*
  
```

m256/a256 95.4% identity in 239 aa overlap

	10	20	30	40	50	60
m256.pep	MLAVRDRGWHGVVVHFRSCGGIANTAPVfyXLGDTAEIAFTLDTFAARYREIYAVGVSLG					
	: : : : :					
a256	MLAVRDRGWNGVVVHFRSCGGVANTAPVfyHLGDTAEIAFTLDTLAARYREIYAVGVSEG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m256.pep	GNALAKYLGEQGKKALPQAAVISAPVDAEAGRRFDSGITRLLYTRYFLRTLIPKAKSL					
	: : : : :					
a256	GNALAKYLGEQGENALPQAAVISAPVDAEAGNRFDSGITRLLYTRYFLRTLIPKARSL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m256.pep	QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHHDYYRQTSCKPLLKHVAKPLLLLNNAVNDP					
	: : : : :					
a256	QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHHDYYRQTSCKPLLKHVAKPLLLLNNAVNDP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m256.pep	FLPPEALPRADEVSEAVTLFQPAYGGHVGFSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	: : : : :					
a256	FLPPEALPRADEVSEAVTLFQPTHGGHVGFSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1011>:

```

g256-1.seq
1   ATGATTTTGA CACCGCCGGA CACGCCCTTT TTCCTCCGCA ACGGCAATGC
51  CGACACGATT GCCGCCAAT TCCTGCAACA CCGGCACCC GCATACCGCC
  
```

```
101 GCGAGATGCT TCCCGACAGC ACGGGTAAAA CCAAAACCGC CTACGACTTT
151 TCAGCAGGCG GCATTTTCGCC CGATGCGCCG CTGGTCGTGC TGTTCACGG
201 TTTGGAAGGA AGCAGCCGCA GCCATTACGC GGTCGAACTG ATGCTCGCGG
251 TACGCAATCG GGGTTGGCAC GCGCGAGTCG TCCATTTCGG CAGCTGCGGC
301 GCGGTAGCGA ACACGCCCCC GGTGTTCTAC CACTTGGGTG ATACCGCCGA
351 AATCGCCTTT GCTTTGGACA CGCTCACCGC GCGTTACCGT GAAATATACG
401 CCCTCGGCGT ATCGCTGGGC GGCAACGCGC CGGCAAAATA TTTGGGCGAA
451 CAGGGCAAAA AGGCATTGCC GCACGCCTCG GCCGCCGTAT CCGCCCCCGT
501 TGATGCAGAG GCGGCAGGCA GCCGCTTCGA CAGCGGCATC ACGCGGCTGC
551 TCTACACGCG CTACTTCCTC CGCACACTGA TACCCAAAGC ACGTTCGCTC
601 CAAGGTTTTT AGACGGCATT TGCCGCAGGG TGCAAAACAC TGGGCGAGTT
651 TGACGACCGT TTCACGCGAC CGCTGCACGG CTTTGCCGAC CGGCACGACT
701 ACTACGCCCA AACTTCCTGC AAACCGCTGC TCAAACACGT TGCCAAACCG
751 CTGCTCCTGC TCAATGCCGC CAACGACCCC TTCCTGCCGC CCGAAGCCCT
801 GCCCGCTGCA GACGAAGCGT CCGAAGCCGT TACCCTGTTT CAACCTGCAC
851 ACGGCGGGCA CGCCGGCTTT GTCAGCAGCA CCGGCGGCAG GCTGCACCTG
901 CAATGGCTGC CGCAGACCGT CCTGTCCTAT TTTGACAGCT TCCGCACAAA
951 CAGGCGTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1012; ORF 256-1.ng>:

g256-1.pep

```
1 MILTPDPTPF FLRNGNADTI AAKFLQHPAP AYRREMLPDS TGKTKTAYDF
51 SAGGISPDAP LVVLFHGLEG SSRSHYAVEL MLAVNRGWH GAVVHFRSCG
101 GVANTAPVYF HLGDTAEIAF ALDTLTARYR EYAVGVSLG GNAPAKYLGE
151 QGKKALPHAS AAVSAPVDAE AAGSRFDSGI TRLLYTRYFL RTLIPKARSL
201 QGFQTAFAAG CKTLGEFDDR FTAPLHGFAD RHDYYRQTSK PLLKHVAKP
251 LLLNNAANDP FLPEALPRA DEASEAVTLF QPAHGHHAGF VSSTGGRLHL
301 QWLPQTVLSY FDSFRTNRR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1013>:

m256-1.seq

```
1 ATGATTTTAA CACCGCCGGA CAGGCCCTTT TTCCTCCGCA ACGGCAATGC
51 CGACACGATT GCCGCCAAAT TCCTGCAACG CCCCAGCGCC GCATACCGCC
101 GAGAGCTGCT TCCCGACAGC ACGGGTAAAA CCAAAGTCGC CTACGACTTT
151 TCAGACGGCA TTTGCCCCGA TGCGCGCTG GTCGTGCTGT TTCACGGTTT
201 GGAAGGAAGC AGCCGCGAGC ATTACGCGGT CGAACTGATG CTTGCGGTAC
251 GCGATCGGGG TTGGCACGGC GTAGTCGTCC ATTTCCGCGC CTGCGGCGGC
301 ATTGCCAACA CCGCTCCGCT GTTCTACCAC TTGGGCGATA CCGCCGAAAT
351 CGCCTTTACT TTGGACACGT TCGCCGCGCG TTACCGTGAA ATATACGCGC
401 TCGGCGTATC GCTGGGCGGC AACGCGCTGG CAAATATTT GGGCGAACAG
451 GGCAAAAAGG CATTGCCGCA AGCCGCTGCC GTCATCTCCG CCGCCGTGTA
501 TGCAGAGGCG GCAGGCAGAC GCTTCGACAG CGGCATCAGC CGGCTGCTCT
551 ACACGCGCTA CTTCTCCGCG ACCCTGATAC CCAAAGCAAA ATCGCTCCAA
601 GGTTTTTCAGA CGGCATTGTC CGCAGGGTGC AAAACACTGG GCGAGTTTGA
651 CGACCGCTTC ACCGCACCGC TGCACGGCTT TGCCGACCGG CACGACTACT
701 ACCGCCAAAC TTCCTGCAAA CCGTGCTCA AACACGTTGC CAAACCGCTG
751 CTCCTGCTCA ATGCCGTCAA CGACCCCTTC CTGCCGCCCG AAGCCCTGCC
801 CCGCGCAGAC GAAGTATCCG AAGCCGTTAC CTTGTTCCAG CCGGCATATG
851 GTGGTCATGT CGGCTTTGTC AGCAGCACCG GCGGCAGGCT GCACCTGCAA
901 TGGCTGCCCG AGACCGTCCT GTCCTATTTC GACAGTTTCC GCACAAACAG
951 GCGTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1014; ORF 256-1>:

m256-1.pep

```
1 MILTPDPTPF FLRNGNADTI AAKFLQRPAP AYRRELLPDS TGKTKVAYDF
51 SDGISPDAPL VVLFHGLEGS SRSHYAVELM LAVDRGWHG VVHFRSCGG
101 IANTAPVYFH LGDTAEIAFT LDTFAARYRE IYAVGVSLGG NALAKYLGEQ
151 GKKALPQAAA VISAPVDAEA AGRRFDSGIT RLLYTRYFLR TLIPKAKSLQ
201 GFQTAFAAGC KTLGEFDDRF TAPLHGFADR HDYYRQTSCK PLLKHVAKPL
251 LLLNAVNDPF LPPEALPRAD EVSEAVTLFQ PAYGGHVGFV SSTGGRLHLQ
301 WLPQTVLSYF DSFRTNRR*
```

m256-1/g256-1 93.1% identity in 319 aa overlap

```
10 20 30 40 50 59
m256-1.pep MILTPDPTPFLLRNGNADTIAAKFLQRPAPAYRRELLPDSTGKTKVAYDFS-DGISPDAP
|||||
g256-1 MILTPDPTPFLLRNGNADTIAAKFLQHPAPAYRREMLPDSTGKTKTAYDFSAGGISPDAP
10 20 30 40 50 60

60 70 80 90 100 110 119
m256-1.pep LVVLFHGLEGSSSRSHYAVELMLAVDRGWHGVVHFRSCGGIANTAPVYFHLGDTAEIAF
```

a256-1.seq

1	ATGATTTTGA	CACCGCCGGA	CACACCCTTT	TTCTCTCGCA	ACGGCAATGC
51	CGACACGATT	GCCCGCAAAT	TCCTGCAACG	CTCCGCACCT	GCATACCGCC
101	CGAGAGTGCT	TCCCGACAGC	ACGGGTAAAA	CAAAAACCCG	CTACGACTTT
151	TCAGACGGCA	TTTCGGCCGA	TGCGCCGCTG	GTCGTGCTGT	TTACCGGGTT
201	GGAGGGCGCG	AGTGGCAGCC	ATTACGCGGT	CGAACTGATG	CTCGCGGTAC
251	GCATTCGGGG	TTGGAACCGC	GTAGTCGTC	ATTTCGCGAG	CTCGCGCGCG
301	TAGCGAACA	CCGCCCCGGT	GTTCTACCA	TTGGGCGATA	CCCGCGAAAT
351	TGCGCTTTAT	TTGGACACGC	TCGCCGCGCG	TTACCGTGAA	ATATACGCCG
401	TCGGCTGATC	GCTGGGCGCG	AACGCGCTGG	CAAAATATTT	GGGCGAACAG
451	CGCGAAACAC	CGCTGCGCGA	AGCCGCGCGC	GTCATCTCCG	CACCCGTCGA
501	TGCAGAGGCG	GCAGGCAACC	GCTTCGACAG	CGGCATCACA	CGCGTGTCT
551	ACACGCGCTA	CTTCTCCCG	ACACTGATAC	CCAAAGCAGC	GTCGCTCCAA
601	GCTTTTCAGA	CGGCATTTCG	CGCAGGGTGC	AAAACACTGG	CGCAGTTTGA
651	CGACCGTTTC	ACCGACACCG	TGCAGCGCCT	TGGCGATCCG	CACGACTACT
701	ACCGCCAAC	TTCTCTGCAA	CCGCTGCTCA	AACACGTTGC	CAAACCGCTG
751	CTCCTGCTCA	ATGCCGTCAA	CGACCCCTTC	CTGCCGCGCG	AAGCGCTGCC
801	CCGCGCAGAC	GAAGTGTCGG	AAGCCGTTAC	CCTGTTCCAG	CGACACACGC
851	GTGGTCATGT	CGGCTTTGTC	GGCAGCACCG	GCGGCAGGCT	GCACCTGCAA
901	TGGTTGCCCG	AGACCGTCCT	GTCCTATTTC	GACAGCTTCC	GCACAAACAG
951	CGGTTAA				

a256-1.ppt

1	MILTPPDTPF	FLRNGNADTI	AAKFLQRSAP	AYRRELLPDS	TGKTKTAYDF
51	SDGISPDAPL	VVLFHGLEGG	SGSHYAVELM	LAVRDGRWNG	VVVFHRS CGG
101	VANTAPVFYH	LGDTAEIAFT	LDTLAARYRE	IYAVGVSLGG	NALAKYLGEO
151	GENALPQAAA	VISAPVDAAE	AGNRFDSGIT	RLLYTRYFLR	TLIPKARSLQ
201	GFQTAFAGC	KTLGEFDDFR	TAPLHGFA DR	HDYYRQTSCK	PLLKHVAKPL
251	LLNAVNDPFF	LPPEALPRAD	EVSEAVTLFR	PTHGGHVGVF	GSTGGRLHLQ
301	WLPOTVLSYF	DSFRNTNR*			

a256-1/m256-1 95.6% identity in 318 aa overlap

	10	20	30	40	50	60
a256-1.pep	MILTPPDP	PFLLRNGNADTIAAKFLQ	RSAPAYRRELLP	DSTGKTKTAYDFS	DGDISPDAPL	
m256-1						
	10	20	30	40	50	60
a256-1.pep	MILTPPDP	PFLLRNGNADTIAAKFLQ	RPAAYRRELLP	DSTGKTKVAYDFS	DGDISPDAPL	
m256-1						
	70	80	90	100	110	120
a256-1.pep	VVLFHGLEGGSGSHYAVELML	AVDRDGRWNGVVVHFRSCGGV	ANTAPVFYHLGDTAEIAFT			
m256-1						
	70	80	90	100	110	120
a256-1.pep	VVLFHGLEGGSSRSHYAVELML	AVDRDGRWGHGVVHFRSCGGI	ANTAPVFYHLGDTAEIAFT			
m256-1						

592

	70	80	90	100	110	120
a256-1.pep	130	140	150	160	170	180
	LDTLAARYREIYAVGVSLGGNALAKYLGEQGENALPQAAAVISAPVDAEAAAGNRFD SGIT					
m256-1	LDTFAARYREIYAVGVSLGGNALAKYLGEQKKALPQAAAVISAPVDAEAAAGRRFD SGIT					
	130	140	150	160	170	180
a256-1.pep	190	200	210	220	230	240
	RLLYTRYFLRTLIPKARSLOGFQTAFAGCKTLGEFDDRFTAPLHGFADRHDIYRQTSCK					
m256-1	RLLYTRYFLRTLIPKAKSLOGFQTAFAGCKTLGEFDDRFTAPLHGFADRHDIYRQTSCK					
	190	200	210	220	230	240
a256-1.pep	250	260	270	280	290	300
	PLLKHVAKPLLLNNAVNDPFLPPEALPRADEVSEAVTLFQPTHGGHVGFGVSTGGRLHLQ					
m256-1	PLLKHVAKPLLLNNAVNDPFLPPEALPRADEVSEAVTLFQPAYGGHVGFGVSSTGGRLHLQ					
	250	260	270	280	290	300
a256-1.pep	310	319				
	WLPQTVLSYFDSFRTNRRX					
m256-1	WLPQTVLSYFDSFRTNRRX					
	310					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1017>:

g257.seq

```

1  atgggcaggc atttcgggcg cagacgtttt ctgacggctg ccgccgttgc
51  tgtggccggt gcggcggttt cttttttgcc gaatcctttt gccgcggcg
101  gcgaaaaacg caacatggat aaaaaacgcg atgaaaatgt gtttttctgg
151  aaaggtgtcg cgctgggttc cggcgcgag ctgcccctgt tcggcgtgga
201  cgacagacag gcggcggtt tggtaataa ggttttggcg gaagtggcg
251  gtttggaata aatgttcagc cttaccgtg aagacagcct gatcagccgt
301  ctgaaccgag acggttatct gacttcgcct ccggcggtt ttttgaact
351  gttgagcctg gccgcgatat tcacgcgctg a

```

This corresponds to the amino acid sequence <SEQ ID 1018; ORF 257.ng>:

g257.pep

```

1  MGRHFGRRRF LTAAAVAVAG AAVSFLPNPF AAGGEKRNMD KKRDENVFFW
51  KGVALGSGAE LRLFGVDDRQ AADLVNKLVA EVARLEKMFS LYREDSLISR
101  LNRDGYLTSP PADFLELLSL AAI FTR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1019>:

m257.seq

```

1  ATGGGCAGGC ATTTCCGGGCG .CAGCGTTTT CTGACGGTTG CCGCCGTTGC
51  GGCGGGGAC. GCGGCGGTTT CTTTCCTGCC GAATCCTTTT GCCGCCGATG
101  ATGAAAAACG CAACGGGGAT GAAAAACGCA ATGAAAATGT GTTTTCTGG
151  AAAGGTGTCT CACTGGGTTC CGGTGCGGA. CTCCGTCTGT TCGGTGTGGA
201  CGACAGGCGT GCGGCGGATT TGGTCAACAA GGTTTGGCG GAAGTGGCGC
251  GTTTGGAATA ATTGTTCAGC CTTTACCGTG AAGACAGCCT GATCAGCCGC
301  CTGAACAGGG ACGGTATCT GACTTCGCCG TCGGCGGATT TTTTGAAC
351  GKTGAGCCTG GCCGCGATAT TCACGCKCTG A

```

This corresponds to the amino acid sequence <SEQ ID 1020; ORF 257>:

m257.pep

```

1  MGRHFGXQRF LTVAAVAAGX AAVSFLPNPF AADDEKRNMD EKRDENVFFW
51  KGVALGSGAX LRLFGVDDR AADLVNKLVA EVARLEKLFS LYREDSLISR
101  LNRDGYLTSP SADFLELXSL AAI FTX*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 257 shows 88.0% identity over a 125 aa overlap with a predicted ORF (ORF 257.ng) from *N. gonorrhoeae*:

m257/g257

10 20 30 40 50 60

593

```

m257.pep  MGRHFGRQRFLTVAAVAAGTAAVSFLPNPFAADDEKRNNGDEKRNENVFFWKGVALGSGAD
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g257      MGRHFGRRRRFLTAAAVAVAGAAVSFLPNPFAAGGEKRNMDKKRDENVFFWKGVALGSGAE
          10      20      30      40      50      60

          70      80      90      100     110     120
m257.pep  LRLFGVDDRRRAADLVNKKVLAEEVARLEKLFSLYREDSLISRLNRDGYLTSPSADFLLELXSL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g257      LRLFGVDDRQAADLVNKKVLAEEVARLEKMFSLYREDSLISRLNRDGYLTSPPADFLLELLSL
          70      80      90      100     110     120

m257.pep  AAIFTXX
          |||||
g257      AAIFTRX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1021>:

```

a257.seq
  1  ATGGGCAGGC  ATTTCTGGGCG  CAGGCGTTTT  TTGACAGTTG  CCGCCGTTGC
51  GCGGCGCGGC  GCGGCGGTTT  CTTTCTTGCC  GAATCCTTTT  GCCGCCGATG
101 ATGAAAAACG  CAATAAAGAT  GAAAAACGCA  ATGAAAATGT  GTTTTTCTGG
151 AAAGGTGTCTG  CACTGGGTTC  CGGTGCGGAG  CTCCGTCTGT  TCGGTGTGGA
201 CGACAGGCGT  GCGGCGGATT  TGGTCAACAA  GGTTTTGGCG  GAAGTGGCGC
251 GTTTGGAAAA  AATGTTTCAGC  CTTTACCGTG  AAGACAGCCT  GATCAGCCGT
301 CTGAACCGTG  ACGGTTATTT  GACTTCGCCG  CCGGCGGATT  TTTTGGAACT
351 GTTGAGCCTG  GCCGTGATAT  TCACGCGCTG  A

```

This corresponds to the amino acid sequence <SEQ ID 1022; ORF 257.a>:

```

a257.pep
  1  MGRHFGRRRF  LTVAAVAAAG  AAVSFLPNPF  AADDEKRNKD  EKRNENVFFW
51  KGVALGSGAE  LRLFGVDDRR  AADLVNKKVLA  EVARLEKMFS  LYREDSLISR
101 LNRDGYLTSP  PADFLELLSL  AVIFTR*

```

m257/a257 92.0% identity in 125 aa overlap

```

          10      20      30      40      50
60
m257.pep  MGRHFGRQRFLTVAAVAAGXAAVSFLPNPFAADDEKRNNGDEKRNENVFFWKGVALGSGAX
          |||||          :|||||:|||||:|||||:|||||:|||||:|||||:
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a257      MGRHFGRRRRFLTVAAVAAAGAAVSFLPNPFAADDEKRNKDEKRNENVFFWKGVALGSGAE
          10      20      30      40      50

          70      80      90      100     110
120
m257.pep  LRLFGVDDRRRAADLVNKKVLAEEVARLEKLFSLYREDSLISRLNRDGYLTSPSADFLLELXSL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
          ||
a257      LRLFGVDDRRRAADLVNKKVLAEEVARLEKMFSLYREDSLISRLNRDGYLTSPPADFLELLSL
          70      80      90      100     110

120

m257.pep  AAIFTXX
          |||||
a257      AVIFTRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1023>:

```

g258.seq
1  atgcgccgct tcctaccgat cgcagccata tgcgccgtcg tcctgctgta
51  cggattgacg gcggcgaccg gcagcaccag ttcgctggcg gattatttct
101 ggtggatagt ctcgttcagc gcaatgctgc tgctggtggt gtccgccgtt
151 ttggcacggt atgtcatatt gctgttgaaa gacaggcgca acggcggtgt
201 cggttcgcag attgccaac gcctttccgg gatgttcacg ctggtcgccg
251 tactgcccgg cttgttctcg ttcggcattt ccgcgcagtt tatcaacggc
301 acgattaatt cgtggttcgg caacgacacc cacgaagccc tcgaacgcag
351 ccttaatttg agcaagtccg cactggattt ggcggcagac aatgccgtca
401 gcaacgccgt tcccgtacag atagacctca tcggcaccgc ctccctgtcg
451 ggcaatatgg gcagtgtgct ggaacactac gccggcagcg gttttgccca
501 gcttgccctg tacaatgccg caagcgggaa aatcgaaaaa agcatcaatc
551 cgcaccaatt cgaccagccg cttcccgaca aagaacattg ggaacagatt
601 cagcagaccg gttcggttcg gagtttgaa agcataggcg gcgtattgta
651 cgcgccagga tgggtgtcgg caggtagcga caacgggcgc gattacgcgc
701 tgttcttccg ccagccgatt cccgaaaatg tggcacagga tgccgttctg
751 attgaaaagg cgcgggcgaa atatgccgaa ttgagttaca gcaaaaaagg
801 tttgcagacc ttttttctgg taacctgtct gattgcctcg ctgctgtcga
851 tttttcttgc gctggtaatg gcactgtatt ttgcccgcg tttcgtcgaa
901 cccattctgt cgcttgccga gggcgcaaag gcggtggcgc aggggtgattt
951 cagccagacg cgccccgtat tgcgcaacga cgagttcggc cgtttgacca
1001 agctgttcaa ccatatgacc gagcagcttt ccatcgccaa agaagcagac
1051 gaacgcaacc gccggcgcg ggaagccgcc cgctactacc tcgagtgcgt
1101 gttggatggg ttgactaccg gtgtggtggt ctctaccctt ctctcttgtt
1151 gccgtaccgc ggtgttttcc acttgtcatt cctccctctt ttcttatttc
1201 taa

```

This corresponds to the amino acid sequence <SEQ ID 1024; ORF 258.ng>:

```

g258.pep
1  MRRFLPIAAI CAVLLYGLT AATGSTSSLA DYFWWIVSFS AMLLLVLSAV
51  LARYVILLK DRNGVFGSQ IAKRLSGMFT LVAVLPGLFL FGISAQFING
101 TINSWFGNDT HEALERSLNL SKSALDLAAD NAVSNAVFPVQ IDLIGTASLS
151 GNMGSVLEHY AGSGFAQLAL YNAASGKIEK SINPHQFDQP LPDKEHWEQI
201 QQTGSVRSLE SIGGVLYAQG WLSAGTHNGR DYALFFRQPI PENVAQDAVL
251 IEKARAKYAE LSYSKGLQT FFLVTLIAS LLSIFLALVM ALYFARRFVE
301 PILSLAEGAK AVAQGDFSQT RPVLRNDEFG RLTKLFNHMT EQLSIAKEAD
351 ERNRRREEAA RHYLECVLDG LTTGVVVSYP LSCCRTAVFS TCHSSPLSYF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1025>:

```

m258.seq
1  ATGCGCCGTT TTCTACCGAT CGCAGCCATA TGCGCCGTCTG TCCTGTTGTA
51  CGGACTGACG GCGGCAACCG GCAGCACCAG TTCGCTGGCG GATTATTTCT
101 GGTGGATTGT TCGTTCAGC GCAATGCTGC TGCTGGTGTT GTCCGCCGTT
151 TTGGCACGTT ATGTCATATT GCTGTTGAAA GACAGGCGCG ACGGCGTATT
201 CGGTTTCGAG ATTGCCAAAC GCCTTTCTGG GATGTTTACG CTGGTTGCCG
251 TACTGCCCAG CGTGTTCCTG TTCGGCGTTT CCGCACAGTT CATCAACGGC
301 ACGATTAATT CGTGGTTCGG CAACGATACC CACGAGGCGC TTGAACGCAG
351 CCTCAATTG AGCAAGTCCG CATTGAATTT GCGGCGAGAC AACGCCCTCG
401 GCAACGCCGT CCCCCTGCAG ATAGACCTCA TCGGCGCGGC TTCCCTGCCC
451 GGGGATATGG GCAGGTGCT GGAACATTAC GCCGGCAGCG GTTTTGCCCA
501 GCTTGCCCTG TACAATGCCG CAAGCGGCAA AATCGAAAAA AGCATCAACC
551 CGCACAAGCT CGATCAGCCG TTTCCAGGTA AGGCGCGTTG GGAAAAAATC
601 CAACGGGCGG GTTCGGTCAG GGATTTGGAA AGCATAGGCG GCGTATTGTA
651 CGCGCAGGGC TGGCTGTCGG CGGGTACGCA CAACGGGCGC GATTACGCCT
701 TGTTTTTCCG TCAGCCGGTT CCCAAAGGCG TGGCAGAGGA TGCCGTCTTA
751 ATCGAAAAGG CAAGGGCGAA ATATGCTGAG TTGAGTTACA GCAAAAAGG
801 TTTGCAGACC TTTTTCCTGG CAACCTGCT GATTGCCTCG CTGCTGTCTGA
851 TTTTCTTGC ACTGGTCATG GCACTGTATT TCGCCCGCGG TTTCTGCGAA
901 CCCGTCTAT CGCTTGCCGA GGGGGCGAAG GCGGTGGCGC AAGGCGATTT
951 CAGCCAGACG CGCCCCGTGT TCGCAACGA CGAGTTCGGA CGCTTGACCA

```

```

1001 AGTTGTTCAA CCACATGACC GAGCAGCTTT CCATCGCCAA AGAAGCAGAC
1051 GAGCGCAACC GCCGGCGCGA GGAAGCCGCC AGGCATTATC TTGAATGCGT
1101 GTTGGAGGGG CTGACCACGG GCGTGGTGGT GTTTGACGAA CAAGGCTGTC
1151 TGAAACsTT CAACAAAGCG GCGGAACAGA TTYTGGGGAT GCCGCTTACC
1201 CCCcTGTTGG GCAGCAGCCG GCACGGTTGG CACGGCGTTT CGGCGCAGCA
1251 GTCCCTGCTT GCCGAAGTGT TTGCCGCCAT CGGCGCGGCG GCAGGTACGG
1301 ACAAACCGGT CCATGTGAAA TATGCCCGCG CGGACGATGC CAAAATCCTG
1351 CTGGGCAAGG CAACCGTCCT GCCCGAAGAC AACGGCAACg GCGTGGTAAT
1401 GGTGATTGAC GACATCACCG TTTTGATACA CGCGCAAAA GAAGCCGCGT
1451 GGGGCGAAGT GGCGaAgCGG CTGGCACACG AAATCCGCAA TCCGCTCACG
1501 CCCATCCAGC TTTCCGCCGA ACgGsTGGCG TkGAAATTGG GCGGGAAGCT
1551 GGATGAGCAG GATGCGCAAA TCCTGACGCG TTCGACCGAC ACCATCGTCA
1601 AACAGGTGGC GGCATTGAAG GAAATGGTCG AAGCATTCGG CAATTATGCG
1651 CGTTCCCTT CGCTCAAATT GGAAATCAG GATTTGAACG CCTTAATCGG
1701 CGATGTGTTG GCATTGTATG AAGCCGGTCC GTGCCGGTTT GCGGCGGACT
1751 TGCCGCGCAA CCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1026; ORF 258>:

m258.pep

```

1 MRRFLPIAAI CAVVLLYGLT AATGSTSSLA DYFWWIVAFS AMLLLVLSAV
51 LARYVILLLK DRRDGVFGSQ IAKRLSGMFT LVAVLPGVFL FGVSAQFING
101 TINSWFGNDT HEALERSLNL SKSALNLAAD NALGNAVVPQ IDLIGAASLP
151 GDMGRVLEHY AGSGFAQLAL YNAASGKIEK SINPHKLDQP FPGKARWEKI
201 QRAGSVRDLE SIGGVLYAQG WLSAGTHNGR DYALFFRQPV PKGVAEDAVL
251 IEKARAKYAE LSYSKKGLQT FFLATLLIAS LLSIFLALVM ALYFARRFVE
301 PVLSLAEGAK AVAQGDFSQT RPYLRNDEFG RLTKLFNHMT EQLSIAKEAD
351 ERNRRREEAA RHYLECVLEG LTTGVVVFDE QGCLKTFNKA AEQILGMPLT
401 PLWGSSRHGW HGVSAQQSLL AEFVFAIGAA AGTDKPVHVK YAAPDDAKIL
451 LGKATVLPED NGNGVVMVID DITVLIHAQK EAAWGEVAKR LAHEIRNPLT
501 PIQLSAERXA XKLGGKLDEQ DAQILTRSTD TIVKQVAALK EMVEAFRNYA
551 RSPSLKLENQ DLNALIGDVL ALYEAGPCRF AADLPANR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 258 shows 90.9% identity over a 386 aa overlap with a predicted ORF (ORF 258.ng) from *N. gonorrhoeae*:

m258/g258

```

              10      20      30      40      50      60
m258.pep  MRRFLPIAAICAVVLLYGLTAATGSTSSLDYFWWIVAFSAML VLSAVLARYVILLLK
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g258      MRRFLPIAAICAVVLLYGLTAATGSTSSLDYFWWIVSFSAM L VLSAVLARYVILLLK
              10      20      30      40      50      60

              70      80      90     100     110     120
m258.pep  DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFINGTINSWFGNDTHEALERSLNL
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g258      DRRNGVFGSQIAKRLSGMFTLVAVLPGLFLFGISAQFINGTINSWFGNDTHEALERSLNL
              70      80      90     100     110     120

              130     140     150     160     170     180
m258.pep  SKSALNLAADNALGNAVVPQIDLIGAASLPDGMGRVLEHYAGSGFAQLALYNAASGKIEK
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g258      SKSALDLAADNAVSNVAVPQIDLIGTASLSGNMGSVLEHYAGSGFAQLALYNAASGKIEK
              130     140     150     160     170     180

              190     200     210     220     230     240
m258.pep  SINPHKLDQPFPGKARWEKIQRAGSVRDLESIGGVLYAQGWLSAGTHNGR DYALFFRQPV
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g258      SINPHQFDQPLPDKEHWEIQQTGSVRSLESIGGVLYAQGWLSAGTHNGR DYALFFRQPI
              190     200     210     220     230     240

```

596

	250	260	270	280	290	300
m258 . pep	PKGVAEDAVLIEKARAKYAELSYSKKGLQTFFLATLLIASLLSIFLALVMALYFARRFVE					
g258	PENVAQDAVLIEKARAKYAELSYSKKGLQTFFLVTLIASLLSIFLALVMALYFARRFVE					
	250	260	270	280	290	300
	310	320	330	340	350	360
m258 . pep	PVLSLAEGAKAVAQGDFSQTRPVLNRNDEFGRLLTKLFNHNMTQELSIAKEADERNRRREEAA					
g258	PILSLAEGAKAVAQGDFSQTRPVLNRNDEFGRLLTKLFNHNMTQELSIAKEADERNRRREEAA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m258 . pep	RHYLECVLEGLTTGVVVVFDEQGLKTFNKAAEQILGMPLTPLWGSSRHGWHGVSAQQSLL					
g258	RHYLECVLDGLTTGVVVSYPVLSCCRFAVFSTCHSSPLSYFX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1027>:

a258 . seq

1	ATGCGCCGTT	TTCTACCGAT	CGCAGCCATA	TGCGCCGTCG	TCCTGTTGTA
51	CGGACTGACG	GCGGCAACCG	GCAGACCAG	TTTCGCTGGCG	GATTATTTCT
101	GGTGGATTGT	TGCGTTCAGC	GCAATGCTGC	TGCTGGTGTT	GTCCGCCGTT
151	TTGGCACGTT	ATGTCATATT	GCTGTTGAAA	GACAGGCGCG	ACGGCGTATT
201	CGGTTTCGAG	ATTGCCAAAC	GCCTTTCCGG	GATGTTTACG	CTGGTTGCCG
251	TACTGCCCGG	CGTGTTCCTG	TTTCGCGGTT	CCGCACAGTT	TATCAACGGC
301	ACGATTAATT	CGTGGTTCGG	CAACGATACC	CACGAGGCGC	TTGAACGCAG
351	CCTCAATTG	AGCAAGTCCG	CATTGAATCT	GGCGGCAGAC	AACGCCCTTG
401	GCAACGCCAT	CCCCGTGCAG	ATAGACCTCA	TCGGCGCGGC	TTCCCTGCCC
451	GGGGATATGG	GCAGGGTGCT	GGAACATTAC	GCCGGCAGCG	GTTTGGCCCA
501	GCTTGCCCTG	TACAATGCCG	CAAGCGGCAA	AATCGAAAAA	AGCATCAACC
551	CGCACAAGCT	CGATCAGCCG	TTTCCAGGTA	AGGCGCGTTG	GGAAAAAATC
601	CAACAGGCGG	GTTTCGGTCAG	GGATTGGGAA	AGCATAGGCG	GCGTATTGTA
651	CGCGCAGGGC	TGGCTGTCTG	CAGGTACGCA	CAACGGGCGC	GATTACGCC
701	TGTTTTTCCG	TCAGCCGGTT	CCCAAAGGCG	TGGCAGAGGA	TGCCGTCTTA
751	ATCGAAAAGG	CAAGGGCGAA	ATATGCTGAG	TTGAGTTACA	GCAAAAAGG
801	TTTGCAGACC	TTTTTCCTGG	CAACCCTGCT	GATTGCCTCG	CTGCTGTCTG
851	TTTTTCTTGC	ACTGGTCATG	GCACTGTATT	TCGCCCGCCG	TTTCGTCTGAA
901	CCCGTCCTAT	CGCTTGCCGA	GGGGGCGAAG	GCGGTGGCGC	AAGCGGATTT
951	CAGCCAGACG	CGCCCCGTGT	TGCGCAACGA	CGAGTTCGGA	CGCTTGACCA
1001	AGTTGTTCAA	CCACATGACC	GAGCAGCTTT	CCATCGCCAA	AGAAGCAGAC
1051	GAGCGCAACC	GCCGGCGCGA	GGAAGCCGCC	AGACATTATC	TGCAATGCGT
1101	GTTGGAGGGG	CTGACCACGG	GCGTGGTGTT	GTTTGACGAA	CAAGGCTGTC
1151	TGAAAACCTT	CAACAAAGCG	GCGGAACAGA	TTTTGGGGAT	GCCGCTTACC
1201	CCCCTGTGGG	GCAGCAGCCG	GCACGGTTGG	CACGGCGTTT	CGGCGCAGCA
1251	GTCCCTGCTT	GCCGAAGTGT	TTGCCGCCAT	CGGCGCGGCG	GCAGGTACGG
1301	ACAAACCGGT	CCATGTGAAA	TATGCCGCGC	CGGACGATGC	CAAAATCCTG
1351	CTGGGCAAGG	CAACCGTCCT	GCCCCAAGAC	AACGGCAACG	GCGTGGTAAT
1401	GGTGATTGAC	GACATACCG	TTTTGATACA	CGCGCAAAAA	GAAGCCGCGT
1451	GGGGCGAAGT	GGCAAAACCG	CTGGCACACG	AAATCCGCAA	TCCGCTCACG
1501	CCCATCCAGC	TTTCTGCCGA	ACGGCTGGCG	TGGAAATTGG	GCGGGAAGCT
1551	GGACGAGCAG	GACGCGCAAA	TCCTGACACG	TTCCAGCCGAC	ACCATCATCA
1601	AACAAGTGGC	GGCATTAAAA	GAAATGGTTC	AGGCATTCCG	CAATTACGCG
1651	CGTTCCCTTT	CGCTCAAATT	GGAAAATCAG	GATTTGAACG	CCTTAATCGG
1701	CGATGTGTTG	GCATTGTACG	AAGCTGGTCC	GTGCCGTTT	GCGGCGGAAC
1751	TTGCCGGCGA	ACCGCTGATG	ATGGCGGCGG	ATACGACCGC	CATGCGGCAG
1801	GTGCTGCACA	ATATTTTCAA	AAATGCCGCC	GAAGCGGCGG	AAGAAGCCGA
1851	TGTGCCCCGA	GTCAGGGTAA	AATCGGAAGC	GGGGCAGGAC	GGACGGATTG
1901	TCCTGACAGT	TTGCGACAAC	GGCAAGGGGT	TCGGCAGGGA	AATGCTGCAC
1951	AATGCCTTCG	AGCCGTATGT	AACGGACAAA	CCGCTGGGAA	CGGGATTGGG
2001	ACTGCCCGTG	GTGAAAAAAA	TCATTGAAGA	ACACGGCGGC	CGCATCAGCC
2051	TGAGCAATCA	GGATGCGGGC	GGCGCGTGTG	TCAGAATCAT	CTTGCCAAAA
2101	ACGGTAGAAA	CTTATGCGTA	G		

This corresponds to the amino acid sequence <SEQ ID 1028; ORF 258.a>:

```
a258.pep
1  MRRFLPIAAI CAVVLLYGLT AATGSTSSLA DYFWWIVAFS AMLLLVLSAV
51  LARYVILLLK DRRDGVFGSQ IAKRLSGMFT LVAVLPGVFL FGVSAQFING
101 TINSWFGNDT HEALERSLNL SKSALNLAAD NALGNAIPVQ IDLIGAASLP
151 GDMGRVLEHY AGSGFAQLAL YNAASGKIEK SINPHKLDQP FPGKARWEKI
201 QQAGSVRDLE SIGGVLYAQQ WLSAGTHNGR DYALFFRQPV PKGVAEDAVL
251 IEKARAKYAE LSYSKKGLQT FFLATLLIAS LLSIFLALVM ALYFARRFVE
301 PVLSLAEGAK AVAQGDFSQT RPVLRNDEFG RLTKLFNHMT EQLSIAKEAD
351 ERNRRREEAA RHYLECVLEG LTTGVVVFDE QGCLKTFNKA AEQILGMPLT
401 PLWGSSRHGW HGVSAQQSLL AEVFAAIGAA AGTDKPVHVK YAAPDDAKIL
451 LGKATVLPED NGNGVVMVID DITVLIHAQK EAAWGEVAKR LAHEIRNPLT
501 PIQLSAERLA WKLGGKLDEQ DAQILTRSTD TTIKQVAALK EMVEAFRNYA
551 RSPSLKLENQ DLNALIGDVL ALYEAGPCRF AAELAGEPLM MAADTTAMRQ
601 VLHNIFKNAA EAAEEADVPE VRVKSEAGQD GRIVLTVCDN GKGFGREMLH
651 NAFEPYVTDK PAGTGLGLPV VKKIIEEHGG RISLSNQDAG GACVRIILPK
701 TVETYA*
```

m258/a258 99.0% identity in 584 aa overlap

```

      10      20      30      40      50      60
m258.pep  MRRFLPIAAICAVVLLYGLTAATGSTSSLA DYFWWIVAFS AMLLLVLSAV LARYVILLLK
          |||
a258      MRRFLPIAAICAVVLLYGLTAATGSTSSLA DYFWWIVAFS AMLLLVLSAV LARYVILLLK
          |||
      70      80      90     100     110     120
m258.pep  DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFINGTINSWFGNDTHEALERSLNL
          |||
a258      DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFINGTINSWFGNDTHEALERSLNL
          |||
     130     140     150     160     170     180
m258.pep  SKSALNLAADNALGNAVVPQIDLIGAASLP GDMGRVLEHYAGSGFAQLALYNAASGKIEK
          |||
a258      SKSALNLAADNALGNAIPVQIDLIGAASLP GDMGRVLEHYAGSGFAQLALYNAASGKIEK
          |||
     190     200     210     220     230     240
m258.pep  SINPHKLDQFPFGKARWEKIQRAGSVRDLESIGGVLYAQQWLSAGTHNGRDYALFFRQPV
          |||
a258      SINPHKLDQFPFGKARWEKIQRAGSVRDLESIGGVLYAQQWLSAGTHNGRDYALFFRQPV
          |||
     250     260     270     280     290     300
m258.pep  PKGVAEDAVLIEKARAKYAE LSYSKKGLQTFFLATLLIASLLSIFLALVMALYFARRFVE
          |||
a258      PKGVAEDAVLIEKARAKYAE LSYSKKGLQTFFLATLLIASLLSIFLALVMALYFARRFVE
          |||
     310     320     330     340     350     360
m258.pep  PVLSLAEGAKAVAQGDFSQTRPVLRNDEFGRLTKLFNHMT EQLSIAKEADERNRRREEAA
          |||
a258      PVLSLAEGAKAVAQGDFSQTRPVLRNDEFGRLTKLFNHMT EQLSIAKEADERNRRREEAA
          |||
     370     380     390     400     410     420
m258.pep  RHYLECVLEGLTTGVVVFDEQGCLKTFNKA AEQILGMPLTPLWGSSRHGW HGVSAQQSLL
          |||
a258      RHYLECVLEGLTTGVVVFDEQGCLKTFNKA AEQILGMPLTPLWGSSRHGW HGVSAQQSLL
          |||
     430     440     450     460     470     480
m258.pep  AEVFAAIGAAAGTDKPVHVKYAAPDDAKILLGKATVLPEDNGNGVVMVIDDITVLIHAQK
          |||
a258      AEVFAAIGAAAGTDKPVHVKYAAPDDAKILLGKATVLPEDNGNGVVMVIDDITVLIHAQK
          |||
```

598

	430	440	450	460	470	480
m258.pep	490	500	510	520	530	540
	EAAWGEVAKRLAHEIRNPLTPIQLSAERXAXKLGGKLDQDAQILTRSTDTIVKQVAALK					
a258						
	EAAWGEVAKRLAHEIRNPLTPIQLSAERLAWKLGGKLDQDAQILTRSTDTIIKQVAALK					
	490	500	510	520	530	540
m258.pep	550	560	570	580	589	
	EMVEAFRNYARSPSLKLENQDLNALIGDVLALYEAGPCRFAADLPANRX					
a258						
	EMVEAFRNYARSPSLKLENQDLNALIGDVLALYEAGPCRFAAELAGEPLMMAADTTAMRQ					
	550	560	570	580	590	600
a258	VLHNIFKNAEAAEEADVPEVRVKSEAGQDGRIVLTVCDNGKGFGREMLHNAFEPYVTDK					
	610	620	630	640	650	660

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1029>:

g259.seq

```

1   atgatgatgc acgcttctgt ccaaagtcgt ttcgcaccga tactttatgt
51  tttgattttc tttgccggtt ttttgaccgc gcaaactctgg ttcaatcaga
101 aagcctatac tgaagagctg cctccgcttc tgtccgcatt gtccgccgtc
151 gcgctggtgt ggctggcgtg ggcgttcgtg tcggtgctgt caaaggctaa
201 ggcagaaaag ttctaccgcg aaaaaatgat acagaacgaa agcatacacc
251 ccgtcctgca cgcttctttg caacacttgg aacacaagcc gcaaactgtc
301 gccctgctgg tcaaaaacca cggcaaaggc atggcggaac aggtcaggtt
351 caaggcggaa gtgctgcccc acgacgaaga cgcgcgacg attgccgccg
401 agttggcaaa aatggatatg ttcgcattgg ggacggacgc ggtcgccctc
451 ggcgaaacct atggcgcgct gtctgccgat attttcgagt tgcggcggc
501 tttggaaagg cgcgcggtca aagggatact gaaactgacg gcggaatata
551 aaaaacatct tcggcgatgc ctgccgttcg gaaacggcgt tggatttggg
601 cgcgctcaat caggcggtga gggaaatctc gaaaacgccg gaaaagccta
651 a

```

This corresponds to the amino acid sequence <SEQ ID 1030; ORF 259.ng>:

g259.pep

```

1   MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SVRSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHGKG MAEQVRFAE VLPDDEDART IAAELAKMDM FALGTDAVAS
151 GETYGRVFAD IFELSAALER RAFKGILKLT AEYKHLRRC LPFGNGVGF
201 RAQSGVEGNL ENAGKA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1031>:

m259.seq (partial)

```

1   ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGTT TTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGGTTCTGT TCGGCGCGTT CAAAGGCCAA
201 GGCAGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCsTGCA CGCCTCTTTG CAACACTTGG AACACAAGCC GCAAATACTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCC ACGACGAAGA CGCGCGCACG ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACKGACGC GGTCGCCTCG
451 GGCGAAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTCGmGGC
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AA.AACATCT TCGmGATGC CTGCCGTTTC GAAACGGCGT TGGAGTTGGG
601 CGCACTCAAT CAGGCGTTGC AGGAGATTTC AAAACATCC GG..

```

This corresponds to the amino acid sequence <SEQ ID 1032; ORF 259>:

m259.pep (partial)

```

1   MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVXHASL QHLEHKPQIL
101 ALLVKNHGKG MAEQVRFAE VLPDDEDART IAAELAKMDM FALGTDAVAS

```

151 GETYGRVFAD IFELSXALEG RAFKGMLKLT AEYKXHLRRC LPFGNGVGVG
201 RTQSGVAGDF KNIR..

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 259 shows 94.3% identity over a 212 aa overlap with a predicted ORF (ORF 259.ng) from *N. gonorrhoeae*:

m259/g259

	10	20	30	40	50	60
m259.pep	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQAYTEELPPLLSALSVALVWLAWAFV					
g259	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQAYTEELPPLLSALSVALVWLAWAFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m259.pep	SARSKAKAEKFYREKMIQNESIHPVXHASLOHLEHKPQILALLVKNHGKMAEQVRFKAE					
g259	SVRSKAKAEKFYREKMIQNESIHPVLHASLOHLEHKPQMLALLVKNHGKMAEQVRFKAE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m259.pep	VLPDDEDARTIAAELAKMDMFALGTD AVASGETYGRVFADIFELSXALEGRAFKGMLKLT					
g259	VLPDDEDARTIAAELAKMDMFALGTD AVASGETYGRVFADIFELSAALERRAFKGILKLT					
	130	140	150	160	170	180
	190	200	210			
m259.pep	AEYKXHLRRC LPFGNGVGGR TQSGVAGDFKNIR					
g259	AEYKXHLRRC LPFGNGVGFGRAQSGVEGNLENAGKAX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1033>:

a259.seq (partial)

1	ATGATGATGC	ACGCTTCTGT	CCAAAGCCGT	TTCGCACCGA	TACTTTATGT
51	TTTGATTTC	TTTGCCGGTT	TTTGACCGC	GCAAATCTGG	TTCAATCAGA
101	AAGCCTATAC	TGAAGAGCTG	CCTCCGCTTC	TGTCGCGATT	GTCCGCCGTC
151	GCGCTGGTGT	GGCTGGCGTG	GGCGTTCGTG	TCGGCGCGTT	CAAAGGCTAA
201	GGCGGAAAAG	TTCTACCGCG	AAAAAATGAT	ACAGAACGAA	AGCATACACC
251	CCGTCCTGCA	CGCTTCTTTG	CAACACTTGG	AACACAAGCC	GCAAATGCTC
301	GCCCTGCTGG	TCAAAAACCA	CGGCAAAGGG	ATGGCGGAAC	AGGTCAGGTT
351	CAAGGCGGAA	GTGCTGCCCG	ACGACGAAGA	CGCGCGCACG	ATTGCCGCCG
401	AGTTGGCAAA	AATGGATATG	TTTGCAATTG	GGACGGACGC	GGTCGCCTCG
451	GGCGAAACCT	ATGGACGCGT	GTTCGCCGAT	ATTTTCGAGT	TGTCGCGCGC
501	TTTGAAGGG	CGCGCGTTCA	AAGGAATGTT	GAAACTGACG	GCGGAATATA
551	AAAA.CATCT	TCGGCGATGC	CTGCCGTTTC	GAAACGGCGT	TGGAGTTGGG
601	CGCGCTCAAT	CAGGCGTTGC	AGGAGATTTC	AAAAACATCG	GAAAAGTCCA
651	A				

This corresponds to the amino acid sequence <SEQ ID 1034; ORF 259.a>:

a259.pep (partial)

1	MMMHASVQSR	FAPILYVLIF	FAGFLTAQIW	FNQAYTEEL	PPLLSALS
51	ALVWLAWAFV	SARSKAKAE	FYREKMIQNE	SIHPVLHASL	QHLEHKPQML
101	ALLVKNHGKG	MAEQVRFKAE	VLPDDEDART	IAAELAKMDM	FALGTD AVAS
151	GETYGRVFAD	IFELSAALEG	RAFKGMLKLT	AEYKXHLRRC	LPFGNGVGVG
201	RAQSGVAGDF	KNIGKVQ			

m259/a259 98.1% identity in 213 aa overlap

	10	20	30	40	50	60
m259.pep	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQAYTEELPPLLSALSVALVWLAWAFV					
a259	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQAYTEELPPLLSALSVALVWLAWAFV					

600

	10	20	30	40	50	60
m259.pep	70	80	90	100	110	120
	SARSKAKAEKIFYREKMIQNESIHPVXHASLQHLEHKPQILALLVKNHKGKMAEQVRFKAE					
a259	70	80	90	100	110	120
	SARSKAKAEKIFYREKMIQNESIHPVLHASLQHLEHKPQMLALLVKNHKGKMAEQVRFKAE					
m259.pep	130	140	150	160	170	180
	VLPDDEDARTIAAELAKMDMFALGTDAVASGETYGRVVFADIFELSALEGRAFKGMLKLT					
a259	130	140	150	160	170	180
	VLPDDEDARTIAAELAKMDMFALGTDAVASGETYGRVVFADIFELSAALEGRAFKGMLKLT					
m259.pep	190	200	210			
	AEYKXHLRRLPFGNGVGVGRQSGVAGDFKNIR					
a259	190	200	210			
	AEYKXHLRRLPFGNGVGVGRAQSGVAGDFKNIGKVQ					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1035>:

g259-1.seq

```

1  ATGATGATGC ACGCTTCTGT CCAAAGTCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GGCCTTCGTG TCGGTGCGTT CAAAGGCTAA
201 GGCAGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATAACCC
251 CCGTCCTGCA CGCTTCTTTG CAACACTTGG AACACAAGCC GCAAATGCTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGC ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCAGC ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACGGACGC GGTGCGCTCG
451 GGCGAAACCT ATGGGCGCGT GTTCGCCGAT ATTTTCGAGT TGTCGGCGGC
501 TTTGGAA

```

This corresponds to the amino acid sequence <SEQ ID 1036; ORF 259-1.ng>:

g259-1.pep

```

1  MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PLLSALSASV
51  ALVWLAWAFV SVRSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHKGK MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDAVAS
151 GETYGRVFAD IFELSAALE

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1037>:

m259-1.seq

```

1  ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GGCCTTCGTG TCGGCGCGTT CAAAGGCCAA
201 GCGGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATAACCC
251 CCGTCCTGCA CGCTTCTTTG CAACACTTGG AACACAAGCC GCAAATACTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCAGC ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACGGACGC GGTGCGCTCG
451 GGCGAAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTCGGCGGC
501 TTTGGAAGGG CGCGCTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AAAACATCTT CGCGGATGCC TGCCGTTCCG AAACGGCGTT GGAGTTGGGC
601 GCACTCAATC AGGCGTTGCA GGAGATTTC AAAACATCGG AAAAGTCCAA
651 ACGGATATTT TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1038; ORF 259-1>:

m259-1.pep

```

1  MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PLLSALSASV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQIL
101 ALLVKNHKGK MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDAVAS
151 GETYGRVFAD IFELSAALEG RAFKGMLKLT AEYKNIFGDA CRSETALELG
201 ALNQLQEIS KTSEKSKRIF_Y*

```

g259-1/m259-1 98.8% identity in 169 aa overlap

601

	10	20	30	40	50	60
g259-1.pep	MMMHASVQSRFAPILYVLIF	FAGFLTAQIWFNQAYTEEL	PPLLSALS	SAVALVWLAWAFV		
m259-1	MMMHASVQSRFAPILYVLIF	FAGFLTAQIWFNQAYTEEL	PPLLSALS	SAVALVWLAWAFV		
	10	20	30	40	50	60
	70	80	90	100	110	120
g259-1.pep	SVRSKAKAEK	FYREKMIQNESIHPVLHASL	QHLEHKPQMLALLVKNHGKGM	AEQVRFKAE		
m259-1	SARSKAKAEK	FYREKMIQNESIHPVLHASL	QHLEHKPQILALLVKNHGKGM	AEQVRFKAE		
	70	80	90	100	110	120
	130	140	150	160	169	
g259-1.pep	VLPDDEDARTIAELAKMDMF	ALGTD	AVASGETYGRVFADIFEL	SAALE		
m259-1	VLPDDEDARTIAELAKMDMF	ALGTD	AVASGETYGRVFADIFEL	SAALEGRAFKGMLKLT		
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1039>:

a259-1.seq

```

1  ATGATGATGC  ACGCTTCTGT  CCAAAGCCGT  TTCGCACCGA  TACTTTATGT
51  TTTGATTTTC  TTTGCCGTT  TTTTGACCGC  GCAAATCTGG  TTCAATCAGA
101 AAGCCTATAC  TGAAGAGCTG  CCTCCGCTTC  TGTCGCATT  GTCCGCCGTC
151 GCGCTGGTGT  GGCTGGCGTG  GCGGTTCTGT  TCGGCGCGTT  CAAAGGCTAA
201 GCGCGAAAAG  TTCTACCGCG  AAAAAATGAT  ACAGAACGAA  AGCATACACC
251 CCGTCTGCA  CGCTTCTTTG  CAACACTTGG  AACACAAGCC  GCAAATGCTC
301 GCCCTGCTGG  TCAAAAACCA  CGGCAAAGGG  ATGGCGGAAC  AGGTCAGGTT
351 CAAGGCGGAA  GTGCTGCCCG  ACGACGAAGA  CGCGCGCAGC  ATTGCCGCCG
401 AGTTGGCAAA  AATGGATATG  TTTGCATTGG  GGACGGACGC  GGTCGCCTCG
451 GGCGAAACCT  ATGGACGCGT  GTTCGCCGAT  ATTTTCGAGT  TGTCGGCGGC
501 TTTGGAAGGG  CGCGCGTTCA  AAGGAATGTT  GAAACTGACG  CGGGAATATA
551 AAAACATCTT  CGGCGATGCC  TGCCGTTCCG  AAACGGCGTT  GGAGTTGGGC
601 GCGCTCAATC  AGGCGTTGCA  GGAGATTTC  AAAACATCGG  AAAAGTCCAA
651 ACGGATATTT  TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1040; ORF 259-1.a>:

a259-1.pep

```

1  MMMHASVQSR  FAPILYVLIF  FAGFLTAQIW  FNQAYTEEL  PPLLSALSAV
51  ALVWLAWAFV  SARSKAKAEK  FYREKMIQNE  SIHPVLHASL  QHLEHKPQML
101 ALLVKNHGKG  MAEQVRFKAE  VLPDDEDART  IAAELAKMDM  FALGTDASAS
151 GETYGRVFAD  IFELSAALEG  RAFKGMLKLT  AEYKNIFGDA  CRSETALELG
201 ALNQAQLEIS  KTSEKSKRIF  Y*

```

a259-1/m259-1 99.5% identity in 221 aa overlap

	10	20	30	40	50	60
a259-1.pep	MMMHASVQSRFAPILYVLIF	FAGFLTAQIWFNQAYTEEL	PPLLSALS	SAVALVWLAWAFV		
m259-1	MMMHASVQSRFAPILYVLIF	FAGFLTAQIWFNQAYTEEL	PPLLSALS	SAVALVWLAWAFV		
	10	20	30	40	50	60
	70	80	90	100	110	120
a259-1.pep	SARSKAKAEK	FYREKMIQNESIHPVLHASL	QHLEHKPQMLALLVKNHGKGM	AEQVRFKAE		
m259-1	SARSKAKAEK	FYREKMIQNESIHPVLHASL	QHLEHKPQILALLVKNHGKGM	AEQVRFKAE		
	70	80	90	100	110	120
	130	140	150	160	170	180
a259-1.pep	VLPDDEDARTIAELAKMDMF	ALGTD	AVASGETYGRVFADIFEL	SAALEGRAFKGMLKLT		
m259-1	VLPDDEDARTIAELAKMDMF	ALGTD	AVASGETYGRVFADIFEL	SAALEGRAFKGMLKLT		
	130	140	150	160	170	180
	190	200	210	220		
a259-1.pep	AEYKNIFGDACRSETALELG	ALNQAQLEISK	TSEKSKRIFYX			
m259-1	AEYKNIFGDACRSETALELG	ALNQAQLEISK	TSEKSKRIFYX			
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1041>:

g260.seq

1	atgggtgctgg	gtgtagtatt	cgttgtcttt	cagccgttct	tcagcctgtt
51	tcgagcgttg	ttcgagggcg	gagtcggtat	agtcgagggg	gcgcacgatg
101	ccgctgaatg	cgacttcttg	tccgaggaat	ttacccgat	ccggatcggg
151	gatgttttta	ttgattcggg	aggtcagata	acggcccggt	tctttcaggc
201	ctttggtgta	aacctctggc	cccttggtgt	acagcagcct	gccttcccgg
251	cccgagagca	ggcgcgcgcg	ggcagcggtt	tcttgcggg	aaacgatttg
301	cgggtgctgc	ataaagacgc	ggtagaagtt	gacatcgatg	gcgggaatac
351	cgtatccgga	cacttcctta	tccggactga	ttttgacgac	ggggatgccg
401	tctgtctgtt	ccaagccgag	gcgcggttcg	ccgccaacgt	agcgcaacac
451	caataccttg	cccggataaa	tcaggtcggg	attgtggatt	tgatcccggg
501	tcgcgcccca	caggggggga	ccattgccac	gggctgtaca	ggtatttgcc
551	cgaataaccc	cacagggtgt	cgcctgtttt	ga	

This corresponds to the amino acid sequence <SEQ ID 1042; ORF 260.ng>:

g260.pcp

```

1  MGAGVVVFVF QPFSLFRAL FEGGVGIVEG AHDAAECDFL SEEFTIRIG
51  DVFIDSVGQI TARFFQAFGV NPGAFGVQQP AFRAREQARR GSGFFAGNDL
101 RVLHKDAVEV DIDGGNTVSG HFLIRTDFFD GDAVCLFOAE ARFAANVAQH
151 QYLARINQVG IVDLIPVRAP QGGTIATGCT GICPKYPTGC RPV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1043>:

m260.seq

1	ATGGGTGCGG	GTATGGTATT	CGTTGTCTTT	CGGCCGTTCT	CCAGCCTGTT
51	TCGAGCGTTG	TTCGAGGACA	GAGTCGGTAT	AGTCGAGGGA	GCGCACGATG
101	CCGCTGAATG	CGACTTCCTG	CCCAGGAAT	TTACCCGTAT	CCGGATCGGT
151	GATGTTTTTA	TTGATTCGGT	AGGTCAGGTA	GCGGCCCGGC	TCTTTCAGGC
201	CTTTGGTGTA	AACCCTGGTG	CCTTTGGTGT	ACAGCAGCCT	GCCTTCCGGG
251	CCCGAGw _r CA	sGCGCGGyGC	GGCAGCGGTT	TCTTTGCGGG	AAACGATTTG
301	CGGATGCCGC	ATAAAGATGC	GGTAGAAGTT	GACATCGATG	GCGGGAATAC
351	CGTATCCGGA	CACTTCCTTA	TCCGGACTCA	TTTGTACGAC	GGGGATGCCG
401	TCTGTCTGTT	CCAAGCCGAG	GCGCGGTTCT	CCGTCAACGT	GGCGCAACAC
451	CAATACTCTGG	TCCGGATAAA	TCAGGTCGGG	ATTGTGGATT	TGATCCCGGT
501	TCGCGTyCCA	CAG			

This corresponds to the amino acid sequence <SEQ ID 1044; ORF 260>:

m260 . pep

```

1  MGAGMVFVFV RPFSSLFRAL FEDRVGIVEG AHDAAECDFL PEEFTRIRIG
51  DVFIDSVGVQV AARLFQAFGV NPGAFGVQQP AFRARXXARX GSGFFAGNDL
101 RMPHKDAVEV DIDGGNTVSG HFLIRTHFDD GDAVCLFQAE ARFAVNVAQH
151 QYLVRINQVG IVDLIPVRVP Q

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 260 shows 89.5% identity over a 171 aa overlap with a predicted ORF (ORF 260.ng) from *N. gonorrhoeae*:

m260/g260

		10	20	30	40	50	60			
m260.pep		MGAGMV	FVFRFP	SSLF	FRALF	FEDRV	GIVEGAHDAECDFLPEEFTRIRIGDVFIDS	VGQV		
		:	:							
g260		MGAGV	VVVFQ	PFSS	LF	FRALF	EGGV	GIVEGAHDAECDFLSEEFTRIRIGDVFIDS	VGQI	
		10	20	30	40	50	60			
		70	80	90	100	110	120			
m260.pep		AARLFQ	AFGVN	PGAF	GVQ	QPAFR	ARXXAR	XSGGFFAGNDL	RMPHKDAVEVDIDGGNTV	SG
		: :								
g260		TARFFQ	AFGVN	PGAF	GVQ	QPAFR	AREQ	ARRGSGGFFAGNDL	RVLHKDAVEVDIDGGNTV	SG
		70	80	90	100	110	120			
		130	140	150	160	170				
m260.pep		HFLIR	THFDD	GDAV	CLFQ	AEARF	AVNVAQH	QYLVRIN	QVGIVDLIPVRVPQ	
g260		HFLIRT	DFDD	GDAV	CLFQ	AEARF	AANVAQH	QYLARIN	QVGIVDLIPVRAPQGGTIATGCT	
		130	140	150	160	170	180			

g260 GICPKYPTGCRPV
190

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1045>:

```
a260.seq
1  ATGGGTGCGG GTATGGTATT CGTTGTCTTT CGGCCGTTCT CCAGCCTGTT
51  TCGAGCGTTG TTCGAGGACA GAGTCGGTAT AGTCGAGGGA GCGCACGATG
101 CCGCTGAATG CGACTTCCTG CCCGAGGAAT TTACCCGTAT CCGGATCGGT
151 GATGTTTTTA TTGATTCGGT AGGTCAGGTA GCGGCCCGGC TCTTTCAGGC
201 CTTTGGTGTA AACCTGGTG CCTTGGTGT ACAGCAGCCT GCCTTCCGGG
251 CCCGAGAGCA GCGCGGGCGC GGCAGCGGTT TCTTGCGGG AAACGATTG
301 CGGGTGCCGC ATAAAGATGC GGTAGAAGTT GACATCGATG GCGGGAATAC
351 CGTATCCGGA CACTTCCTTA TCCGGACTCA TTTGACGAC GGGGATGCCG
401 TCTGTCTGTT CCAAGCCGAG GCGCGGTTTC CCGTCAACGT GCGCGAACAC
451 CAATACCTGG TCCAGATAAA TCAGGTCGGG ATTGTGGATT TGATCCCGGT
501 TCGCGTCCCA CAGGCGGCC. CCATTGCCAC GGGCTGTACA GGTATTTGCC
551 CGAAATGCCC CACAGGTGTG CGCCCTGTTT GA
```

This corresponds to the amino acid sequence <SEQ ID 1046; ORF 260.a>:

```
a260.pep
1  MGAGMVFVVF RPFSSLFRL FEDRVGIVEG AHDAAECDL PEEFTRIRIG
51  DVFIDSVQV AARLFQAFV NPGAFGVQQP AFRAREQARR GSGFFAGNDL
101 RVPHKDAVEV DIDGGNTVSG HFLIRTHFDD GDAVCLFQAE ARFAVNVAQH
151 QYLQINQVG IVDLIPVRVP QAAXIATGCT GICPKCPTGC RPV*
```

m260/a260 97.1% identity in 171 aa overlap

	10	20	30	40	50	60
m260.pep	MGAGMVFVVF RPFSSLFRL FEDRVGIVEG AHDAAECDL PEEFTRIRIG DVFIDSVQV					
a260	MGAGMVFVVF RPFSSLFRL FEDRVGIVEG AHDAAECDL PEEFTRIRIG DVFIDSVQV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m260.pep	AARLFQAFGVNPGA FG VQQP AFRARXXARXGSGFFAGNDLRMPHKDAVEVDIDGGNTVSG					
a260	AARLFQAFGVNPGA FG VQQP AFRAREQARRGSGFFAGNDLRVPHKDAVEVDIDGGNTVSG					
	70	80	90	100	110	120
	130	140	150	160	170	
m260.pep	HFLIRTHFDDGDAVCLFQAEARFAVNVAQH QYLVRINQVG IVDLIPVRVPQ					
a260	HFLIRTHFDDGDAVCLFQAEARFAVNVAQH QYLQINQVG IVDLIPVRVPPQAAXIATGCT					
	130	140	150	160	170	180
a260	GICPKCPTGCRPVX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1047>:

```
g261.seq
1  atggagcttg ggcataatcgt attccttggtg ctttgcgcg cgttcagacgg
51  cctttttact ttccagacat tccgccagcc cgcgttcg cgaagatacag
101 ctcgggcatt cgcggcagcc gccgacgata cccttgtagc aggtgtgggt
151 ctggttcg cgg atgtagtcca acacgccc attcgtccg aacgcccacg
201 tttgcgcctt ggtcaggtag atcagcgcg tgtggattt gaaatcgtag
251 tccatcgcca gattaagggg aacgttcatt gatttgacga acacgccg cgcg
301 gcagtcggga tagcccgaaa aatcggtttc gcacacgccc gcgatgatgt
351 gccggatacc ctgccctttg gcaaaaatgg cggcgtaaag caggaaaagc
401 gcgttacgcc cgtccacaaa ggtattggga acgcccgttg cggcggtttc
451 gatggcgggc gtttcgatgg cggcggtttc gtccatcagg gcgttggtgcg
501 taatctgccg catcaggctc aaatcgagta cggtttgact gacacccaaa
551 tcctgcgcga tccactctgc gcgttcagc tcgacggcat ggcgttgccc
601 gtatcggaag gtgatggctt ggacgttttc gcgccgtag gtttgattg
```

This corresponds to the amino acid sequence <SEQ ID 1048; ORF 261.ng>:

g261.pep

1	<u>MELGHIVFLV</u>	<u>LCARSDGLFT</u>	<u>FQTFRQPAFA</u>	QDTARAFAAA	ADDTLVAGVG
51	LFADVVOQAH	FVRQRPRRLR	GQVHQRRVDL	KIVVHRQIKG	NVHGFDDEHAA
101	AVGIARKIGF	AHARDDVPDT	LPFGKNGGVK	QEKRVTPVHK	GIGNAVVGGF
151	DGGVGFDGGF	VHQGVVNRNP	HQAQIEYGLT	DTQILRDPLC	AFQLDGMALP
201	VSEGDLDFV	APVGLDCLNQ	AGGRILTARE	DDQGLFV*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1049>:

m261.seq

1	ATGGAGCTTG	GGCATATCGT	ATTCTTATG	GTTTGC GCGT	GTTCAGACGG
51	CCTTTTTACT	TTCCAGATAT	TCCGCCAGCC	cGcGTTGCGC	CAAGATACAG
101	CTCGGGCATT	CGCGgCAGCC	GCCGACGATG	CCGTTATAGC	AGGTGTGGGT
151	TTGCTCGCGG	ATATAGTCCA	GCACGCCCAT	TTCTGTCGCC	AACGCCCCACG
201	TTTTCGCTTA	GGTCAGATAC	ATCAGCGGCG	TGTGGATTTG	AAAATCATAG
251	TCCATCGCTA	AATTAAGGGT	AACGTTTCATC	GATTTGACAA	ACACGTCGCG
301	GCAGTCGGGA	TAGCCGGAGA	AGTCGGTTTC	GCACACGCCC	GCGATGATGT
351	GCCGTATCCC	CTGCCCTTTG	GCGTAAATCG	CGGCATAGAG	CAGGAAAAGC
401	gCGTTGCGGC	CGTCTACAAA	GGTATTCGGA	ACGCCGTTTT	CGGCAGTTTC
451	GATGGCGGCG	GTGTCGTCCA	TCAGGGCATT	GTGCGTAATC	TGCCGCATCA
501	GgCTcAAGTC	GAGTACGGTT	TGTTTGACGC	CCAAATCCTG	CGCAATCCAG
551	CGGCGACGTT	CCAGCTCGAC	GCGATGGCGT	TGCCCGTATT	GGAAAGTAAT
601	GGCTTGACG	TTTTCGCGCC	CGTAGGTTTG	GATTGCCTGA	ATCAGGCAGG
651	TGGTCGAATC	CTGACCGCCC	GAAAAGATGA	CCAAGGCTTG	TTGTTTTGA

This corresponds to the amino acid sequence <SEQ ID 1050; ORF 261>:

m261.pep

1	<u>MELGHIVFLM</u>	<u>VCACSDGLFT</u>	<u>FQIFRQPAFA</u>	QDTARAFAAA	ADDAVIAGVG
51	LLADIVQHAH	FVRQRPRRLR	GQIHQRRVDL	KIIVHRQIKG	NVHRFDKHVA
101	AVGGIAGEVGF	AHARDDVPYP	LPFGVNRGIE	QEKRAAVYK	GIRNAVFGSF
151	DGGVGVHQGI	VRNLPQAQV	EYGLFDAQIL	RNPAGTFOLD	GMALPVLESN
201	GLDVFAVPGL	DCLNQAGGRI	LTARKDOGL	LV*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 261 shows 79.7% identity over a 237 aa overlap with a predicted ORF (ORF 261.ng) from *N. gonorrhoeae*:

m261/g261

		10	20	30	40	50	60
m261.pep		MELGHIVFLMVCACSDGLFTFQIFRQPAFAQD	TARAF	AAAADD	AVIAGVGLLADIVQHAH		
		::			::	::	
g261		MELGHIVFLVLCARSDGLFTFQTFRQPAFAQD	TARAF	AAAADDTLVAGVGLFADVVQHAH			
		10	20	30	40	50	60
		70	80	90	100	110	120
m261.pep		FVRQRPRRLRGQIHQRVVDLKIIVHRQIKGNVHR	FDKHVA	AVGIAGEVGF	AHARD	DDVPYP	
		::					
g261		FVRQRPRRLRGQVHQRRVDLKIVVHRQIKGNVHG	FDHAA	AVGIARKIG	AHARD	DDVPDT	
		70	80	90	100	110	120
		130	140	150	160	170	
m261.pep		LPFGVNRGIEQEKRVAAVYKGINNAVFGSFDGGGV	----	VHQGIVRNLP	HQAQV	EYGLF	
		::					
g261		LPFGKNGGVKQEKRVTPVHKGINAVVGGFDGGG	FDGGGFVHQGVVRNLP	HQAQIEYGLT			
		130	140	150	160	170	180
		180	190	200	210	220	230
m261.pep		DAQILRNPA	GTG	FQDGMALPV	LESNGLDVF	APVGLDCLN	QAGGRILTARKDDQGLLVX
		::	:	::	:	::	::
g261		DTQILRDPL	CAFQDGMALPV	SEGDGLDVF	APVGLDCLN	QAGGRILTAREDDQGLLVX	
		190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1051>:

```
a261.seq
1  ATGGAGCTTG GGCATATCGT ATTCCTTATG GTTTGCGCGT GTTCAGACGG
51  CCTTTTACT TTCCAGATAT TCCGCCAGCC CGCGTTCGCG CAAGATACAG
101 CTCGGGCATT CGCGGCAGCC GCCGACGATG CCGTTATAGC AGGTGTGGGT
151 TTGCTCGCGG ATATAGTCCA GCGCGCCCAT TTCGTCCGCC AACGCCCAG
201 TTTGCGCCTT GGTGAGATAC ATCAGCGGCG TGTGGATTTC AAAATCATAG
251 TCCATCGCCA GATTAAGGGT AACGTTTCATG GATTTGACAA ACACGTCACG
301 GCAGTCGGGA TAGCCGAGGA AGTCGGTTTC GCACACGCC CCGATGATGT
351 GCCGTATCCC CTGCCCTTTG GCGTAAATCG CGGCATAGAG CAGGAAAAGC
401 GCGTTGCGGC CGTCTACAAA GGTATTCGGA ACGCCGTTTT CCGCAGTTTC
451 GATGGCGGCG GTGTCGTCCA TCAGGCGATT GTGCGTAATC TGCCGCATCA
501 GGCTCAAGTC GAGTACGGTT TGTGTTGACGC CCAAATCCTG CGCAATCCAG
551 CGGGCACGTT CCAGCTCGAC GGCATGGCGT TGCCCGTATT GGAAAGTAAT
601 GGCTTGACG TTTTCGCGCC CGTAGGTTTG GATTGCCTGA ATCAGGCAGG
651 TGGTCGAATC CTGACCGCCC GAAAAGATGA CCAAGGCTTT TTGGTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1052; ORF 261.a>:

```
a261.pep
1  MELGHIVFLM VCACSDGLFT FQIFRQPAFA QDTARAFAAA ADDAVIAGVG
51  LLADIVQRAH FVRQRPRLRL GQIHQRRVDL KIIVHRQIKG NVHGFDPKHT
101 AVGIAGEVGF AHARDDVPYP LPFGVNRGIE QEKRVAAVYK GIRNAVFGSF
151 DGGGVVHQGI VRNLPHQAV EYGLFDAQIL RNPAGTFQLD GMALPVLESN
201 GLDVFAFVGL DCLNQAGGRI LTARKDDQGF LV*
```

m261/a261 97.8% identity in 232 aa overlap

	10	20	30	40	50	60
m261.pep	MELGHIVFLMVCACSDGLFTFQIFRQPAFAQDTARAFAAAADDAVIAGVG	LLADIVQRAH				
a261	MELGHIVFLMVCACSDGLFTFQIFRQPAFAQDTARAFAAAADDAVIAGVG	LLADIVQRAH				
	10	20	30	40	50	60
m261.pep	FVRQRPRLRLGQIHQRRVDLKIIVHRQIKGNVHRFDKHVA	AVGIAGEVGF				
a261	FVRQRPRLRLGQIHQRRVDLKIIVHRQIKGNVHRFDKHVT	AVGIAGEVGF				
	70	80	90	100	110	120
m261.pep	AVGIAGEVGF	AHARDDVPYP				
a261	AVGIAGEVGF	AHARDDVPYP				
	70	80	90	100	110	120
m261.pep	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGVVHQGI	VRNLPHQAV				
a261	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGVVHQGI	VRNLPHQAV				
	130	140	150	160	170	180
m261.pep	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGVVHQGI	VRNLPHQAV				
a261	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGVVHQGI	VRNLPHQAV				
	130	140	150	160	170	180
m261.pep	RNPAGTFQLDGMALPVLESNGLDVFAFVGLDCLNQAGGRI	LTARKDDQGLLVX				
a261	RNPAGTFQLDGMALPVLESNGLDVFAFVGLDCLNQAGGRI	LTARKDDQGLLVX				
	190	200	210	220	230	
m261.pep	RNPAGTFQLDGMALPVLESNGLDVFAFVGLDCLNQAGGRI	LTARKDDQGLLVX				
a261	RNPAGTFQLDGMALPVLESNGLDVFAFVGLDCLNQAGGRI	LTARKDDQGLLVX				
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1053>:

```
g263.seq
1  atggcacgtt taaccgtaca caccctcgaa accgccccg aagccgcca
51  accgcgctga gaggccgtac caaaaaaca cggctttatc cccaacctca
101 tcggcgctatt ggcaaagcgc cccgaagctt tggcgtttta ccaagaagtc
151 ggcaaagctca acgcccgcga cagcctgacc gccgcggaag tcgaagtgat
201 ccggatcatc gccgtccgca ccaaccaatg cagcttctgc gtggcagggc
251 acaccaaact cgcaacctg aaaaaactcc tgtccgagca atccctcaat
301 gccgccccgc ctttgccggc aggtaaatct gacgatgcc aactcggcgc
351 gcttgccgcc ttcacccaag ccgtaatggc gaaaaaaggc gcagtatccg
401 acgacgaact caacgccttc ctcgaagcgg gctacaaccg gcagcaggca
```

451 gtcgaagtcg taatgggcgt agccttggca actttgtgca actacgcaa
501 caacctcgcc caaacccaaa tcaaccccaa attgcaggca tacgcctaa

This corresponds to the amino acid sequence <SEQ ID 1054; ORF 263.ng>:

g263.pep

1	MARLTVHTLE	TAPEAAKPRV	EAVPKNNGFI	PNLIGVLANA	PEALAFYQEV
51	GKLNAANSLT	AGEVEVIRII	AVRTNQCSFC	VAGSTTKLATL	KKLLSEQSLN
101	AARALAAGKS	DDAKLGALAA	FTQAVMAKQ	AVSDDELNAF	LEAGYNRQQA
151	VEVVMGVALA	TLCNYANNLA	QTEINPKLQA	YA*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1055>:

```
m263.seq (partial)
1 ..GCAGCAGGCG AATTGACGA TGCCAAACTC GGCGCGCTCG CCGCCTTCAC
51 CCAAGCCGTA ATGGCGAAAA AAGGCGCGGT ATCCGACGAG GAACTCAAAG
101 CATTTTTCGA TGCGGGCTCA AACCACGACG AGGCAGTCGA AGTCGTGATG
151 GGCGT.AsyC TGGCAACCTT GTGCAACTCG GTCAACAACC TCGGACAAAC
201 CGAAATCAAC CCCGAATTGC AGGCTTACGC CTGA
```

This corresponds to the amino acid sequence <SEQ ID 1056; ORF 263>:

m263.pep (partial)

1	..GCAGCAGGCG	AATTTGACGA	TGCCAAACTC	GGCGCGCTCG	CCGCCTTCAC
51	CCAAGCCGTA	ATGGCGAAAA	AAGGCGCGGT	ATCCGACGAG	GAACTCAAAG
101	CATTTTTCGA	TGCGGGCTAC	AACCAAGCAG	AGGCAGTCGA	AGTCGTGATG
151	GGCGT.AsyC	TGCAACCCCT	GTGCAACTAC	GTCAACAACC	TCGGACAAAC
201	CGAAATCAAC	CCCGAATTGC	AGGCTTACGC	CTGA	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 263 shows 85.7% identity over a 77 aa overlap with a predicted ORF (ORF 263.ng) from *N. gonorrhoeae*:

m263 / g263

```
m263.pep      10          20          30  
               AAGEFDDAKLGALAAFTQAVMAKKGAVSDE  
g263           |||:|||||:|||||:|||||:|||||:  
       QCSFCVAGHTKLATLTKLLSEQSLNAARALAAGKSDDAKLGALAAFTQAVMAKKGAVSD  
             80        90        100         110        120        130  
  
              40        50        60        70  
m263.pep     ELKAFFDAGYNQQQAVEVVMGVXLATLCNYVNNLGQTETNPQLQAYAX  
            |:|::|:|||||:|||||:|||||:|||||:  
g263         ELNMFLEAGYNRQQAVEVVMGVALATLCNYANNLAQTETINPKLQAYAX  
             140        150        160        170        180
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1057>:

a263.seq

1	ATGGCACGTT	TAACCGTACA	CACCCTCGAA	ACCGCCCCCG	AAGCCGCCAA
51	AGCGCGCGTC	GAGGCGGTAC	TTCAAAACAA	CGGCTTTATC	CCCAACCTTA
101	TCGGCGTATT	ATCAAACGCC	CCCCAAGCCT	TGGCGTTTTA	CCAGAAGTC
151	GGCAAGCTCA	ACGCCGCCAA	CAGCCTGACC	GCCGGCGAAG	TCGAAGTAAT
201	CCAGATTATT	GCCGCCCGCA	CCAACCAATG	CGGCTTCTGC	TGGCAGGGC
251	ACACCAAAC	CGCAACCCTG	AAAAAACTCC	TTTCCGAACA	ATCCGTCAA
301	GCCGCGCGCG	CTTTGGCGGC	AGGCGAATTT	GACGATGCTA	AACTCGGCGC
351	GCTCGCCGCC	TTTACCCAAG	CCGTAATGCG	AAAAAAAGGC	GCGGTATCCG
401	ACGAGGAAC	CAAAGCATTT	TTTGATGCGG	GCTCAACCCA	GCAGCAGGCA
451	GTCGAAGTCG	TGATGGGCGT	AGCCTTGSCA	ACTTTGTGCA	ACTACGTCAA
501	CAACCTCGGA	CAAACCGAAA	TCAACCCCGA	ATTGCAGGCT	TACGCCTGA

This corresponds to the amino acid sequence <SEQ ID 1058; ORF 263.a>:

a263.pep

1	MARLTVHTLE	TAPEAAKARV	EAVLQNNGFI	PNLIGVLSNA	PEALAFYQEV
51	GKLNAANSLT	AGEVEVIQII	AARTNQCGFC	VAGHTKLATL	KKLLSEQSVK
101	AARALAAGEF	DDAKLAGLAA	FTQAVMAKKG	AVSDEELKAF	FDAGYNQQQA
151	<u>VEVVMGVALA</u>	<u>TLCNYVNNLG</u>	<u>QTEINPELOA</u>	YA*	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1059>:

This corresponds to the amino acid sequence <SEQ ID 1060; ORF 264.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1061>:

This corresponds to the amino acid sequence <SEQ ID 1062; ORF 264>:

BNSDOCID: <WO 9957280A2 | >

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 264 shows 91.6% identity over a 239 aa overlap with a predicted ORF (ORF 264.ng) from *N. gonorrhoeae*:

m264/g264

```

      10      20      30      40      50      60
m264 . pep  LTLTRKTLFLLTAAFGTHSLQTASADAVVKA EKLHASANRSYKVAGKRYTPKNQVAEFTQ
      |||||
g264        LTLTRKTLFLLTAAFGTHSLQTASADAVV KPEKLHASANRSYKVA-----EFTQ
      10      20      30      40

      70      80      90     100     110     120
m264 . pep  TGNASWYGGRFHFGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP
      |||||
g264        TGNASWYGGRFHFGRKTSGGDRYDMNAFTA AHKTLPIPSHVRVTNTKNGKSVIVRVNDRGP
      50      60      70      80      90     100

      130     140     150     160     170     180
m264 . pep  FHGNRIIDVSKAAQKLG FVNQGT AHVKIEQIVPGQSAPVAENKDIFIDLKSFSGTEHEAQ
      |||||
g264        FHGNRIIDVSKAAQKLG FVSQGT AHVKIEQIVPGQSAPVAENKDIFIDLKSFSGTEHEAQ
      110     120     130     140     150     160

      190     200     210     220     230     240
m264 . pep  AYLNQAAQNFAVSSSGTNLSVEKR RYEVVVKMGPF TSQERAAEAEQA RGMVRAVLTAGX
      |||||
g264        AYLNQAAQNFAASSSSPNLSVEKR RYEVVVKMGPFASQERAAEAEQA RGMVRAVLTSGX
      170     180     190     200     210     220

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1063>:

a264 . seq

```

1   TTGACTTTAA CCCGAAAAAC CCTTTTCCTC CTCACCGCCG CATTCCGGCAT
51  ACATTCCTTT CAGACGGCAT CCGCCGACGC AGTGGTCAGG GCAGAAAAAC
101 TGCACGCCTC CGCCAACCGC AGCTACAAAG TCGCCGGAAA ACGCTACACG
151 CCGAAAAAAC AAGTCGCCGA ATTCACGCAA ACCGGCAACG CCTCGTGGTA
201 CGGCGGCAGG TTTCACGGGC GCAAAACTTC CGGCGGAGAA CGATACGATA
251 TGAACGCCTT TACCGCCGCC CACAAAACCC TGCCCATCCC CAGCTATGTG
301 CGCGTAACCA ATACCAAAAA CGGCAAAAGC GTCATCGTCC GCGTCAACGA
351 CCGCGGCCCC TTCCACGGCA ACCGCATCAT CGACGTATCC AAAGCCGCCG
401 CGCAAAAATT GGGCTTTGTC AACCAAGGGA CGGCGCACGT CAAAATCGAA
451 CAAATCGTCC CGGGCCAATC CGCACC GGTT GCCGAAAACA AAGACATCTT
501 CATCGACTTG AAATCTTTTC GTACGGAACA CGAAGCACAA GCCTATCTGA
551 ACCAAGCCGC CCAAAACCTG GCTTCATCGG CATCAAACCC GAACCTCTCG
601 GTTGAAAAAC GCCGTTACGA ATACGTCGTC AAAATGGGAC CGTTTGCCTC
651 GCAGGAACGC GCCGCCGAGG CCGAAGCTCA GGCGCGCGGT ATGGTTCCGG
701 CGGTATTAAAC CGCCGGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1064; ORF 264.a>:

a264 . pep

```

1   LTLTRKTLFL LTAAFGIHSF QTASADAVVR AEKLHASANR SYKVAGKRYT
51  PKNQVAEFTQ TGNASWYGGR FHGRKTS GGE RYDMNAFTA HKTLPIPSYV
101 RVTNTKNGKS VIVRVNDRGP FHGNRIIDVS KAAQKLG FV NQGT AHVKIE
151 QIVPGQSAPV AENKDIFIDL KSFGTEHEAQ AYLNQAAQN ASSASNP NLS
201 VEKR RYEVV KMGPFASQER AAEEAEQA RGMVRAVLTAG*

```

m264/a264 96.2% identity in 239 aa overlap

```

      10      20      30      40      50      60
m264 . pep  LTLTRKTLFLLTAAFGTHSLQTASADAVVKA EKLHASANRSYKVAGKRYTPKNQVAEFTQ
      |||||
a264        LTLTRKTLFLLTAAFGIHSFQTASADAVVRAEKLHASANRSYKVAGKRYTPKNQVAEFTQ
      10      20      30      40      50      60

```

609

	70	80	90	100	110	120
m264 . pep	TGNASWYGGRFHGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
a264	TGNASWYGGRFHGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m264 . pep	FHGNRIIDVSKAAAQKLG FVNQGT AHVKIEQIVPGQSAPVAENK DIFIDLKSFSGTEHEAQ					
a264	FHGNRIIDVSKAAAQKLG FVNQGT AHVKIEQIVPGQSAPVAENK DIFIDLKSFSGTEHEAQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m264 . pep	AYLNQAAQNFAVSSSGTNLSVEKRRYEVVVKMGPF T SQERAAEAE AQARGMVR AVL TAGX					
a264	AYLNQAAQNLASSASNPNLSVEKRRYEVVVKMGPF ASQERAAEAE AQARGMVR AVL TAGX					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1065>:

```

m265 . seq
1   ATGTCGGTGA TTTTGCCGCC GACACGCGCC AACGCTGCTT TTTCGGCTTG
51  GGCGCGGCTG ATGATTTTGT CTTGTTTGTG GTGTTGGTGT GCGGCGTGTC
101 CGTGGTCGTC ATCGCCGTGT CCGTCGTGGT GGGCGAGCGC GGGGCGGAA
151 ATGCTCAGCA GTGCGGTTGC GCGGAGGTC AAGAGAAGGT GTTTGATGTT
201 CATAT .TTTT GCCTTTGTAA ATCGTGGGTT GGAAATGTG GATATTAATA
251 AGGTATCAAA TAACCGTCAG CCGGCGGTCA ATACCGCCCG AACCATAACCG
301 CGCGCCTGAG CTTCGGCTTC GCGGCGCGCT TCCTGCGAGG TAAACGGTCC
351 CATTTTGACG ACGTATTCGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1066; ORF 265>:

```

m265 . pep
1   MSVILPPTRA NAAFAWARL MILSCLLCWC AACPWSSSPC PSWWASAGAE
51  MLSSAVAAEV KRRCLMFI XFVNRGLNV DINKVSNNRQ PAVNTARTIP
101 RAXASASAAR SCEVNGPILT TYS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 265 shows 88.6% identity over a 123 aa overlap with a predicted ORF (ORF 265.ng) from *N. gonorrhoeae*:

m265/g265	10	20	30	40	50	60
m265 . pep	MSVILPPTRANA AFAWARLMILSCLLCWCAACPWSSSPCPSWWASAGA EMLSSAVAAEV					
g265	MSVILPPTRAQA AFAWARLMILSCLPCWCAACPWSSSPCPSWWASAGA EMPNSAVAAAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m265 . pep	KRRCLMFI XFAFVNRGLNV DINKVSNNRQ PAVNTARTI PRAXASASAARSCEVNGPILT					
g265	KRRCLMFI -FALVNQGLKNG DINKVSNNRQ PEVSTARTI PRACASASAARSCEANGPILT					
	70	80	90	100	110	
m265 . pep	TYSX					
g265	TYSX					
	120					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1067>:

a265.seq

```

1   ATGTCGGTGA TTTTGCCGCC GACACGCGCC AACGCTGCTT TTTCGGCTTG
51  GGCGCGGCTG ATGATTTTGT CTTGTTTGCT GTGTTGGTGT GCGGCGTGTC
101 CGTGGTCGTC ATCGCCGTGT CCGTCGTGGT GGGCGAGTGC GGGGGCGGAA
151 ATGCCCATCA GTGCGGTTGC GCGGCGGTC AAGAGAAGGC GTTTGAAGTT
201 CATTTTGTCT CCTGCGAAGT ATCTGGT... ..GGTGT TTGAAGGACG
251 TAAAGGCGGG ACATCAACCG GCGGTTAATA CCGCCGAAC CATACCGCGC
301 GCCTGAGCTT CGGCCTCGGC GCGCGTTCC TCGAGGCAA ACGGTCCCAT
351 TTTGACGACG TATTCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1068; ORF 265.a>:

a265.pep

```

1   MSVILPPTRA NAAFSAWARL MILSCLLCWC AACPWSSSPC PSWWASAGAE
51  MPISAVAAAV KRRRLKFIFA PAKYLX..XC LKDVKAGHQP AVNTARTIPR
101 A*ASASAARS CEANGPILTT YS*

```

m265/a265 79.7% identity in 123 aa overlap

	10	20	30	40	50	60
m265.pep	MSVILPPTRANAAFSAWARLMILSCLLCWCAACPWSSSPCPSWWASAGAEMLSAVAAEV					
a265	MSVILPPTRANAAFSAWARLMILSCLLCWCAACPWSSSPCPSWWASAGAEMPISAVAAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m265.pep	KRRCLMFIKFAFVNRGLNVNDINKVSNRQPAVNTARTIPRAXASASAARSCEVNGPILT					
a265	KRRRLKFI---FAPAKYLXXCLKDVKAGHQP VNTARTIPRAXASASAARSCEANGPILT					
	70	80	90	100	110	
m265.pep	TYSX					
a265	TYSX					
	120					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1069>:

g266.seq

```

1   agttcagacg gcatcgccgc cgacaatgcc caaacagaaa gcccacatcatg
51  accgcatcca tgtacatcct tttggtcttg gcactcatct ttgccaacgc
101 ccccttcctc acgaccagac tggtcgcgct ggccgcgctc aagcgcaaac
151 atttcggaca ccacctgatc gagctggcgg cagggttcgc gctgaccgcc
201 tctcttgccct acatcctcga atcccgctgc ggagcggtac acaatcaggg
251 ttgggagttt tacgccaccg tcgtctgcct gtacctcatt ttcgccttcc
301 cgtgtttcgt gcggcggtat ttttggcaca cgcgcaacag ggaataa

```

This corresponds to the amino acid sequence <SEQ ID 1070; ORF 266.ng>:

g266.pep

```

1   MQFRRHRRRO CPNRKPIMTA SMYILLVLAL IFANAPFLT RLFGVAALKR
51  KHFGHHLIEL AAGFALTASL AYILES RAGA VHNQGW EFWA TVVCLYLIFA
101 FPCFVRRYFW HTRNRE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1071>:

m266.seq

```

1   ATGCCGTTCC GCAACGCGtT cAGACGGCAT CGCCGCCGAC AACGCCTAAA
51  CAGAAAGCCC ACCATGACCG CATCCATGTA CATCCTTTTG GTCTTGGCAC
101 TCATCTTTGC CAACGCCCCC TTCCTCACGA CCAGACTGTT CGGCGTGGCC
151 rCACTCAAGC GCAAACATTT CGGACACCAC ATGATCGAGC TGGCGGCAGG
201 TTTCGCGCTG ACCGCCGTTT TTGCCTACAT CCTsGAATCC CGTGCAAGAT
251 CGGTACACGA TCAGGGTTGG GAGTTTTATG CCACAGTCGT CTGCCTGTAC
301 CTGATTTTTG CGTTTCCATG TTTTGTGTGG CGGTATTTTT GGCACACGCG
351 CAACAGGGAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 1072; ORF 266>:

```
m266.pep
  1  MPFRNAFRRH RRRQRLNRKP TMTASMYILL VLALIFANAP FLTTRLFGVA
 51  XLKRKHFGHH MIELAAGFAL TAVLAYILES RAGSVHDQGW EFYATVVCLY
101  LIFAFPCFVW RYFWHTRNRE *
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 266 shows 92.1% identity over a 114 aa overlap with a predicted ORF (ORF 266.ng) from *N. gonorrhoeae*:

m266/g266

```

              10      20      30      40      50      60
m266.pep      MPFRNAFRRHRRRQRLNRKPTMTASMYILLVLALIFANAPFLTTRLFGVAXLKRKHFGHH
              |||||  |||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g266           MQFRRHRRRQCPNRKPIMTASMYILLVLALIFANAPFLTTRLFGVAALKRKHFGHH
              10      20      30      40      50

              70      80      90      100     110     120
m266.pep      MIELAAGFALTAVLAYILES RAGSVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNREX
              :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||
g266           LIELAAGFALTASLAYILES RAGAVHNQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNREX
              60      70      80      90      100     110
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1073>:

```
a266.seq
  1  ATGCCGTTCC GCAATGCGTT CAGACGGCAT CGCCGCCGAC AATGCCCAAA
 51  CAGAAAGCCC GCCATGACCG CATCCATGTA CATCCTTTTG CTGCTTGCTT
101  TGATTTTTCG CAACGCCCCC TTCCTCACGA CCAAGCTGTT CGGCATCGTA
151  CCGCTCAAGC GCAAACATTT CGGACACCAC CTGATCGAGC TGGCGGCAGG
201  TTTCGCGCTG ACCGCCGTTT TTGCCTACAT CCTCGAATCC CGTGCGGGAG
251  CGGTACACGA TCAGGGTTGG GAGTTTACG CCACCGTCGT CTGCCTGTAC
301  CTGATTTTTC CGTTTCCCTG TTTCGTGTGG CGGTATTTT GGCACACGCG
351  CAACAGGGAA TAG
```

This corresponds to the amino acid sequence <SEQ ID 1074; ORF 266.a>:

```
a266.pep
  1  MPFRNAFRRH RRRQCPNRKP AMTASMYILL LLALIFANAP FLTTKLFGIV
 51  PLKRKHFGHH LIELAAGFAL TAVLAYILES RAGAVHDQGW EFYATVVCLY
101  LIFAFPCFVW RYFWHTRNRE *
```

m266/a266 91.7% identity in 120 aa overlap

```

              10      20      30      40      50      60
m266.pep      MPFRNAFRRHRRRQRLNRKPTMTASMYILLVLALIFANAPFLTTRLFGVAXLKRKHFGHH
              |||||  |||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a266           MPFRNAFRRHRRRQCPNRKPAMTASMYILLLLALIFANAPFLTTLKLFIVPLKRKHFGHH
              10      20      30      40      50      60

              70      80      90      100     110     120
m266.pep      MIELAAGFALTAVLAYILES RAGSVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNRE
              :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||  :|||
a266           LIELAAGFALTAVLAYILES RAGAVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNRE
              70      80      90      100     110     120
```

```
m266.pep      X
              |
a266           X
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1075>:

g267.seq

g267.pcp

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1077>:

1	GTGCAAGTCG	CCTTTTTTCT	CGCCGTGGTA	TTCAAAAATA	TGGGTTTCCA
51	CAATCGCATC	AGTCGGGCAT	GCCTCTTCGC	AGAAACCGCA	GAAGATGCAC
101	TTGGTCAGGT	CGATGTCGTA	ACGCTTGGTG	CGGCGCGTAC	CGTCTTCACG
151	TTCTTCCGAT	TCGATGTTAA	TCGCCATTGC	CGGACACACT	GCCTCACACA
201	ACTTACACGC	GATACACCGC	TCTTCGCCGT	TCGGATACCG	CcGCTGCGCG
251	TGCAGACCCG	GAAACCGCAC	GGATTGCGGC	GTTTTCTCTT	CGGGGAAATA
301	AATTGTGTCT	TTGCGGGCGA	AAGAGTTTTT	GACGCTTACG	CCCATACCTT
351	TTACCAATTC	GCCAAGCAGA	AAGGTTTTTA	CTAA	

m267.pcp

Computer analysis of this amino acid sequence gave the following results:

ORF 267 shows 82.7% identity over a 127 aa overlap with a predicted ORF (ORF 267.ng) from *N. gonorrhoeae*:

```

m267.pep      10      20      30      40      50      60
               VQVAFFLAVVFKNMGFHNRI SRACLFAETAEDALGQVDVVTLGAARTVFTFFRFDVNRHC
               : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
g267          10      20      30      40      50      60
               MQVAFFLAVVFKNMGFHNRI GRAGLFAETAEDALGQVDVVTLGAAGAVFAFFRFDVDRHC

m267.pep      70      80      90      100     110     120
               RTHCLTQLTRDTPLFAVRIPPLRVQTAETHGLRRFLFG EINC VFAGEKV FERYAHTFYQF
               ||| : |||| : ::|| ||||| : ||||| : ||||| : ||||| : ||||| : |||||
g267          70      80      90      100     110     120
               RTHRLAQFTRDAAFLSVRK TALRVQTAETHGLRRFLFG KINC VFAGKKV FERYAHAFDQF

m267.pep      AKQKGFFX
               |||||
g267          AKQKGFFX

```

a267.seq

BNSDOCID: <WO__9957280A2_1>

This corresponds to the amino acid sequence <SEQ ID 1080; ORF 267.a>:

```
m267.pep
  1  VQVAFFLAVV FKNMGFHNRI GRAGFFAETA EDALGQVDVV TLGAARAVFA
 51  FFRFDVDRHC GANGFTQFTR DAAFLAVWIT ALRVQTAETH GLRRFLFGKI
101  NRVFAGKKVF ERYAHTFYQF AKQKGFY*
```

m267/a267 82.7% identity in 127 aa overlap

	10	20	30	40	50	60
m267.pep	VQVAFFLAVV	FKNMGFHNRI	SRACLFAETA	EDALGQVDVV	TLGAARTV	FTFFRFDVNRHC
a267	VQVAFFLAVV	FKNMGFHNRI	GRAGFFAETA	EDALGQVDVV	TLGAARAV	FAFFRFDVDRHC
	10	20	30	40	50	60
	70	80	90	100	110	120
m267.pep	RTHCLTQLTRD	TPFAVRI	PPLRVQTAETH	GLRRFLFGE	INCVFAGEK	VFERYAHTFYQF
	:::	:::				
a267	GANGFTQFTR	DAAFLAVWIT	ALRVQTAETH	GLRRFLFGK	INRVFAGKK	VFERYAHTFYQF
	70	80	90	100	110	120
m267.pep	AKQKGFYX					
a267	AKQKGFYX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1081>:

```
G268.seq
  1  atgaaaaaaa atttaccgcg actggcattg gcaagtatgc tgattttgtc
 51  gggctgcgac cgtttgggaa taggcaaccc gttttccgga aaggaaattt
101  cctgcggaag cgaagagact aaagagatgt tgggtcaaact ggtccgcgac
151  aatgtcgaag gtgaaaccgt caaaactttt gacgacgacg cattcaaaga
201  ccaagcattt gccgatatcg gcatatcgca tatccgcaga atggtcgaac
251  gtttgggcat aaccgtcgat gaagtccgaa ctaccgagaa aaccgacacg
301  tccagcaaac tcaaatgtga agccgcgtta aaactggacg tgcccgcacg
351  tgttgtcgat tatgccgtcg ccgccaacca atctataggc aacagccata
401  agaaaacgcc cgactttttt gaaccctact accgcaaaga aggcgcgtat
451  tatgtcaaaa ctatttctta cagcgtccag ccgacagacg acaaaagcaa
501  aatctttgcc gaactcagtc aggcacacga tatcatccat ccgctcagcg
551  agctgggtgtc tatggcactg attaaagagc cggttgacaa agcgaaacaa
601  aggaacgaaa aacttgaagc ggcagaagcc accgcgcagg aagcgaggga
651  ggcagaagaa gcggcggcgc aggaggcatt gggctggggg caggaagccg
701  cccgcgtatc cgaatgggaa gaacgctaca agctgtcgcg cagcgagttc
751  gagcagtttt ggaaaggatt gcctcaaact gtacagaata agctgcaagc
801  ctgcgcagaaa acatggaaaa gcggtatgga caagatctgt gccacaatat
851  cgaaagccga aggtgaaacg ccaaaccgca taaaagtcag tgagttggcg
901  tgtaaaacgg cagaaaccga agcacgcttg gaagagctgc acaaccgtaa
951  aaaagccctt atcgacgaaa tggtcaggga agaggacaag aaagaactgc
1001 caaagcggct ctga
```

This corresponds to the amino acid sequence <SEQ ID 1082; ORF 268.ng>:

```
m268.pep
  1  MKKNLPALAL ASMLILSGCD RLGIGNPFSG KEISCGSEET KEILVKLVDR
 51  NVEGETVKTF DDDAFKDQAF ADIGISHIRR MVERLGITVD EVRTTEKTD
101  SSKLKCEAAL KLDVDDVVD YAVAANQSIG NSHKKTPDFF EPYRKEGAY
151  YVKTISYSVQ PTDDKSKIFA ELSQAHDIIH PLSELVSMAL IKEPLDKAKQ
201  RNEKLEAAEA TAQEAREAE AAAQEALGRE QEAAVSEWE ERYKLSRSEF
251  EQFWKGLPQT VQNKLQASQK TWKSGMDKIC ANNAKAEGET PNGIKVSELA
301  CKTAETEARL EELHNRKKAL IDEMVREEDK KELPKRL*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1083>:

```
m268.seq (partial)
  1  ..ATGGCACTGA TTAAAGAGCC GTTGACAAA GTGAAACAAA GGAACGAAGA
```

```

51   ACTTGAAGCG GCAGAAGAAG CGGCGGCGCA GGAGGCATTG GGTCTGGGAGC
101  AGGAAGCCGC CCGCGTATCC GAATGGGAAG AACGCTACAA GCTGTCGCGC
151  AG.CAGTTCG AGCAGTTCTG GAAAGGATTG CCTCAAACCG TACAGAATAA
201  GCTGCAACCh TCACAGAAAA CATGGAAAAG CGGGATGGAT AAAATCTGTG
251  CCAACAATGC GAAAGCTGAA GGTAAAACGC CAAACGGCAT AAAATTCAGC
301  GAACTGGCAT GCAAAACGGC GAAAACCGAA GCACGCTTGG AAGAGCTGCA
351  CAACCGTAAA AAAGCCCTTA TCGACGAAAT GGyCAGGGAA GCGGACAmGA
401  AAGAACTGTC AAAGCGGCTs TGA

```

This corresponds to the amino acid sequence <SEQ ID 1084; ORF 268>:

```

m268.pep (partial)
1   .MALIKEPLDK VKQRNEELEA AEEAAAQEAL GREQEAAARVS EWEERYKLSR
51  XQFEQFWKGL POTVQNKLP SQKTWKSGMD KICANNAKAE GKTPNGIKFS
101 ELACKTAKE ARLEELHNRK KALIDEMXRE ADKKELSKRL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 268 shows 86.0% identity over a 150 aa overlap with a predicted ORF (ORF 268.ng) from *N. gonorrhoeae*:

m268/g268

```

m268.pep                               10      20
                                     MALIKEPLDKVKQRNEELEAAE-----
g268                                |||||:|||||:|||||
SVQPTDDKSKIFAELSQAHDIIHPLSELVSMALIKEPLDKAKQRNEKLEAAEATAQEARE
160      170      180      190      200      210

m268.pep                               30      40      50      60      70      80
--EAAAQEALGREQEAAARVSEWEERYKLSRSQFEQFWKGLPQTVQNKLP SQKTWKSGMD
g268                                |||||:|||||:|||||:|||||:|||||:|||||
AEEAAAQEALGREQEAAARVSEWEERYKLSRSEFEQFWKGLPQTVQNKLP SQKTWKSGMD
220      230      240      250      260      270

m268.pep                               90      100     110     120     130     140
KICANNAKAE GKTPNGIKFSELACKTAKEARLEELHNRKKALIDEMXREADKKELSKRLX
g268                                |||||:|||||:|||||:|||||:|||||:|||||
KICANNAKAEGETPNGIKVSELACKTAETEARLEELHNRKKALIDEMVREEDKKELPKRLX
280      290      300      310      320      330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1085>:

```

a268.seq
1   ATGGCACTGA TTAAAGAGCC GTTGGACAAA GCGAAACAAA GGAACGAAGA
51  ACTTGAAGCG GCAGAAGAAG CGGCGGCGCA GGAGGCATTG GGTCTGGGAGC
101 AGGAAGTCGA CCGCGTATCC GAATGGGAAG AACGCTACAA GCTGTCGCGC
151 AGCGAGTTCG AGCAGTTCTG GAAAGGATTG CCTCAAACCG TACAGAATAA
201 GCTGCAAGCC TCACAGAAAA CATGGAAAAG CGGGATGGAT AAAATCTGTG
251 CCAACAATGC GAAAGCTGAA GGTGAAAACGC CAAACGGCAT AAAATTCAGC
301 GAACTGGCAT GCAAAACGGC GGAAACCGAA GCACGCTTGG AAGAGCTGCA
351 CAACCGTAAA AAAGCCCTTC TCGACGAAAT GGCCAGGGAA GCGGACAAGA
401 AAGAACTGCC AAAGCGGCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1086; ORF 268.a>:

```

a268.pep
1   MALIKEPLDK AKQRNEELEA AEEAAAQEAL GREQEVDRVS EWEERYKLSR
51  SEFEQFWKGL POTVQNKLP SQKTWKSGMD KICANNAKAE GETPNGIKFS
101 ELACKTAETE ARLEELHNRK KALLDEMARE ADKKELPKRL *

```

m268/a268 91.4% identity in 140 aa overlap

```

m268.pep          10      20      30      40      50      60
MALIKEPLDKVKQRNEELEAAEEAAAQEALGREQEAAARVSEWEERYKLSRXQFEQFWKGL
|||||:|||||:|||||:|||||:|||||:|||||
a268              MALIKEPLDKAKQRNEELEAAEEAAAQEALGREQEVDRVSEWEERYKLSRSEFEQFWKGL

```

615

	10	20	30	40	50	60
	70	80	90	100	110	120
m268.pep	PQTVQNKLPQSQKTWKSMDKICANNAKAEGKTPNGIKFSELACKTAKTEARLEELHNRK					
a268	PQTVQNKLPQSQKTWKSMDKICANNAKAEGKTPNGIKFSELACKTAKTEARLEELHNRK					
	70	80	90	100	110	120
	130	140				
m268.pep	KALIDEMXREADXKELSKRLX					
	:					
a268	KALLDEMAREADKKELPKRLX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1087>:

m268-1.seq

```

1  GTGCAATCCC GATATGATGG TTTGCATAAA TTAAACATA TATGTTCCGC
51  AGCTATGGCA CTGATTAAAG AGCCGTTGGA CAAAGTGAAA CAAAGGAACG
101 AAGAACTTGA AGCGGCAGAA GAAGCGGCGG CGCAGGAGGC ATTGGGTCGG
151 GAGCAGGAAG CGCCCGCGT ATCCGAATGG GAAGAACGCT ACAAGCTGTC
201 GCGCAGCGAG TTCGAGCAGT TCTGGAAAGG ATTGCCTCAA ACCGTACAGA
251 ATAAGCTGCA AGCCTCACAG AAAACATGGA AAAGCGGGAT GGATAAAATC
301 TGTGCCAACA ATGCGAAAGC TGAAGGTAAA ACGCCAAACG GCATAAAATT
351 CAGCGAACTG GCATGCAAAA CGGCGAAAAC CGAAGCACGC TTGGAAGAGC
401 TGCACAACCG TAAAAAAGCC CTTATCGACG AAATGGCCAG GGAAGCGGAC
451 AAGAAAGAAC TGTCAAAGCG GCTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1088; ORF 268-1>:

m268-1.pep

```

1  VQSRDGLHKH FKHICSAAMA LIKEPLDKVK QRNEELEAAE EAAAEALGR
51  EQEAAARVSEW EERYKLSRSE FEQFWKGLPQ TVQNKLPQASQ KTWKSGMDKI
101 CANNAKAEGK TPNGIKFSEL ACKTAKTEAR LEELHNRKKA LIDEMAREAD
151 KKELSKRL*

```

m268-1/g268 82.3% identity in 164 aa overlap

		10	20	30	
m268-1.pep		VQSRDGLHKHFKHICSAAMALIKEPLDKVKQRNE			
		:	:	:	:
g268	KEGAYVYKTISYSVQPTDDKSKIFAELSQAHDIHPLSELVS--MALIKEPLDKAKQRNE				
	150 160 170 180 190 200				
	40 50 60 70 80				
m268-1.pep	ELEAAE-----EAAAEALGREQEAARVSEWEERYKLSRSEFEQFWKGLPQTVQN				
	:				
g268	KLEAAEATAQEAREAEAEAAAEALGREQEAARVSEWEERYKLSRSEFEQFWKGLPQTVQN				
	210 220 230 240 250 260				
	90 100 110 120 130 140				
m268-1.pep	KLQASQKTWKSMDKICANNAKAEGKTPNGIKFSELACKTAKTEARLEELHNRKKALIDE				
g268	KLQASQKTWKSMDKICANNAKAEGKTPNGIKVSELACKTAKTEARLEELHNRKKALIDE				
	270 280 290 300 310 320				
	150 159				
m268-1.pep	MAREADKKELSKRLX				
	:				
g268	MVREEDKKELPKRLX				
	330				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1089>:

a268-1.seq

```

1  GTGCAATCCC GATATGATGG TTTGCATAAA TTAAACATA TATGTTCCGC
51  AGCTATGGCA CTGATTAAAG AGCCGTTGGA CAAAGCGAAA CAAAGGAACG
101 AAGAACTTGA AGCGGCAGAA GAAGCGGCGG CGCAGGAGGC ATTGGGTCGG
151 GAGCAGGAAG TCGACCGCGT ATCCGAATGG GAAGAACGCT ACAAGCTGTC
201 GCGCAGCGAG TTCGAGCAGT TCTGGAAAGG ATTGCCTCAA ACCGTACAGA
251 ATAAGCTGCA AGCCTCACAG AAAACATGGA AAAGCGGGAT GGATAAAATC
301 TGTGCCAACA ATGCGAAAGC TGAAGGTGAA ACGCCAAACG GCATAAAATT
351 CAGCGAACTG GCATGCAAAA CGGCGGAAAC CGAAGCACGC TTGGAAGAGC

```

401 TGCACAACCG TAAAAAGCC CTTCTGACG AAATGGCCAG GGAAGCGGAC
451 AAGAAAGAAC TGCCAAAGCG GCTCTGA

This corresponds to the amino acid sequence <SEQ ID 1090; ORF 268-1.a>:

a268-1.pep

1 VQSRDGLHK FKHICSAAMA LIKEPLDKAK QRNEELEAAE EAAAEALGR
51 EQEVDVSEW EERYKLSRSE FEQFWKGLPQ TVQNKLOASQ KTWKSGMDKI
101 CANNAKAEGE TPNGIKFSEL ACKTAETEAR LEELHNRKKA LDEMAREAD
151 KKELPKRL*

a268-1/m268-1 95.6% identity in 158 aa overlap

	10	20	30	40	50	60
a268-1.pep	VQSRDGLHKFKHICSAAMALIKEPLDKAKQRNEELEAAE	EAQALGREQEVDRVSEW				
m268-1	VQSRDGLHKFKHICSAAMALIKEPLDKVQRNEELEAAE	EAQALGREQEAARVSEW				
	10	20	30	40	50	60
a268-1.pep	EERYKLSRSEFEQFWKGLPQTVQNKLOASQKTWKS	GMKICANNAKAEGETP	NGIKFSEL			
m268-1	EERYKLSRSEFEQFWKGLPQTVQNKLOASQKTWKS	GMKICANNAKAEGKTP	NGIKFSEL			
	70	80	90	100	110	120
a268-1.pep	EERYKLSRSEFEQFWKGLPQTVQNKLOASQKTWKS	GMKICANNAKAEGETP	NGIKFSEL			
m268-1	EERYKLSRSEFEQFWKGLPQTVQNKLOASQKTWKS	GMKICANNAKAEGKTP	NGIKFSEL			
	70	80	90	100	110	120
a268-1.pep	ACKTAETEARLEELHNRKKALLDEMAREADKKELPKRLX					
m268-1	ACKTAETEARLEELHNRKKALLDEMAREADKKELSKRLX					
	130	140	150	159		
a268-1.pep	ACKTAETEARLEELHNRKKALLDEMAREADKKELPKRLX					
m268-1	ACKTAETEARLEELHNRKKALLDEMAREADKKELSKRLX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1091>:

g269.seq

1 atggtttggc gtgtgaattg cgcggaacg gcggcgctga ttttttcgct
51 cagcccttgg atttgggcgg tgggtggtg gtggtcgcgg tcggtttttt
101 cctgcaaacc ttgcgccagc cttgacgcgt ccagtgcgcc ggcgttggcg
151 gtttcgccgt gggactttat ccggaacacg gcttcgcccc aggtgtcggc
201 ggctttgatg cacagtttta aaaccagggc tttggggcgg ttttctgcgc
251 cgcccggttc cattttgctg tccaatcgcg ggggttaaaaa accgttgctg
301 tttaagtcgc cgtccgtcca agtcgatacg agcgcgcttc tttgccttcc
351 attgcggtct tggtaa

This corresponds to the amino acid sequence <SEQ ID 1092; ORF 269.ng>:

g269.pep

1 MVWRVNCAAT AALIFSSSPW IWAVVWWSR SAFSCKPCAS LDASSAPALA
51 VSPWDFIRNT ASPKVSAAIM HSFKTRALGR FSAPPVAILL SNRGVKKPLS
101 FKSPSVQVDT SALLCLSLRS S*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1093>:

m269.seq

1 ATGTTTGGC GTGTGAATTG CGCGGCAACG GCGGTGCTGA TTTTTCGTC
51 CAGCCCTTGG ATTTGGGCGG CGGTGTGGGT GTGCTCTCGG TCGGCTTTGT
101 CTTGCAAACC TTGCGCCaCG TGCCCGCGTC CAGCGCTGCG GTTGATGGTT
151 TCGCCGTGGG ACTTTATCCA AAACACGGCT TCGCCCAAGG TGTCGGCGGC
201 TTTGATGCAC AGTTTAAAA CCAGGGCTTT GGGGCGGTTT TCGTCGCCGC
251 CTGTCGCCAT TTTGCTGTCC GAGCGCGGGG TTAAAAAGCC GTTGTCGTTT
301 AAATTTTCGT CCGTCCAAGT CGATACGAGC GCGCTTCTCT GCCTTTCGTT
351 GCGGTCTTCG TAA

This corresponds to the amino acid sequence <SEQ ID 1094; ORF 269>:

m269.pep

1 MVWRVNCAAT AVLIFSSSPW IAAVWWSR SALSCKPCAT CPRPAPALMV
51 SPWDFIQNTA SPKVSAAIMH SFKTRALGRF SSPPVAILLS ERGVKKPLSF
101 KFSSVQVDT SALLCLSLRS *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 269 shows 87.6% identity over a 121 aa overlap with a predicted ORF (ORF 269.ng) from *N. gonorrhoeae*:

```

m269.pep  MVWRVNCAATAVLIFSSSPWIWAAVVWWSRSALSCKPCATCP-RPAPALMVSPWDFIQNT  59
          |||||||||:|||||||:|||||||:|||||||:  ||| |||||||:|
g269      MVWRVNCAATAALIFSSSPWIWAVVWWSRSASFCKPCASLDASSAPALAVSPWDFIRNT  60

m269.pep  ASPKVSAAALMHSEFKTRALGRFSSPPVAILLSERGVKKPLSFKFSSVQVDTALLCLSLRS  119
          |||||||||:|||||||:|||||||:|||||||:  ||| |||||||:|
g269      ASPKVSAAALMHSEFKTRALGRFSAPPVAILLSNRGVKKPLSFKSPSVQVDTALLCLSLRS  120

m269.pep  SX  121
          ||
g269      SX  122

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1095>:

```

a269.seq
1  ATGGTTTGGC GTGTGAATTG CGCGGCAACG GCGGTGCTGA TTTTTCGTC
51 CAGCCCTTGG ATTTGGGCGG CGGTGTGGGT GTGGGCGCGG TCTGCTTTGT
101 CTTGGAGGTT TTGCGCCAGC GTGCCCGCGT CCAGCGCGCC GGC GTTGACG
151 GTTTCGCCGT GGGACTTTAT CCAGAACACG GCTTCGCCCCA AGGTGTCGGC
201 GGCTTTGATG CACAGTTTTA AAACCCAGGC TTTGGGGCGG TTTTCGTCGC
251 CGCCTGTCGC CATTTTGCTG TCCGGGCGCG GGGTTAAAAA GCCGTTGTCG
301 TTAAATTTT CGTCCGTCCA AGTCGATACG AGCGCGCTTC TCTGCCTTTC
351 GTTGTGGTCT TCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1096; ORF 269.a>:

```

a269.pep
1  MVWRVNCAAT AVLIFSSSPW IWA AVVWWAR SALSWRFCAS VPASSAPALT
51 VSPWDFIQNT ASPKVSAAAL HSEFKTRALGR FSSPPVAILL SGRGVKKPLS
101 FKFSSVQVDT SALLCLSLWS S*

```

m269/a269 90.1% identity in 121 aa overlap

```

m269.pep  10 20 30 40 50 59
          MVWRVNCAATAVLIFSSSPWIWA AVVWWSRSALSCKPCATCP-RPAPALMVSPWDFIQNT
a269      10 20 30 40 50 60
          MVWRVNCAATAVLIFSSSPWIWA AVVWWSRSALSCKPCATCP-RPAPALMVSPWDFIQNT

m269.pep  60 70 80 90 100 110 119
          ASPKVSAAALMHSEFKTRALGRFSSPPVAILLSERGVKKPLSFKFSSVQVDTALLCLSLRS
a269      60 70 80 90 100 110 120
          ASPKVSAAALMHSEFKTRALGRFSSPPVAILLSERGVKKPLSFKFSSVQVDTALLCLSLRS

m269.pep  120
          SX
a269      120
          SX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1097>:

```

g270.seq
1  atgaataaaa accgcaaatt actgcttgcc gcactgctgc tgactgcctt
51 tgccgccttc aagctcgttt tgttgcaatg gtggcaggcg cagcagccgc
101 aagccgtggc ggcgcaatgc gatttgaccg aggggtgcac gctgccggac
151 ggaagccgtg tccgcgcccgc cgcggtttca accaaaaaac cgtttgatat
201 ttatatcgaa cacgcgcccgc ccggcacgga acaggtcagc atcagcttca
251 gtatgaaaaa tatggatatg gggttcaacc gctatatgtt cgagcggcaa
301 ccgtcgggga cttggcaggc agcacgcacg cgcctgcccg tctgtgtcga
351 aggcaggcgc gattttacgg cggacattac aatcggcagc cggacatttc
401 agacggcatt taccgcccga taa

```

This corresponds to the amino acid sequence <SEQ ID 1098; ORF 270.ng>:

g270.pep

```

1  MNKNRKLLLA ALLLTAFAAF KLVLLQWWQA QQPQAVAAQC DLTEGCTLPD
51  GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ
101 PSGTWQAARI RLPVCVEGRR DFTADITIGS RTFQTAFTAE*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1099>:

m270.seq

```

1  ATGAATAAAA ACCGTAAATT ACTGCTTGCC GCACTGCTGC TGATTGCCTT
51  TGCCGCCGTC AAGCTCGTTT TGTGCAATG GTGGCAGGCG Ca. CAGCCGC
101 AAGCTGTGGC GGCGCAATGC GATTTGACCG AGGGTTGCAC GCTGCCGGAC
151 GGAAGCCGCG TCCGCGCCGC CGCCTTTTCA ACCAAAAAAC CGTTTGATAT
201 TTATATCGAA CACGCGCCCG CCGGCACGGA ACAGGTCAGC ATCAGCTTCA
251 GTATGAAAAA TATGGATATG GGTTCaACC GCTATATGTT CGAGCGGCAA
301 CCGTCGGGGA CTTGGCAGGC AGTACGCATC CGCCTGCCCA TCTGTGTCGA
351 AGGCAGGCGC GATTTTACGG CGGACATTAC AATCGGCAGT CGGACATTTT
401 AGACGGCATT TACCGCCGAA TAA
```

This corresponds to the amino acid sequence <SEQ ID 1100; ORF 270>:

m270.pep

```

1  MNKNRKLLLA ALLLIAFAAV KLVLLQWWQA XQPQAVAAQC DLTEGCTLPD
51  GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ
101 PSGTWQAVRI RLPICVEGRR DFTADITIGS RTFQTAFTAE *
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 270 shows 96.4% identity over a 140 aa overlap with a predicted ORF (ORF 270.ng) from *N. gonorrhoeae*:

m270/g270

	10	20	30	40	50	60
m270.pep	MNKNRKL LLA AALLLIAFAAVKLVLLQWWQAXQPQAVAAQC					
g270	MNKNRKL LLA AALLLTAF AAF KLVLLQWWQAQQPQAVAAQC					
	10	20	30	40	50	60
	70					
m270.pep	TKKPFDIYIEHAPAGTEQVSISFSMKNMDMGFNRYMFERQPSGTWQAVRIRLPICVEGRR					
g270	TKKPFDIYIEHAPAGTEQVSISFSMKNMDMGFNRYMFERQPSGTWQAARIRLPICVEGRR					
	70	80	90	100	110	120
	70					
m270.pep	DFTADITIGSRTFQTAFTAEX					
g270	DFTADITIGSRTFQTAFTAEX					
	130	140				
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1101>:

a270.seq

```

1  ATGAATAAAA ACCGTAAATT ACTGCTTGCC GCACTGCTGC TGATTGCCTT
51  TGCCGCCGTC AAGCTCGTTT TGTGCAATG GTGGCAGGCG CAGCAGCCGC
101 AAGCTGTGGC GGCGCAATGC GATTTGACCG AGGGTTGCAC GCTGCCGGAC
151 GGAAGCCGCG TCCGCGCCGC CGCCGTTTCA ACCAAAAAAC CGTTTGATAT
201 TTATATCGAA CACGCGCCCG CCGGCACGGA ACAGGTCAGC ATCAGCTTCA
251 GTATGAAAAA TATGGATATG GGTTCaACC GCTATATGTT CGAGCGGCAA
301 CCGTCGGGGA CTTGGCAGGC AGTACGCATC CGCCTGCCCA TCTGTGTCGA
351 AGGCAGGCGC GATTTTACGG CGGACATTAC AATCGGCAGC CGGACATTTT
401 AGACGGCATT TACCGCCGAA TAA
```

This corresponds to the amino acid sequence <SEQ ID 1102; ORF 270.a>:

a270.pep

```

1  MNKNRKLLLA ALLLIAFAAV KLVLLQWWQA QQPQAVAAQC DLTEGCTLPD
51  GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ
```

101 PSGTWQAVRI RLPICVEGRR DFTADITIGS RTFQTAFTAE *

m270/a270 99.3% identity in 140 aa overlap

	10	20	30	40	50	60
m270.pep	MNKNRKL	LLAALL	IAFAAV	KLVL	LQWQ	AXQPQ
a270	MNKNRKL	LLAALL	IAFAAV	KLVL	LQWQ	AXQPQ
	10	20	30	40	50	60
	70	80	90	100	110	120
m270.pep	TKKPF	DIYIE	HAPAG	TEQVS	ISFS	MKNMD
a270	TKKPF	DIYIE	HAPAG	TEQVS	ISFS	MKNMD
	70	80	90	100	110	120
	130	140				
m270.pep	DFTAD	ITIGS	RTFQT	AFTAE		
a270	DFTAD	ITIGS	RTFQT	AFTAE		
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1103>:

g271.seq

1	atgttcagtt	cgcggtatggc	gaggatttgg	gcgacggggg	taacgttgtg
51	tatggtcagt	ccgtgtccgg	cgttgacgac	caagcccaaa	tcgccggcga
101	aatgcgcgcc	gttttggatg	cgctcgaact	gcctgatttg	ttcggcggtg
151	ctttgtgctg	cgccatgatg	gccggtgtgc	agctcgacaa	cgggcgcgcc
201	gacatcacgg	gcggtcttga	tttgctgtgc	gtcggcatcg	ataaacaagg
251	acacgcgtat	gcccgcgtcg	gtcaggattt	tggcgaattc	ggcgattttt
301	tcctgttgcg	ccaatacgtc	caaaccgcct	tcggtcgtga	tttcctgccg
351	tttttcaggc	acgatgcaca	cgtcttccgg	catcacttta	agcgcgtttt
401	cgagcatttc	ttccgtcaac	gccatttcaa	ggttcaggcg	cgtgcggatg
451	gcgtttttga	cgggcaatac	atccgcgtct	ttgatgtggc	ggcggtcttc
501	gcgcaggtgc	atggtaatac	ggtctgcacc	gtgcgtttcg	gcaaccagtg
551	ccgcctccac	ggggctggga	taa		

This corresponds to the amino acid sequence <SEQ ID 1104; ORF 271.ng>:

g271.pep

1	MFSSRMARIW	ATGVTL	CMVS	PCPAL	TTKPK	SPAKCA	PFWM	RSNCLIC	SAW
51	LCASAYAPVC	SSTTGAPT	SR	AAWICL	SSAS	INKDTR	MPAS	VRILANS	AI
101	SCCANTSKPP	SVVISCRF	SG	TMHTSS	GITL	SAFSSI	SVN	AISRFR	RVRM
151	AFLTANTSAS	LMWRRSS	RRC	MVIRSA	PCVS	ATSAAS	TGLG*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1105>:

m271.seq

1	AwGTTCAgTT	CGCGGATGGC	GAGGATTtGG	GCGATGGGGG	TAACGTTGTG
51	TATGGTCAGT	CCGTGTCCGG	CGTTGACGAC	CAAGCCCAAA	TCGCCGGCGA
101	AATGCGCGCC	GTTTTGGATG	CGCTCGAACT	GCCTGATTtG	TTCCGGCGTG
151	CTGCGCGCGT	CGGCATACGC	GCCTGTGTGC	AGCTCGACAA	CGGGCGCGCC
201	GACATCACGG	GCGGCTTGA	TTTGCCTGTC	GTCGGCATCG	ATAAACAAAG
251	ACACGCGTAT	GCCTGCGTCG	GTCAGGATTt	TGGTGAACCC	GGCGATTtTT
301	TCCTGTTGCG	CCAATACGTC	CAAACCGCCT	TCGGTCGTGA	TTTCCTGACG
351	TTTTTCAGGC	ACGATGCACA	CGTCTTCCGG	CATCACTTTC	AAAGCGTTtT
401	CCAACATTTC	TTCCGTCAAC	GCCATTtCAA	GGTTCAGGCG	CGTGCGGATG
451	GCGTTTTTGA	CGGCAACAC	GTCCGCGTCT	TTGATGTGGC	GGCGGTCTTC
501	GCGCAGGTGC	ATGGTAATCA	AATCCGCACC	GTGCGTTTCG	GCAACCAGTG
551	CCGCCTCCAC	GGGGCTGGGA	TAA		

This corresponds to the amino acid sequence <SEQ ID 1106; ORF 271>:

m271.pep

1	XFSSRMARIW	AMGVTL	CMVS	PCPAL	TTKPK	SPAKCA	PFWM	RSNCLIC	SAW
51	LRASAYAPVC	SSTTGAPT	SR	AAWICL	SSAS	INKDTR	MPAS	VRILVNP	AI
101	SCCANTSKPP	SVVISXRF	SG	TMHTSS	GITF	KAFSNI	SVN	AISRFR	RVRM
151	AFLTANTSAS	LMWRRSS	RRC	MVIKSA	PCVS	ATSAAS	TGLG *		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 271 shows 95.2% identity over a 189 aa overlap with a predicted ORF (ORF 271.ng) from *N. gonorrhoeae*:

m271/g271

	10	20	30	40	50	60
m271 .pep	XFSSRMARIWAMGVTLCMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLRLASAYAPVC					
g271	MFSSRMARIWATGVTLCMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLCASAYAPVC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m271 .pep	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNPAIFSCCANTSKPPSVVISXRFSG					
g271	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILANS AIFSCCANTSKPPSVVISCRFSG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m271 .pep	TMHTSSGITLFAFSNIISSVNAISRFRVRMAFLTANTSASLMWRRSSRRCMVIRSAAPCVS					
g271	TMHTSSGITLSAFSSIISSVNAISRFRVRMAFLTANTSASLMWRRSSRRCMVIRSAAPCVS					
	130	140	150	160	170	180
	190					
m271 .pep	ATSAASTGLGX					
g271	ATSAASTGLGX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1107>:

a271 .seq

```

1  ATGTTTCAGTT  CGCGGATGGC  GAGGATTTGG  GCGATGGGGG  TAACGTTGTG
51  TATGGTCAGT  CCGTGTCCGG  CGTTGACGAC  CAAGCCCAAA  TCGCTGGCAA
101 AATGCGCGCC  GTTTTGGATG  CGCTCGAACT  GCCTGATTG  TTCGGCGTGG
151 CTGCGCGCGT  CGGCATACGC  GCCTGTGTGC  AGCTCGACAA  CGGGCGCGCC
201 GACATCACGG  GCGGCTTGGA  TTTGCCTGTC  GTCGGCATCG  ATAAACAAGG
251 ACACGCGTAT  GCGGCGGTCG  GTCAGGATTT  TGGTGAATTC  GGCAATTTTG
301 TCTTGTGTCG  CCAATACGTC  CAAGCCGCCT  TCGGTCGTGA  TTTCTGTACG
351 TTTTCCGGC  ACGATGCACA  CGTCTCCGG  CATCACTTTA  AGCGCGTTTT
401 CGAGCATTTC  TTCCGTCAAC  GCCATTTCAA  GGTTCAGGCG  CGTGC GGATG
451 GCGTTTTTGA  CAGCAAACAC  GTCCGCGTCT  TTGATGTGGC  GCGCGTCTTC
501 GCGCAGGTGC  ATGGTAATCA  GGTCCGCACC  GTGCGTTTCG  GCAACCAAGT
551 CCGCCTCCAC  GGGGCTGGGA  TAA

```

This corresponds to the amino acid sequence <SEQ ID 1108; ORF 271.a>:

a271 .pep

```

1  MFSSRMARIW  AMGVTLCMVS  PCPALTTKPK  SLAKCAPFWM  RSNCLICSAW
51  LRASAYAPVC  SSTTGAPTSR  AAWICLSSAS  INKDTRMPAS  VRILVNSAIL
101 SCCANTSKPP  SVVIS*RFSG  TMHTSSGITL  SAFSSIISSV  NAISRFRVRM
151 AFLTANTSAS  LMWRRSSRRC  MVIRSAAPCV  ATSAASTGLG  *

```

m271/a271 96.3% identity in 189 aa overlap

	10	20	30	40	50	60
m271 .pep	XFSSRMARIWAMGVTLCMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLRLASAYAPVC					
a271	MFSSRMARIWAMGVTLCMVSPCPALTTKPKSLAKCAPFWMRSNCLICSAWLRLASAYAPVC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m271 .pep	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNPAIFSCCANTSKPPSVVISXRFSG					
a271	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNSAILSCCANTSKPPSVVISXRFSG					

621

	70	80	90	100	110	120
	130	140	150	160	170	180
m271.pep	TMHTSSGITFKAFNSNISSVNAISRFRVRMAFLTANTSASLMWRRSSRRRCMVKSAPCVS					
a271	:: :					
	130	140	150	160	170	180
	190					
m271.pep	ATSAASTGLGX					
a271						
	ATSAASTGLGX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1109>:

g272.seq

```

1  atgactgcaa aggaagaact gttcgcattg ctgcgccata tgaacaaaaa
51  caaagggtcc gacctgttg tgacgacca tttcccgccc gctatgaagc
101 tggacggcaa aatcaccgc atcacggacg aaccgctgac ggcggaaaaa
151 tgtatggaaa tcgccttttc gattatgagt gcgaagcagg cggaagaatt
201 ttcacgcacc aacgagtgcg atttcgccat cagcctgccg gacaccagcc
251 gcttccgcgt caatgcgatg atacagcgcg gtgcgacggc gttggtattc
301 cgcgcgatta ccagcaagat tcccaagttt gaaagcctga acctgccgcc
351 ggcttgaag gatgttgccg tgaaaaaacg cgggctggtt atttttgtcg
401 gcggcaccgg ctccgggcaa tcgacttcgc tcgcctcgct tatcgactac
451 cgcaatgaaa attcgttcgg acacatcatc accatcgaa atccgatcga
501 gtttgtccac gaacacaaaa actgcatcat taccagcgcg gaggtcggcg
551 tggacacgga aaactggatg gcggcggttg aaaatacgct gcgtcaggcg
601 ccgatgtgta tccttatcgg cgaaatccgc gaccgtgaaa caatggacta
651 cgccatcgcc tttgccgaaa cggggcattt gtgtatggcg acgctgcacg
701 ccaacagcac caatcaggcg ctgcaccgca tcatcaactt cttcccgag
751 gagcggcgcg aacaattgct gacggatttg tcgctcaacc ttcaggcggt
801 tatttcgcaa cgctcgttc cgcgagacgg cggcaagggc aggggtggcg
851 cagtgcaggt gctgctcaat tcgcccctga tttcggagtt gattcacaac
901 ggcaacatcc atgaaatcaa agaagtgatg aaaaaatcca ctaccctggg
951 tatgcagacc ttcgaccaac acctttacca attgtatgaa aaaggcgaga
1001 tttccttgca ggatgccttg aaaaatgccg attccgcaca tgatttgcgt
1051 ttggcggtac agttgcgcag ccgcagggca caaagtccg accccgattt
1101 ggaactgctc tga

```

This corresponds to the amino acid sequence <SEQ ID 1110; ORF 272.ng>:

g272.pep

```

1  MTAKEELFAW LRHMNKNKGS DLFVTTHFPP AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFSST NECNFAISLP DTSRFRVNAM IQRGATALVF
101 RAITSKIPKF ESLNLPPALK DVALKKRGLV IFVGGTSGSK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYAIA FAETGHLMA TLHANSTNQA LDRIINFFPE
251 ERREQLLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMQT FDQHLQLYE KGEISLQDAL KNADSAHDLR
351 LAVQLRSRRA QSSDPDELL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1111>:

m272.seq

```

1  ATGACCGCAA AGGAAGAACT GTTCGCATGG CTGCGCCATA TGAwCCAAAA
51  CAAAGGTTCC GACCTGTTCC TGACAACCCA TTTCCCGCCC GCAATGAAGC
101 TGGACGGCAA AATCACCAGC ATCAGGACG AACCCTGAC GCGCGAAAAA
151 TGTATGAAAA TCGCCTTTTC GATTATGAGT GCGAAGCAGG CGGAAGAATT
201 TTCATCGACC AACGAGTGCA ACTTCGCCAT CAGCCTGCCG GACACCAGCC
251 GCTTCCGCGT CAATGCGATG ATACAGCGCG GCGCGACGGC GTTGGTATTC
301 CGTACGATTA CCAGCAAGAT TCCCAAGTTT GAAAGCCTGA ACCTGCCGCC
351 AGTCTTGAAG GATGTCGCGC TGAAAAAACG CGGGCTGGTT ATTTTGTGCG
401 CGGACACCGG CTCGGGTAAA TCGACTTCGC TTGCCTCGCT TATCGACTAC
451 CGCAATGAAA ATTCGTTCCG ACACATCATC ACCATCGAAG ACCCGATCGA
501 GTTTGTCCAC GAACACAAAA ACTGCATCAT CACCCAGCGC GAGGTGCGCG

```

```

551 TGGATACGGA AACTGGATG GcGGCGTTGA AAAACACGCT GCGTCAGGCG
601 CCTGATGTCA TCCTTATCGG CGAAATCCGT GACCGCGAAA CAATGGACTA
651 CGCCATTGCC TTTGCCGAAA CGGGGCATTT GTGTATGGCG ACGCTGCACG
701 CCAACAGCAC CAATCAGGCA CTCGACCGCA TCATCAACTT TTCCCCGAG
751 GAGCGGCGCG AACAAATGCT GACGGATTG TCGCTCAACC TTCAGGCGTT
801 TATTTGCAA CGCCTCGTTC CGCGAGACGG CGGCAAGGGC AGGGTGGCGG
851 CAGTCGAGGT GCTGCTCAAT TCGCCCtGA TTTCGGAGTT GATTACAAC
901 GGCAACATCC ATGAAATCAA AGAAGTGATG AAAAAATCCA CTACCCTGGG
951 TATGCAGACC TTCGATCAAC ACCTTTACCA ATTGTATGAA AAAGGCGATA
1001 TTTCCCTGCA AGAAGCATTG AAAAAATGCCG ATTCCGCACA CGATTTGCGT
1051 TTGGCGGTAC AGTTGCGCAG CCGCCGCGCG CAaAGTTyCA GCCCCGATTT
1101 GGnACTGCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1112; ORF 272>:

m272.pep

```

1  MTAKEELFAW LRHMxQNKGS DLFVTTTFPP AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFSST NECNFAISLP DTSRFRVNAI IORGATLVF
101 RTITSKIPKF ESLNLPVVK DVALKKRGLV IFVGGTSGSK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYIA FAETGHLCA TLHANSTNQA LDRIINFPE
251 ERREQLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMQT FDQHLQLYE KDISLQAL KNADSAHDLR
351 LAVQLRSRRA QXSPDLXLL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 272 shows 97.6% identity over a 370 aa overlap with a predicted ORF (ORF 272.ng) from *N. gonorrhoeae*:

m272/g272

m272.pep	10	20	30	40	50	60
	MTAKEELFAWLRHMxQNKGS DLFVTTTFPPAMKLDGKITRITDEPLTAEK CMEIAFSIMS					
g272	MTAKEELFAWLRHMKNKGS DLFVTTTFPPAMKLDGKITRITDEPLTAEK CMEIAFSIMS					
	10	20	30	40	50	60
m272.pep	70	80	90	100	110	120
	AKQAEFSSTNECNFAISLPDTSRFRVNAI IORGATLVFRTITSKIPKFESLNLPVVK					
g272	AKQAEFSSTNECNFAISLPDTSRFRVNAI IORGATLVFRAITSKIPKFESLNLPALK					
	70	80	90	100	110	120
m272.pep	130	140	150	160	170	180
	DVALKKRGLVIFVGGTSGSKSTSLASLIDYRNENSFGHIIITIEDPIEFVHEHKNCIITQR					
g272	DVALKKRGLVIFVGGTSGSKSTSLASLIDYRNENSFGHIIITIEDPIEFVHEHKNCIITQR					
	130	140	150	160	170	180
m272.pep	190	200	210	220	230	240
	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETMDYIAFAETGHLCA TLHANSTNQA					
g272	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETMDYIAFAETGHLCA TLHANSTNQA					
	190	200	210	220	230	240
m272.pep	250	260	270	280	290	300
	LDRIINFPEERREQLTDL SLNLQAFISQRLVPRDGGKGRVA AAVEVLLN SPLISELIHN					
g272	LDRIINFPEERREQLTDL SLNLQAFISQRLVPRDGGKGRVA AAVEVLLN SPLISELIHN					
	250	260	270	280	290	300
m272.pep	310	320	330	340	350	360
	GNIHEIKEVMKKSTTLGMQTFDQHLQLYE KDISLQALKNADSAHDLRLAVQLRSRRA					
g272	GNIHEIKEVMKKSTTLGMQTFDQHLQLYE KGEISLQDALKNADSAHDLRLAVQLRSRRA					
	310	320	330	340	350	360

```

          370
m272 . pep    QSXSPDLXLLX
              || :||| |||
g272         QSSDPDLELLX
              370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1113>:

```

a272 . seq
1  ATGACCGCAA AGGAAGAACT GTTCGCATGG CTGCGCCATA TGAACAAAAA
51  CAAAGGTTCC GACCTGTTCC TGACGACCCA TTTCCCGCCC GCAATGAAGC
101 TGGACGGCAA AATCACCCGC ATCACGGACG AACCGCTGAC GGCGGAAAAA
151 TGTATGGAAA TCGCCTTTTC GATTATGAGT GCGAAGCAGG CGGAAGAATT
201 TTCATCGACC AACGAGTGCA ACTTCGCCAT CAGTCTGCCG GACACCAGCC
251 GCTTCCGCGT CAATGCGATG ATACAGCGCG GTGCGACGGC GTTGGTATTC
301 CGTGCGATTA CCAGCAAGAT TCCCAAGTTT GAAAGCCTGA ACCTGCCGCC
351 GGTCTTGAAG GATGTCGCGC TGAAAAAACG CGGGCTGGTT ATTTTGTGTCG
401 GCGGCACCGG CTCGGGCAAA TCGACTTCGC TTGCCTCGCT TATCGACTAC
451 CGCAATGAAA ATTCGTTCCG ACACATCATC ACCATCGAAG ACCCGATCGA
501 GTTTGTCCAC GAACACAAA ACTGCATCAT CACCCAGCGC GAGGTCGGCG
551 TGGATACGGA AACTGGATG GCGGCGTTGA AAAACACGCT GCGTCAGGCA
601 CCGGATGTGA TTCTGATCGG CGAAATCCGC GACCGCGAAA CAATGGACTA
651 CGCCATTGCT TTTGCCGAAA CGGGGCATTT GTGTATGGCG ACGCTGCACG
701 CCAACAGCAC CAATCAGGCA CTCGACCGCA TCATCAACTT TTTCCCGAG
751 GAGCGGCGCG AACAATTGCT GACGGATTTG TCGCTCAACC TTCAGGCATT
801 TATTTGCGAA CGCCTCGTTC CGCGAGACGG CGGCAAGGGC AGGGTGGCGG
851 CAGTCGAGGT GCTGCTCAAT TCGCCCCTGA TTTCGGAGTT GATTACAAC
901 GGCAATATCC ATGAAATCAA AGAAGTGATG AAAAAATCCA CTACCCTGGG
951 TATGCAGACT TTCGACCAAC ACCTTTACCA ATTGTATGAA AAAGGCGAGA
1001 TTTCTTGCA GGATGCCTTG AAAAATGCCG ATTCCGCACA CGATTGCGT
1051 TTGGCGGTAC AGTTGCGCAG CCGCCAGGCG CAAAGTCCG GTCCCGATT
1101 GGAAGTCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1114; ORF 272.a>:

```

a272 . pep
1  MTAKEELFAW LRHMNKNKGS DLFVTTTHFPP AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFSST NECNFAISLP DTSRFRVNAI IQRGATALVF
101 RAITSKIPKF ESLNLPVLK DVALKKRGLV IFVGGTGSBK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYIAI FAETGHLCA TLHANSTNQA LDRIINFFPE
251 ERREQLLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMQT FDQHLQLYE KGEISLQDAL KNADSAHDLR
351 LAVQLRSRQA QSSGPDELL *

```

m272/a272 97.6% identity in 370 aa overlap

```

          10      20      30      40      50      60
m272 . pep    MTAKEELFAWLRHMNKNKGS DLFVTTTHFPPAMKLDGKITRITDEPLTAEK CMEIAFSIMS
              ||||| :||| |||
a272         MTAKEELFAWLRHMNKNKGS DLFVTTTHFPPAMKLDGKITRITDEPLTAEK CMEIAFSIMS
              10      20      30      40      50      60

          70      80      90      100     110     120
m272 . pep    AKQAEFSSTNECNFAISLPDTSRFRVNAI IQRGATALVFRTITSKIPKFESLNLPVLK
              ||||| :||| |||
a272         AKQAEFSSTNECNFAISLPDTSRFRVNAI IQRGATALVFRAITSKIPKFESLNLPVLK
              70      80      90      100     110     120

          130     140     150     160     170     180
m272 . pep    DVALKKRGLVIFVGGTGSBKSTSLASLIDYRNENSFGHII TIEDPIEFVHEHKNCIITQR
              ||||| :||| |||
a272         DVALKKRGLVIFVGGTGSBKSTSLASLIDYRNENSFGHII TIEDPIEFVHEHKNCIITQR
              130     140     150     160     170     180

```

	190	200	210	220	230	240
m272.pep	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETM DY A I A F A E T G H L C M A T L H A N S T N Q A					
a272	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETM DY A I A F A E T G H L C M A T L H A N S T N Q A					
	190	200	210	220	230	240
	250	260	270	280	290	300
m272.pep	LDRIINFPEERREQLLTDSLNLQAFISQRLVPRDGGKGRVAAVEVLLNSPLISELIHN					
a272	LDRIINFPEERREQLLTDSLNLQAFISQRLVPRDGGKGRVAAVEVLLNSPLISELIHN					
	250	260	270	280	290	300
	310	320	330	340	350	360
m272.pep	GNIHEIKEVMKKSTTLGMOTFDQHL Y Q L Y E K G D I S L Q E A L K N A D S A H D L R L A V Q L R S R R A					
a272	GNIHEIKEVMKKSTTLGMOTFDQHL Y Q L Y E K G E I S L Q D A L K N A D S A H D L R L A V Q L R S R Q A					
	310	320	330	340	350	360
	370					
m272.pep	Q S X S P D L X L L X					
	:					
a272	Q S S G P D L E L L X					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1115>:

g273.seq

```

1  atgagtccttc aggcgggtatt tatatacccc ccaagccgta cgcacaata
51  caacgaaaat caggaaaacg gcggtaaagc tcataaacag ggacaaagcg
101 gcaaacacac cgaccgccgt caggatatag gcgtattcga ggccggaact
151 ccattcaccg ttttcctgcc gtttcctgtc gcttttgaaa taaaggatga
201 tgccggcaag cagcgcgcca gccgcgccg acattggcat tgtgttcatt
251 gttgttcctt aacggttaaa aaccgcgccg gccgtgcaac cgttttaagg
301 cgggaaattg caaaatttgt ttgcggggcg gtgcgctga aatcaaggcg
351 gtttgagaag tgtttcenac gcgcccgcgc tatgtgccga aatattattt
401 gtcgctcacc tgcaaaatcg ccaagaacgc gctttgcgga atttccacgt
451 tgcccacttg tttcatacgg cgtttgccctg ctttttgctt ttcaagcagt
501 tttttcttac gcgtaa

```

This corresponds to the amino acid sequence <SEQ ID 1116; ORF 273.ng>:

g273.pep

```

1  MSLQAVFIYP PSRTAQYNEN QENGGAHKQ GQSGKHTDRR QDIGVFEAGT
51  PFTVFLPFLV AFEIKDDAGK QRGSRARHWH CVHCCSLTVK NPPGRATVLR
101 REIAKFVCGR VPLKSRRFEK CFXRARPMCR NIICRSPAKS PRTRFAEFPR
151 CPLVSYGVCL LFVFQAVFSY A*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1117>:

m273.seq

```

1  ATGAGTCTTC AGGCGGTATT TATATACCCm CCAAGCCGTA CCGCACAATA
51  CAACGAAAAT CAGGAAAACG GCGGTAAAGC TCAYAAACAG GGACAAAGCG
101 GCAAACACGC CGACCGCTGT CAGGATATAG GCGTATTCAA GGCCGGAAC
151 CCATTCCCCG TTTTCCTGCC GCTTCTTGTC GCTTTTGAAA TAAAGGATGA
201 TGCCGGCAAG CAGCGCGGCA GCCGCGCCCG ACATTAGCAT TGTGTTTCATT
251 GTTGTTCCTT AATGCTTAAA AACC CGCTG TCCGTGCAAC CGTTTTAAGG
301 CGGCAAATTG CAAAATTGTG TTGCGGGCGC GTGCCCTGA AATCAGGGCG
351 GTTTGAGGGG TGTCCCGAC GCGCCGCCCT GTGTGCCGGA GTTATTTGTC
401 GCTCACCTGC AAAATCGCCA AGAACGCGCT TTGCGGAATT TCCACATTGC
451 CCACTTGTTT CATACGGCGT TTACCTGCCT TTTGTkTwTC AAGCAGTTTT
501 TTCTTACGCG TAA

```

This corresponds to the amino acid sequence <SEQ ID 1118; ORF 273>:

m273.pep

```

1  MSLQAVFIYP PSRTAQYNEN QENGGAHKQ GQSGKHADRC QDIGVFKAGT
51  PFPVFLPLL V AFEIKDDAGK QRGSRARH*H CVHCCSLMLK NPPVRATVLR
101 RQIAKFVCGR VPLKSGRFEG CSRRALCAG VICRSPAKSP RTRFAEFPHC
151 PLVSYGVYLP FVXQAVFSYA *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 273 shows 86.0% identity over a 171 aa overlap with a predicted ORF (ORF 273.ng) from *N. gonorrhoeae*:

m273/g273

	10	20	30	40	50	60
m273.pep	MSLQAVFIYPPSRTAQYNENQENGGAHKQGGSGKHADRCQDIGVFKAGTPFPVFLPLL					
g273	MSLQAVFIYPPSRTAQYNENQENGGAHKQGGSGKHADRRQDIGVFEAGTFPTVFLPLFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m273.pep	AFEIKDDAGKQGRSRRHXHCVHCCSLMLKNPPVRATVLRRIAKFVCGRVPLKSGRFEG					
g273	AFEIKDDAGKQGRSRRHWHCVHCCSLTVKNPPGRATVLRREIAKFVCGRVPLKSGRFEK					
	70	80	90	100	110	120
	130	140	150	160	170	
m273.pep	CSRRRA-ALCAGVICRSPAKSPRTRFAEFPHCPLVSYGVYLPFVXQAVFSYAX					
g273	CFXRARPMCRNIICRSPAKSPRTRFAEFPRCPLVSYGVCLLFVFQAVFSYAX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1119>:

a273.seq

```

1   ATGAGTCTTC AGGCGGTATT TGTATACCCC CCAAGCCGTA CCGCACAAATA
51  CAACGAAAT  CAGGAAAACG GCGGTAAAGC TCATAAACAG GGACAAAGCG
101 GCAAACACGC  CGACCGCCGT  CAGGATATAG GCGTATTCCA GACCGGAACT
151 CCATTACCG  TTTTCCTGCC  GCTTTTGTG  GCTTTTGAAA TAAAGGATGA
201 TGCCGGCAAG  CAGCGCGGCA  GCCGCGCCCG ACATTAGCAT AATGTTCATT
251 GTTGTTCCTT AACGGTTAAA  AACCCGCCCG TCCGTGCAAC CGTTTTTAAAG
301 AGGCGGTAAA  TCACAAAGTT  TGTGCGCGGA CGTGCTCTCT TACAATCAGG
351 GCGGTTTAA  GGGCATGATG  CACTGCCCCG TGTGCCGGAT ATTATTTGTC
401 GCTCACCTGC AAAATTGCCA  AGAACGCGCT TTGCGGGATT TCCACATTGC
451 CCACTTGTTT CATACGGCGT  TTGCCTGCTT TTTGTTTTTC AAGCAGTTTT
501 TTCTTACGCG TAA

```

This corresponds to the amino acid sequence <SEQ ID 1120; ORF 273.a>:

a273.pep

```

1   MSLQAVFVYP PSRTAQYNEN QENGGAHKQ  GQSGKHADRR QDIGVFQGTG
51  PFTVFLPLFV AFEIKDDAGK QGRSRRAR*H NVHCCSLTVK NPPVRATVFK
101 RR*ITKFVGG  RALLQSGRFK GHDALPRVPD IICRSPAKLP RTRFAGFPHC
151 PLVSYGVCLL  FVFQAVFSYA *

```

m273/a273 80.1% identity in 171 aa overlap

	10	20	30	40	50	60
m273.pep	MSLQAVFIYPPSRTAQYNENQENGGAHKQGGSGKHADRCQDIGVFKAGTPFPVFLPLL					
a273	MSLQAVFVYPPSRTAQYNENQENGGAHKQGGSGKHADRRQDIGVFQGTGTFPTVFLPLFV					
	10	20	30	40	50	60
	70	80	90	100	110	119
m273.pep	AFEIKDDAGKQGRSRRARHXHCVHCCSLMLKNPPVRATVLR-RRQIAKFVCGRVPLKSGRFE					
a273	AFEIKDDAGKQGRSRRARHXHNVHCCSLTVKNPPVRATVFKRRXITKFVGGRALLQSGRFK					
	70	80	90	100	110	120
	120	130	140	150	160	170
m273.pep	GCSRRRAALCAGVICRSPAKSPRTRFAEFPHCPLVSYGVYLPFVXQAVFSYAX					
a273	GHDALPRV-PDIICRSPAKLPRTFAGFPHCPLVSYGVCLLFVFQAVFSYAX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1121>:

```
g274.seq
  1  ATGGCGGGGC  CGATTTTGT  CGTCatCGCC  AgcgTCGCTA  TGTTTTTTGT
 51  CGCGCAGCAG  CACGCGACAG  ATTTGGTTAC  GGACGATTAT  TATAAGGATG
101  GCAAGCATAT  CGACATCCAG  CTTTCATCGG  ATGAAGAAGC  CGTCAGACGG
151  CATATCGGGG  TGCAGGTCCT  CATTCTCCCC  GATATGAATG  CGGCAAAAGT
201  GTTTGTCGGC  ggCgagtTTG  ACGGCAAACA  GCCTTTGAAC  CTGCTGCTGA
251  TGCACCCGAC  CCGCAAGGCG  GACGATCAAA  CCGTCGCCCT  CAAGCCCGTC
301  GGCAGCGCGC  AGAACGGCAG  GCGGAATAT  GAGGCGGTgt  tcaaAACCCCT
351  TCCGCCGGCC  AACCCTGGT  ATGTGCGCGT  GGAggacgCG  GCAGGCGTGT
401  GGCAGCGTCGA  GAACAAATGG  ATTACCAGCC  AGGGCAATGC  GGTCGATTTG
451  ACCCCGATGG  ACAAACTTTT  CAATAATGCA  GGAAGCAAAT  AA
```

This corresponds to the amino acid sequence <SEQ ID 1122; ORF 274.ng>:

```
g274.pep
  1  MAGPIFVVIA  SVAMFFVAQQ  HATDLVTDDY  YKDGHIDIQ  LHRDEEAVRR
 51  HIGVQVLISP  DMNAAKVFG  GEFDGKQPLN  LLLMHPTRKA  DDQTVALKPV
101  GSAQNGRAEY  EAVFKTLPPA  NHWYVRVEDA  AGVWRVENKW  ITSQNAVDL
151  TPMDKLFNNA  GSK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1123>:

```
m274.seq
  1  ATGGCGGGGC  CGATTTTGT  CGTCATCGCC  AGCGTCGCTA  TGTTTTTTGT
 51  CGCGCAGCAG  CACGCGACAG  ATTTGGTTAC  GGACGATTAT  TATAAAGACG
101  GCAAACATAT  CGACATCCAG  CTTTCATCGG  ATGAAGAAGC  CGTCAGACGG
151  CATATCGGGG  TGCAGGTTCT  CATTCTCCCC  GATATGAATG  CGGCAAAAGT
201  GTTTGTCGGC  GCGGAGTTTG  ACGGCAAACA  GCCTTTGAAC  CTGCTGCTGA
251  TGCACCCGAC  CCGCAAGGCG  GACGATCAAA  CCGTCGCCCT  CAAGCCCGTC
301  GGCAGCGCGC  AGAACGGCAG  GCGGAATAT  GAGGCGGTGT  TCAAACCCCT
351  TTCGCCGACC  AACCCTGGT  ATGTGCGCGT  GGAGGACGCG  GCAGGCGTGT
401  GGCAGCGTCGA  GAACAAATGG  ATTACCAGCC  AAGGCAATGC  GGTCGATTTG
451  ACCCCGATGG  ACAAGCTTTT  CAATAATACT  GAAAGCAAAT  AA
```

This corresponds to the amino acid sequence <SEQ ID 1124; ORF 274>:

```
m274.pep
  1  MAGPIFVVIA  SVAMFFVAQQ  HATDLVTDDY  YKDGHIDIQ  LHRDEEAVRR
 51  HIGVQVLISP  DMNAAKVFG  GEFDGKQPLN  LLLMHPTRKA  DDQTVALKPV
101  GSAQNGRAEY  EAVFKTSLPT  NHWYVRVEDA  AGVWRVENKW  ITSQNAVDL
151  TPMDKLFNNT  ESK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 274 shows 97.5% identity over a 163 aa overlap with a predicted ORF (ORF 274.ng) from *N. gonorrhoeae*:

g274/m274

	10	20	30	40	50	60
g274.pep	MAGPIFVVIASVAMFFVAQQHATDLVTDDYKDGKHIDIQ LHRDEEAVRRHIGVQVLISP					
m274	MAGPIFVVIASVAMFFVAQQHATDLVTDDYKDGKHIDIQ LHRDEEAVRRHIGVQVLISP					
	10	20	30	40	50	60
g274.pep	DMNAAKVFGGEFDGKQPLNLLLMHPTRKADDQTVALKPVGSAQNGRAEY EAVFKTLPPA					
m274	DMNAAKVFGGEFDGKQPLNLLLMHPTRKADDQTVALKPVGSAQNGRAEY EAVFKTSLPT					
	70	80	90	100	110	120
g274.pep	DMNAAKVFGGEFDGKQPLNLLLMHPTRKADDQTVALKPVGSAQNGRAEY EAVFKTLPPA					
m274	DMNAAKVFGGEFDGKQPLNLLLMHPTRKADDQTVALKPVGSAQNGRAEY EAVFKTSLPT					
	70	80	90	100	110	120
g274.pep	NHWYVRVEDAAGVWRVENKWITSQNAVDLTPMDKLFNNAGSKX					
m274	NHWYVRVEDAAGVWRVENKWITSQNAVDLTPMDKLFNNTESKX					
	130	140	150	160		
g274.pep	NHWYVRVEDAAGVWRVENKWITSQNAVDLTPMDKLFNNAGSKX					
m274	NHWYVRVEDAAGVWRVENKWITSQNAVDLTPMDKLFNNTESKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1125>:

```
a274.seq
1   ATGGCGGGGC CGATTTTGT CGTCATCGCC AGCGTCGCTA TGTTTTTTGT
51  CGCGCAGCAG CACGCGACAG ATTTGGTTAC GGACGATTAT TATAAAGACG
101 GCAAGCATAT CGACATCCAG CTTTCATCGG ATGAAGAAGC CGTCAGACGG
151 CATATCGGGG TGCAGGTTCT CATTTCCTCC GATATGAATG CGGCAAAAGT
201 GTTTGTCGGC GCGGAGTTTG ACGGCAAACA GCCTTTGAAC CTGCTGCTGA
251 TGCACCCGAC CCGCAAGGCG GACGATCAA CCGTCGCCCT CAAGCCCCTC
301 GGCAGCGCGC AGAACGGCAG GCGGGAATAT GAGGCGGTGT TCAAAACCTT
351 TTCGCCGACC AACCCTGGT ATGTGCGCGT GGAGGACGCG GCAGGCGTGT
401 GGCAGCGTCG GAACAAATGG ATTACCAGCC AAGGCAATGC GGTCGATTG
451 ACCCCGATGG ACAAACCTTT CAATAATACT GAAAGCAAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 1126; ORF 274.a>:

```
a274.pep
1   MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR
51  HIGVQVLISP DMNAAKVFGV GEFDGKQPLN LLLMHPTRKA DDQTVALKPV
101 GSAQNGRAEY EAVFKTSLPT NHWYVRVEDA AGVWRVENKW ITSQGNVDL
151 TPMDKLFNNT ESK*
```

m274/a274 100.0% identity in 163 aa overlap

	10	20	30	40	50	60
m274.pep	MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR HIGVQVLISP					
a274	MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR HIGVQVLISP					
	10	20	30	40	50	60
m274.pep	DMNAAKVFGV GEFDGKQPLN LLLMHPTRK ADDQTVALKPV GSAQNGRAEY EAVFKTSLPT					
a274	DMNAAKVFGV GEFDGKQPLN LLLMHPTRK ADDQTVALKPV GSAQNGRAEY EAVFKTSLPT					
	70	80	90	100	110	120
m274.pep	DMNAAKVFGV GEFDGKQPLN LLLMHPTRK ADDQTVALKPV GSAQNGRAEY EAVFKTSLPT					
a274	DMNAAKVFGV GEFDGKQPLN LLLMHPTRK ADDQTVALKPV GSAQNGRAEY EAVFKTSLPT					
	70	80	90	100	110	120
m274.pep	NHWYVRVEDA AGVWRVENKW ITSQGNVDL TPMDKLFNNTESKX					
a274	NHWYVRVEDA AGVWRVENKW ITSQGNVDL TPMDKLFNNTESKX					
	130	140	150	160		
m274.pep	NHWYVRVEDA AGVWRVENKW ITSQGNVDL TPMDKLFNNTESKX					
a274	NHWYVRVEDA AGVWRVENKW ITSQGNVDL TPMDKLFNNTESKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1127>:

```
g276.seq
1   atgattttgc cgccatccat gacgatgatg cggtcggcgg attcgacggt
51  ggtcaggcgg tgggcgacga tgatgccggt gcggttttcc atcaggcggt
101 cgagcgcttg ttggacgagg cggtcggatt cggtgtccaa tgcgctggtg
151 gcttcgtcca ataataatat cggcgcgtct ttcaaatagg cgcgggcatg
201 ggcgacgcgt tgccgctgtc cgccggataa gttgctgccg ttcgatccga
251 tgggctggtg cagtcgagc ggggatgcgt cgatcaggct ttgcagggtg
301 gcggcttggg gggcgacag gacttcggct tcgcccgcgt cgggacggct
351 gtatcggacg ttttcaaca ggggtgtcgt aaacaggaat acgtcttggg
401 agacgagggc gaattggcgc cgcaggcagt cgagtttgat gtcggcgatg
451 tcgataccgt ctatgcagat gttgccggca gacggttcga caaagcgggg
501 cagaagggtg acgacggtg atttgccgct gccggaacgt ccgaccaggg
551 cgacgcgttc gccttgtctg atgtcgaggt tgaagttgtc gagggctttg
601 atgccgtctg aacggtattc gacatcgacg ttgcggaagc tgatgcgccc
651 ttcgacacgc tgcggcgca gcgtgccttt gtccgtgttc ggcgggggtg
701 cgagaaatgc acatacgccg tcggcgcgca ggaacatcgt ctgcataggg
751 atgctgatgt tggcaaggct tttgatgggg gcgtacattt gcagcatcgc
801 gacgatgaat gccataaatt cgccgatggt ggtgtag
```

This corresponds to the amino acid sequence <SEQ ID 1128; ORF 276.ng>:

```
g276.pep
```

```

1  MILPPSMTMM RSADSTVVRR WATMMPVRFS IRRSSACWTR RSDSLSNALV
51  ASSNNNIGAS FKMARAMATR CRCPPDKLLP FDPMGWCSPS GDASIRLCRL
101 AAWRADRTSA SPASGRLYRT FSNRVSSNRN TSWETRANWA RRQSSLMSAM
151 SIPSMQMLPA DGSTKRGRRRL TTVDLPLPER PTRATRSPCL MSRLKLSRAL
201 MPSERYSTST LRKLMPSTR CGASVPLSCS GGVSRNAHTP SAARNIVCIG
251 MLMLARLLMG AYICSIATMN AINSPMVV*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1129>:

m276.seq

```

1  ATGATTTTGC CGTCGTCAT CACGATGATG CGGTCGGCCC CTTGATGGT
51  GGTCAGGCGG TGGGCGACGA TGATGCCGGT GCGGTTTTCC ATCAGGCGTT
101 CGAGCGCCTG TTGGACGAGG CGTTCGGATT CGTTGTCTAA TGCGCTGGTG
151 GCTTCGTCCA ATAATAATAT CGGCGCGTCT TTCAAATCGA CGCGGGCAAT
201 GGCGACGCGT TGCCGCTGTC CGCCGGATAA GTTGCTGCCG TTCGATCCGA
251 TGGGCTGGTG CAGTCCGAGC GGGGAGCTGT CAATCAGGCT TTGCAGGTTG
301 GCGGTTTGGA GGGCGAACAG GACTTCGGCT TCGCCCGCGT CGGGACGGCT
351 GTATCGGACG TTTTCAAACA GGGTGTGCTC AAACAGGAAT ACCTCTGGG
401 AGACGAGGGC GAATTGGGCG CGCAGGCAGT CGAGTTTGAT GTCGGCGATG
451 TCGATACCGT CTATGCAGAT GTTGCCGGCA GACGGTTCGA CAAAGCGGGG
501 CAGCAGGTG ACGACGGTGG ATTTGCCGCT GCCGGAACGT CCGACCAGGG
551 CGACGCGTTC GCCTTGCTCTG ATGTCGAGGT TGAAGTTGTC GAGGGCTTTG
601 ATGCCGCTG AACGGTATTC GACATCGACG TTGCGGAAGC TGATGCGCCC
651 TTCGACACGC TGCGGTGCGA GCGTGCCCTT GTCCTGTTCG GGCGGGGTGT
701 CGAGAAATGC ACATACACCG TCGGCGGCGA GGAACATCGT CTGCATAGGG
751 ATGCTGATGT TGGCAAGGCT TTTGATGGGG GCGTACATTT GCAGCATCGC
801 GACGATGAAT GCCATAAAT CGCCGATGGT GGTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1130; ORF 276>:

m276.pep

```

1  MILPSSITMM RSAPSMVVRW WATMMPVRFS IRRSSACWTR RSDSLSNALV
51  ASSNNNIGAS FKMARAMATR CRCPPDKLLP FDPMGWCSPS GELSIRLCRL
101 AVWRANRTSA SPASGRLYRT FSNRVSSNRN TSWETRANWA RRQSSLMSAM
151 SIPSMQMLPA DGSTKRGSRLL TTVDLPLPER PTRATRSPCL MSRLKLSRAL
201 MPSERYSTST LRKLMPSTR CGASVPLSCS GGVSRNAHTP SAARNIVCIG
251 MLMLARLLMG AYICSIATMN AINSPMVV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 276 shows 96.8% identity over a 278 aa overlap with a predicted ORF (ORF 276.ng) from *N. gonorrhoeae*:

m276/g276

	10	20	30	40	50	60
m276.pep	MILPSSITMMRSAPSMVVRWATMMPVRFSIRRSSACWTRRSDSLSNALVASSNNNIGAS					
g276	MILPSSITMMRSADSTVVRRWATMMPVRFSIRRSSACWTRRSDSLSNALVASSNNNIGAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m276.pep	FKMARAMATRCRCPPDKLLPFDPMGWCSPSGELSIRLCRLAVWRANRTSASPASGRLYRT					
g276	FKMARAMATRCRCPPDKLLPFDPMGWCSPSGDASIRLCRLAAWRADRTSASPASGRLYRT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m276.pep	FSNRVSSNRNTSWETRANWARRQSSLMSAMSIPSMQMLPADGSTKRGSRLLTTVDLPLPER					
g276	FSNRVSSNRNTSWETRANWARRQSSLMSAMSIPSMQMLPADGSTKRGSRLLTTVDLPLPER					
	130	140	150	160	170	180
	190	200	210	220	230	240
m276.pep	PTRATRSPCLMSRLKLSRALMPSERYSTSTLRKLMPSTRCGASVPLSCSGGVSRNAHTP					
g276	PTRATRSPCLMSRLKLSRALMPSERYSTSTLRKLMPSTRCGASVPLSCSGGVSRNAHTP					
	190	200	210	220	230	240

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	250	260	270	279
m276.pep	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX			
g276	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX			
	250	260	270	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1131>:

a276.seq

1	ATGATTTTGC	CGTCGTCCAT	TACGATGATG	CGGTCGGCCC	CTTCGATGGT
51	GGTCAGGCGG	TGGGCGACGA	TGATGCCGGT	GCGGTTTTTC	ATCAGGCGTT
101	CGAGCGCCTG	TTGGACGAGG	CGTTCGGATT	CGTTGTCCAA	TGCGCTGGTG
151	GCTTCGTCCA	ATAATAATAT	CGGCGCGTCT	TTCAAATGG	CGCGGGCAAT
201	GGCAACGCGT	TGCCGCTGTC	CGCCGGATAA	GTTGCTGCCG	TTCGATCCGA
251	TGGGCTGGTG	CAGTCCGAGC	GGTGATGCGT	CGATCAGGCT	TTGCAGGTTA
301	GCGGCTTGGA	GGGCGGATAG	GACTTCGGCT	TCGCCC GCGT	CGGGACGGCT
351	ATATCGGACG	TTTTCAAACA	GGGTGTCGTC	AAACAGGAAT	ACGTCTTGGG
401	AGACGAGGGC	AAATTGGGCG	CGCAGGCAGT	CGAGTTTGAT	GTCGGCGATG
451	TCGATACCGT	CTATGCAGAT	GTTGCCGGCA	GACGGTTCGA	CAAAGCGGGG
501	CAGCAGGTTG	ACGACGGTGG	ATTTGCCGCT	GCCGGAACGT	CCGACCAGGG
551	CGACGCGTTC	GCCTTGCTGT	ATGTCGAGGT	TGAAGCCGTC	GAGGGCTTTG
601	ATGCCGTCCG	AACGGTATTC	GACATCGACG	TTGCGGAAGC	TGATCGCCCC
651	TTGACACGCG	TGCGGTGCGA	GCGTGCCTTT	GTCCTGTTCT	GGCGGGGTGT
701	CGAGAAATGC	ACATACGCCG	TCGGCGGCGA	GGAACATCGT	CTGCATAGGG
751	ATGCTAATGT	TGGCAAGGCT	TTTGATGGGG	GCGTACATTT	GCAGCATCGC
801	GACGATGAAT	GCCATAAATT	CGCCGATGGT	GGTGTAG	

This corresponds to the amino acid sequence <SEQ ID 1132; ORF 276.a>:

a276.pep

1	MILPSSITMM	RSAPSMVVR	WATMMPVRF	IRRSSACWTR	RSDSLSNALV
51	ASSNNNIGAS	FKMARAMATR	CRCPPDKLLP	FDPMGWCSPS	GDASIRLCRL
101	AAWRADRTSA	SPASGRLYRT	FSNRVSSNRN	TSWETRANWA	RRQSSILMSAM
151	SIPSMQMLPA	DGSTKGRSRL	TTVDLPLPER	PTRATRSPCL	MSRLKPSRAL
201	MPSEYSTST	LRKLMPSTR	CGASVPLSCS	GGVSRNAHTP	SAARNIVCIG
251	MLMLARLLMG	AYICSIATMN	AINSPMVV*		

m276/a276 98.2% identity in 278 aa overlap

	10	20	30	40	50	60
m276.pep	MILPSSITMMRSAPSMVVRWATMMPVRF					
a276	MILPSSITMMRSAPSMVVRWATMMPVRF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m276.pep	FKMARAMATRCRCPPDKLLPFDPMGWCSPSGELSI					
a276	FKMARAMATRCRCPPDKLLPFDPMGWCSPSGELSI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m276.pep	FSNRVSSNRNTSWETRANWARRQSSILMSAMS					
a276	FSNRVSSNRNTSWETRANWARRQSSILMSAMS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m276.pep	PTRATRSPCLMSRLKLSRALMPSEYSTSTLRKLMPSTR					
a276	PTRATRSPCLMSRLKPSRALMPSEYSTSTLRKLMPSTR					
	190	200	210	220	230	240
	250	260	270	279		
m276.pep	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX					
a276	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1133>:

```
g277.seq (partial)
1  ..atggtacacg tcgccgtagc ttacggtatt gccgtccggc gtttttgccc
51  aaacgaggtc atagacgttt tccacgcctt gcaggtacat cgccaagcgt
101 tcgatgccgt aggtaatctt gccgagtagc ggcgtgcaat cgataccgcc
151 gacttggttg aaataggtaa actgggttac ttccatgccg ttgagccaga
201 cttcccagcc caaaccacac gcaccgaggg tgggggtttc ccagtcgtct
251 tcgacaaagc ggatgtcgtg gactttggga tcgatgccca attcgcgcag
301 ggagtcgaga tagaggtctt ggatattggc gggggcgggt ttgaggcgca
351 cttggaattg gtaatagtgt tgcaggcggg tgggggtgtc gccgtagcgg
401 ccgtcttttg ggcggcggct ggggttgacg taggcggcaa accaaggctc
451 gggggccgagc gcgcgcaggc aggtggcggg atgggatgtg ccggcaccga
501 cttccatgtc gaagggttg atgacgggtc agcctttgtc tgcccagaag
551 gtttgcagtt tgaagatgat ttggtggaag gtaagcatgg cttattgttc
601 gataaaataa aggttttatt ttactgtttc catagccgct tgaatagatt
651 tatctcgaag acagcctga
```

This corresponds to the amino acid sequence <SEQ ID 1134; ORF 277.ng>:

```
g277.pep (partial)
1  ..MVHVAVAYGI AVRRFCPNEV IDVFHALQVH ROAFDAVGNF AEYGRAIDTA
51  DLLEIGKLG Y FHAVEPDFPA QTPRTEGGVF PVVFDKADV DFGIDAQFAQ
101 GVEIEVL D I GGGFEGDLEL VIVLQAVGVV AVAAVFGAAA GLDVGGKPR L
151 GAERAQAGG MGCAGTDFHV EGLDDGA AFV CPEGLQFEDD LLEGKHGLLF
201 DKIKVLFYCF HSRLNRFISK TA*
```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1135>:

```
m277.seq
1  ATGCCCCGCT TTGAGGACAA GCTCGTAGGC AGGCAGGGCG AGGGCGGCGT
51  TTTCTTCGGC AAGCAGGCGT TTGGCTTGCG CTTCGTAGTC GTTGAACTGG
101 CGCAGCAGCC AGTCGGCATC GCTGTATTCTG AAGTTGTAGG TGGATTGCTC
151 GACTTCGTTT TGGTGGTACA CGTCGCCGTA GGTGACGGTG TTGCCGTGCA
201 GCGTTTTTGC CCAAACGAGG TCGTAGACGT TTTCTACACC TTGCAAGTAC
251 ATCGCCAAGC GTTCGATGCC GTAGGTGATT TCGCCGAGTA CGGGCGTGCA
301 GTCGATGCCG CCGACTTGTT GGAAATAGGT AACTGGGTT ACTTCCATGC
351 CGTTGAGCCA GACTTCCCAG CCCAAACCCC ACGCGCCGAG GGTGGGGTTT
401 TCCCAGTCGT CTTGACAAA GCGGATGTCG TGGACTTTGG GATCGATGCC
451 CAATTGCGC AGAGAGTCGA GATAGAGGTC TTGGATATTG GCGGGAGCGG
501 GCTTGAGGGC GACTTGGAAT TGGTAATAGT GTGCAGGCG GTTGGGGTTG
551 TCGCCGTAGC GGCCGTCTTT GGGGCGGCGG CTGGGTTGGA CGTAGGCGGC
601 AAACCAAGG TCGGGGCCGA GTGCGCGCAG GCAGGTGGCG GGATGGGATG
651 TGCCGGCACC GACTTCCATG TCGAAGGGT GGATGACGGT GCAGCCTTTG
701 TCTGCCAGA ATGTTTGCA TTTGAAGATG ATTTGTTGGA AGGTAAGCAT
751 GGCTTATGA
```

This corresponds to the amino acid sequence <SEQ ID 1136; ORF 277>:

```
m277.pep
1  MPRFEDKLVG RQEGGVFFG KQAFGLRFV VELAQQPVG AVFEVVGGLL
51  DFVLVVHVAV GDGVAVERFC PNEVVDVFT LQVHRQAFDA VGDFAEYGRA
101 VDAADLLEIG KLG Y FHAVEP DFPAQTPRAE GGVFPVVDK ADVVDFGIDA
151 QFAQRVEIEV LDIGSGLEG DLELVIVLQA VGVVAVAAVF GAAAGLDVGG
201 KPRLGAECAQ AGGGMGCAGT DFHVEGLDDG AAFVCPCEQL FEDDLLEGKH
251 GL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 277 shows 90.0% identity over a 221 aa overlap with a predicted ORF (ORF 277.ng) from *N. gonorrhoeae*:

g277/m277

g277.pep

10 20 30
MVHVAVAYGIAVRRFCPNEVIDVFHALQVH

631

```

                                :|||:|:|:|:|:|:|:|:|:|:|:|
m277      GLRFVVVELAQQPVGIAVFEVVGGLLDFVLVVHVAVGDGVAVERFCPNEVDVFYTLQVH
           30      40      50      60      70      80

           40      50      60      70      80      90
g277.pep   RQAFDAVGNFAEYGRAIDTADLLEIGKLGYPHVEPDPFAQTPTREGGVFPVFDKADV
           |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
m277      RQAFDAVGDFAEYGRAVDAADLLEIGKLGYPHVEPDPFAQTPRAEGGVFPVFDKADV
           90      100     110     120     130     140

           100     110     120     130     140     150
g277.pep   DFGIDAQFAQGVIEVLDIGGGFEGDLELVIVLQAVGVVAVAAVFGAAAGLDVGGKPRL
           |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
m277      DFGIDAQFAQGVIEVLDIGGGFEGDLELVIVLQAVGVVAVAAVFGAAAGLDVGGKPRL
           150     160     170     180     190     200

           160     170     180     190     200
g277.pep   GAERAQAGGGMGCAGTDFHVEGLDDGAAAFVCPEGLQFEDDLLEGKHGLL
           |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
m277      GAECAQAGGGMGCAGTDFHVEGLDDGAAAFVCPECLQFEDDLLEGKHGLX
           210     220     230     240     250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1137>:

```

a277.seq
1  ATGCCCCGCT TTGAGGACAA GCTCGTAGGC AGGCAGGGCG AGGGCGGCGT
51  TTTCTTCGCG AAGCAGGCGT TTGGCTTGCG CTTCTAGTGC GTTGAAC TGG
101 CGCAGCAGCC AATCGGCATC GCTGTATTGC AAGTTGTAGG TGGATTGTTT
151 GACTTCGTTT TGGTGGTACA CGTCGCCGTA AGTTACTGTA TTACCGTCCA
201 GCGTTTTTGC CCAAACGAGG TCATAGACGT TTTCCACGCC TTGCAGGTAC
251 ATCGCCAAGC GTTCGATGCC GTAGGTGATT TCGCCGAGTA CGGGGGTGCA
301 GTCGATGCCG CCGACTTGTT GGAAATAGGT GAACTGGGTT ACTTCCATAC
351 CGTTGAGCCA GACTTCCCAG CCCAAACCCC ACGCGCCGAG GGTGGGGTTT
401 TCCCAGTCGT CTTGACAAA GCGGATGTCG TGCAC TTTGG GGTGATGCC
451 CAATTCGCGC AGGGAGTCTG GATAGAGGTC TTGGATATTG GCGGGAGCGG
501 GCTTGAGGGC GACTTGGAAT TGGTAATAGT GTTGACAGCG GTTGGGGTTG
551 TCGCCGTAGC GACCGTCTTT GGGCGCGCGG CTGGGTGGA CGTAGGCGGC
601 AAACCAAGGC TCGGGGCCGA GTGCGCGCAG ACAGGTGGCG GGATGGGATG
651 TGCCGGCACC GACTTCCATG TCGAAGGGTT GGATGACGGT GCAGCCTTTG
701 TCTGCCCAGA ATGTTTGCAG TTTGAAGATG ATTTGTTGGA AGGTAAGCAT
751 GGCTTATGA

```

This corresponds to the amino acid sequence <SEQ ID 1138; ORF 277.a>:

```

a277.pep
1  MPRFEDKLVG RQEGGVFFG KQAFGLRFVV VELAQQPIGI AVFEVVGGLF
51  DFVLVVHVAV SYCITVQRFC PNEVIDVFHA LQVHRQAFDA VGDFAEYGGA
101 VDAADLLEIG ELGYFHTVEP DFPAQTPRAE GGVFPVFDK ADVVHFGVDA
151 QFAQGVIEV LDIGGSGLEG DLELVIVLQA VGVVAVATVF GAAAGLDVGG
201 KPRLGAECAQ TGGGMGCAGT DFHVEGLDDG AAFVCPECLQ FEDDLLEGKH
251 GL*

```

m277/a277 92.5% identity in 252 aa overlap

```

           10      20      30      40      50      60
m277.pep   MPRFEDKLVG RQEGGVFFG KQAFGLRFVV VELAQQPIGI AVFEVVGGLDFVLVVHVAV
           |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
a277      MPRFEDKLVG RQEGGVFFG KQAFGLRFVV VELAQQPIGI AVFEVVGGLDFVLVVHVAV
           10      20      30      40      50      60

           70      80      90      100     110     120
m277.pep   GDGVAVERFCPNEVDVFYTLQVHRQAFDAVGDFAEYGRAVDAADLLEIGKLGYPHVEP
           : :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
a277      SYCITVQRFCPNEVIDVFHALQVHRQAFDAVGDFAEYGGAVDAADLLEIGELGYFHTVEP
           70      80      90      100     110     120

           130     140     150     160     170     180

```

```

m277.pep    DFPAQTPRAEGGVFPVVFDAKADVDFGIDAQFAQRVEIEVLDIGGSGLEGDLELVIVLQA
a277        DFPAQTPRAEGGVFPVVFDAKADVVFHFGVDAQFAQGVIEVLDIGGSGLEGDLELVIVLQA
              130      140      150      160      170      180

              190      200      210      220      230      240
m277.pep    VGVVAVAAVFGAAAGLDVGGKPRLGAECAQAGGMGCAGTDFHVEGLDDGAAFVCPECLQ
a277        VGVVAVATVFGAAAGLDVGGKPRLGAECAQTGGGMGCAGTDFHVEGLDDGAAFVCPECLQ
              190      200      210      220      230      240

              250
m277.pep    FEDDLLEGKHGLX
a277        FEDDLLEGKHGLX
              250

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1139>:

```

g278.seq (partial)
1   ttgctgcaa tcacgcccgg tgcgattttt tcgacagggg cgggtcaaagt
51  tgtattaatc ggacctttgc cgtcgatagg ccgacccaat gcatcgacga
101 cgcgtccgac caattcgcgt cgcaccggca cttctaaaat acggccggta
151 caggtaaccg tgcgccttc tttaatatgt tcgtactcgc ccaacactac
201 ggcaccgacg gactcgcgct ccaggttcat cgccaagcct aaagtgttac
251 ccgggaattc gagcatctca ccttgcatg catctgacaa accatggatg
301 cgaacgatac cgtcagttac cgaaatcacc gtaccacggg tactcacttc
351 ggcatttaca gacagatttt cgatcttggc tttaatcaga tcgctaattt
401 cagcaggatt aagctgcatg aaaactctcc taattcgtca tagtcgtgta
451 caaagcactc agtttgctt gtacagacaa atccaaaacc tgatcaccca
501 cttcaacttt ta...

```

This corresponds to the amino acid sequence <SEQ ID 1140; ORF 278.ng>:

```

g278.pep (partial)
1   LRAITPGAIF STGAVKVLI GPLPSIGRPN ASTTRPTNSR PTGTSKIRPV
51  QVTVSPSLIC SYSPNTTAPT ESRSRFIAKP KVLPGNSSIS PCIASDKPWM
101 RTIPSVTEIT VPRVLTSFT DRFSILALIR SLISAGLSM KTLIRHSRV
151 QSTQFALYRQ IQNLITHFNF...

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1141>:

```

m278.seq..
1   TTGCGCGCAA TCACGCCCCG TGCGATTTTT TCGATAGGGG CGGTCAAAGT
51  TGTATTAATC GGGCCTTTGC CGTCGATAGG CCGACCCAAT GCATCAACGA
101 CCGCTCCGAC CAGTTCGCGT CCGACCGGCA CTTCCAAGAT ACGACCGGTA
151 CAGGTAACCG TGTCGCCTTC TTTAATGTGT TCGTACTCGC CCAACACTAC
201 GCGGCCGACG GAGTCGCGCT CCAGGTTTAT CGCCAAGCCG AAAGTGTTAC
251 CCGGGAATTC GAGCATCTCA CCTTGCATTG CATCTGACAA ACCATGGATG
301 CGAACGATAC CGTCAGTTAC CGAAATTACC GTACCACAGG TACGCACTTC
351 GGCATTTACA GACAGATTTT CGATCTTGGC TTTAATCAAA TCGCTAATTT
401 CAGCAGGATT AAGCTGCATG AAAACTCTCC TAATTCGTCA TAGTCGTGTA
451 CAAGGCACTC AATTTGCCTT GTACAGACAA ATCCAAAACC TGATCACCCA
501 CTTCAACTTT TATGCCGCCA ATCAGCTCCG GTTCGATTTC GACAGAGATT
551 TTCAGCTCGC TGTCGAAACG CTTATTCAGC ATTTGCACCA ACTCGCCGAC
601 CTGTTTGTCT GTCAACGGAT AGGCACTGTA AATGACGGCA GATTTGATAT
651 GGTGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1142; ORF 278>:

```

m278.pep
1   LRAITPGAIF SIGAVKVLI GPLPSIGRPN ASTTRPTSSR PTGTSKIRPV
51  QVTVSPSLMC SYSPNTTAPT ESRSRFIAKP KVLPGNSSIS PCIASDKPWM
101 RTIPSVTEIT VPOVRTSFT DRFSILALIK SLISAGLSM KTLIRHSRV
151 QGTQFALYRQ IQNLITHFNF YAANQLRFDL DRDFQLAVET LIQHLHQLAD
201 LFVQQRIGTV NDGRFDMVE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 278 shows 95.9% identity over a 170 aa overlap with a predicted ORF (ORF 278.ng) from *N. gonorrhoeae*:

g278/m278

	10	20	30	40	50	60
g278.pep	LRAITPGAIFSTGAVKVVLI	GPLPSIGRPNASTTRPTNSRPTGTSKIRPVQVTVSPSLIC				
m278	LRAITPGAIFSIGAVKVVLI	GPLPSIGRPNASTTRPTSSRPTGTSKIRPVQVTVSPSLMC				
	10	20	30	40	50	60
	70	80	90	100	110	120
g278.pep	SYPNTTAPTESRSRFIAKPKVLP	GNSSISPCIASDKPWMRTIPSVTEITVPRVLTSAFT				
m278	SYPNTTAPTESRSRFIAKPKVLP	GNSSISPCIASDKPWMRTIPSVTEITVPRVLTSAFT				
	70	80	90	100	110	120
	130	140	150	160	170	
g278.pep	DRFSILALIRSLISAGLS	CMKTLIRHSRVQSTQFALYRQIQNLITHFNF				
m278	DRFSILALIKSLISAGLS	CMKTLIRHSRVQSTQFALYRQIQNLITHFYAANQLRFDF				
	130	140	150	160	170	180
m278	DRDFQLAVETLIQHLHQLADLFV	QGRIQTVNDGRFDMVE*				
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ.ID 1143>:

a278.seq

```

1   TTGCGCGCAA TCACGCCCGG TCGGATTTTT TCGATAGGGG CGGTCAAAGT
51  TGTATTAATC GGGCCTTTGC CGTCGATAGG CCGACCCAAT GCATCAACGA
101 CGCGTCCGAC CAGTTCGCGT CCGACCGGCA CTCCAAGAT ACGACCGGTA
151 CAGGTAACCG TGTCGCCTTC TTTAATATGT TCGTGCTCGC CCAACACTAC
201 GGCGCCGACG GAGTCGCGCT CCAGGTTTCAT CGCCAAGCCG AAAGTGTTAC
251 CCGGGAATTC GAGCATCTCA CCTTGCATTG CATCTGACAA ACCATGGATG
301 CGAACGATAC CGTCAGTTAC CGAAATCACC GTACCACGGG TACGCACTTC
351 GGCATTTACA GACAGATTTT CGATCTTGGC TTTAATCAAA TCGCTAATTT
401 CAGCAGGATT AAGCTGCATG AAAACTCTCC TAATTCGTCA TAGTCGTGTA
451 CAAGGCACTC AATTTGCCTT GTACAGACAA ATCCAAAACC TGATCACCCA
501 CTTCAACTTT TATGCCGCCA ATCAGCTCCG GTTCGATTTT GACAGAGATT
551 TTCAGCTCGC TGTCGAAACG CTTATTCAGC ATTTGCGCCA ACTCGCCGAC
601 CTGTTTGTCG GTCAACGGAT AGGCACTGTA AATGACGGCA GATTTGATAT
651 GGTGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1144; ORF 278.a>:

a278.pep

```

1   LRAITPGAIF SIGAVKVVLI GPLPSIGRPN ASTTRPTSSR PTGTSKIRPV
51  QTVVSPSLIC SCSPTTAPT ESRSRFIAKP KVLPGNSSIS PCIASDKPWM
101 RTIPSVTEIT VPRVRTSAFT DRFSILALIK SLISAGLSCM KTLIRHSRV
151 QGTQFALYRQ IQNLITHFNF YAANQLRFDF DRDFQLAVET LIQHLRQLAD
201 LFVGQRIGTV NDGRFDMVE*

```

m278/a278 98.2% identity in 219 aa overlap

	10	20	30	40	50	60
m278.pep	LRAITPGAIFSIGAVKVVLI	GPLPSIGRPNASTTRPTSSRPTGTSKIRPVQVTVSPSLMC				
a278	LRAITPGAIFSIGAVKVVLI	GPLPSIGRPNASTTRPTSSRPTGTSKIRPVQVTVSPSLIC				
	10	20	30	40	50	60
	70	80	90	100	110	120
m278.pep	SYPNTTAPTESRSRFIAKPKVLP	GNSSISPCIASDKPWMRTIPSVTEITVPRVLTSAFT				
a278	SCSPNTTAPTESRSRFIAKPKVLP	GNSSISPCIASDKPWMRTIPSVTEITVPRVLTSAFT				
	70	80	90	100	110	120

	130	140	150	160	170	180
m278.pep	DRFSILALIKSLISAGLSCKMTLLIRHSRVQGTQFALYRQIQNLITHFNFYAANQLRFDF					
a278	DRFSILALIKSLISAGLSCKMTLLIRHSRVQGTQFALYRQIQNLITHFNFYAANQLRFDF					
	130	140	150	160	170	180
	190	200	210	220		
m278.pep	DRDFQLAVETLIQHLQLADLFVQGRIQTVNDGRFDMVEX					
a278	DRDFQLAVETLIQHLQLADLFVQGRIQTVNDGRFDMVEX					
	190	200	210	220		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1145>:

q279.seq

1	atgacgcgga	tttgcggctg	cttgatttca	acggttttga	gtgtttcggc
51	aagtttgtcg	gcggcggtt	tcatacaggct	gcaatgggaa	ggaacggata
101	ccggcagcgg	cagggcgcgt	ttggctccgg	cttctttggc	ggcagccatg
151	gtgcgtccga	cggcgcgggc	gttgctgca	atcacgactt	gtccggggcg
201	gttgaaattg	acggcttcga	ccacttcgcc	ctgtgcggat	tcggcacaaa
251	tctgcctgac	ctgttcattt	tccaaaccca	aaatggccgc	cattgcgctt
301	acgccttgcg	gtacggcgga	ctgcatcagt	tcggcgcgca	ggcggaacgag
351	tttgcagcga	tcggcaaaat	ccaatgcttc	ggcggcgaca	agcgcggtgt
401	attcgccgag	gctgtgtccg	gcaacggcgg	caggcgtttt	gccgcccaat
451	tccaaataac				

This corresponds to the amino acid sequence <SEQ ID 1146; ORF 279.ng>:

q279 . pep

```

1  MTRICGCLIS TVLSVSASLS AAGFIRLQWE GTDTGSGRAR LAPASLAAAM
51  VRPTAAALPA ITTCPGELKL TASTTSPCAD SAQICLTCSS SKPKMAAIAP
101 TPCGTADCIS SARRRTSLTA SAKSNASAAT SAVYSPRLCP ATAAGVLPPT
151 SK*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1147>:

m279.seq

1	ATAACGCGGA	TTTGC GGCTG	CTTGATTTC	ACGGTTTTCA	GGGCTTCGGC
51	AAGTTTGTCG	GCGGCGGGTT	TCATCAGGCT	GCAATGGGAA	GGTACGGACA
101	CGGGCAGCGG	CAGGGCGCGT	TTGGCACCGG	CTTCTTTGGC	GGCAGCCATG
151	GCGCGTCCGA	CGGCGGCGGC	GTTGCCTGCA	ATCACGATTT	GTCCGGGTGA
201	GTTGAAGTTG	ACGGCTTCGA	CCACTTCGCT	TTGGGCGGCT	TCGGCACAAA
251	TGGCTTTAAC	CTGCTCATCT	TCCAAGCCGA	GAATCGCCGC	CATTGCGCCC
301	ACGCCTTGCG	GTACGGCGGA	CTGCATCAGT	TCGGCGCGCA	GGCGCACGAG
351	TTTGACCGCG	TCGGCAAAAT	TCAATGCGCC	GGCGGCAACG	AGTGCGGTGT
401	ATTGCCCGAG	GCTGTGTCCG	GCAACGGCGG	CAGGCGTTTT	GCCGCCCGCT
451	TCTAAATAG				

This corresponds to the amino acid sequence <SEQ ID 1148; ORF 279>:

m279.pep

```

1  ITRICGCLIS TVFRASASLS AAGFIRLQWE GTDTGSGRRAR LAPASLAAAM
51  ARPTAAALPA ITICPGELKL TASTTSLWAA SAQMALTCSS SKPRIAAIAP
101 TPCGTADCIS SARRRTSLTA SAKFNAPAAT SAVYSPRLCP ATAAGVLP
151 SK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 279 shows 89.5% identity over a 152 aa overlap with a predicted ORF (ORF 279.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m279.pep	ITRICGCLISTVFRASASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMARPTAAALPA					
	: : : : : : : : : : : :					
g279	MTRICGCLISTVLSVSASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMVRPTAAALPA					
	10	20	30	40	50	60
	70	80	90	100	110	120

a279.seq

1	ATGACNCNGA	TTTGC GGCTG	CTTGATTTCA	ACGGTTTNNNA	GGGCTTCGGC
51	GAGTTTGTCG	GCGGCGGGTT	TCATGAGGCT	GCAATTGGGA	GGTACNGACA
101	CNCGCAGCGG	CAGGCGCGCT	TTGGCGCCGG	CTCTTTTGGC	GGCAAGCATA
151	GCGCGCTCGA	GCGGCGCGGC	ATTGCCTGCA	ATCACGACTT	GTCGCGGCGA
201	GTTGAAGTTG	ACGGCTTCAA	CCACTTCATC	CTGTGCGGAT	TCGGCGCAAA
251	TTTGTTTAC	CTGTTTCATCT	TCCAAGCCGA	GAATCGCCGC	CATTGCGCCC
301	ACGCCTTGCG	GTACGGCGGA	CTGCATCAGT	TCGGCGCGCA	NGCGCACGAG
351	TTTGACCGCG	TCGGCAAAAT	CCAATGCGCC	GGCGGCAACN	AGTGCGGTGT
401	ATTGCGCGAN	GCTGTGTCCG	GCAACGGCGG	CAGGCGTTTT	GCCGCCCGCT
451	TCCGAATAG				

```
a279.pep
1  MTXICGCLIS TVXRASASLS AAGFMRLQWE GTDTGSGRAR LAPASLAASI
51  ARSTAAALPA ITTCPGELKL TASTTSSCAD SAQICFTCSS SKPRIAAIAP
101 TPCGTADCIS SARXRTSLTA SAKSNAPAAAT SAVYSPXLCP ATAAGVLPPA
151 SE*
```

	10	20	30	40	50	60
m279.pep	ITRICGCLISTVFRASASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMARPTAAALPA					
	: : :					
a279	MTXICGCLISTVXRASASLSAAGFMRLQWEGTDTGSGRARLAPASLAASIARSTAAALPA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m279.pep	ITICPGELKLTAFTTSLWAASAQMALTCSSSKPRIAAIAPTTCGTADCISSARRRTSLTA					
	:					
a279	ITTCPGELKLTAFTTSSCADSAQICFTCSSSKPRIAAIAPTTCGTADCISSARXRTSLTA					
	70	80	90	100	110	120
	130	140	150			
m279.pep	SAKFNAPAATSAVYSPRLCPATAAGVLPPASKX					
a279	SAKSNAPAATSAVYSPXLCPPATAAGVLPPASEX					
	130	140	150			

BNSDOCID: <WO 8957280A2 | >

1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 279 and the amino acid sequence encoded thereby is provided herein.

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1151>:

g280.seq

```

1  atgaaacacc tcaaacttac ccttattgcc gcattgctgg ccaccgccgc
51  aactgccgca ccccttccgg ttgtaaccag tttcagcatt ttaggcgacg
101 tagccaaaca aatcggcggt gagcgcgtag ccgtacaaag cctcgtcgga
151 gccaaaccaag atactcatgc ctatcacatg accagtggcg acattaaaaa
201 aatccgcagt gcaaaactcg tcctgctcaa cggcttggga cttgaagccg
251 ccgacatcca acgcgcgcgtc aaacagagca aagtatccta tgccgaagcg
301 accaaaggca tccaaccctt caaagccgaa gaagaaggcg gacaccatca
351 cgaccaccat cagaccacg atcatgacca cgaaggacac caccacgacc
401 acggcgcaata tgaccccccac gtctggaacg accctgttct tatgtccgac
451 tatgccc aaa acgtcgctga aacctgata aaggccgac cgaaggcaa
501 agtttattat caacaacgct tgggcaacta ccaaagcag cttaaaaaac
551 tgcacagcga cgcacaagcc gcatttaatg ccgtccctgc cgccaaacgc
601 aaagtccctga ccgggcacga cgcattttcc tacatgggca accgctacaa
651 catcagcttc atcgccccgc aaggcgtgag cagcgaagcc gagccgtccg
701 ccaaacaagt cgccgccatc atccggcaaa tcaaacgcga aggcacaaa
751 gccgtatttta ccgaaaatat caaagacacc cgcattggtg accgcacgc
801 caaagaaacc ggcgtaacg tcagcggcaa actgtattcc gacgcactcg
851 gcaacgcgcc cgcagacacc tacatcgcca tgtaccgcca caacgtcgaa
901 gccttgacca acgcgatgaa gcaataa

```

This corresponds to the amino acid sequence <SEQ ID 1152; ORF 280.ng>:

g280.pep

```

1  MKHLKLTLIA ALLATAATAA PLPVVTSFSI LGDVAKQIGG ERVAVQSLVG
51  ANQDTHAYHM TSGDIKKIRS AKLVLLNGLG LEAADIQRAV QSKVSYAEA
101 TKGIQPLKAE EGGHHHDH HDHHDHDEGH HHDHGEYDPH VWNDPVLMDS
151 YAQNVAETLI KADPEGKVYY QQRLGNYQMQ LKKLHSDAQA AFNAVPAKR
201 KVLTHGDAFS YMGNRYNISF IAPQVSSEA EPSAKQVAI IRQIKREGIK
251 AVFTENIKDT RMDRIAKET GNVVSGKLYS DALGNAPADT YIGMYRHVNE
301 ALTNAMKQ*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1153>:

m280.seq

```

1  ATGAAACACC TCAAACCTCAC CTTATTGCC GCATTGCTGA CCGCCTCCGC
51  AACTGCCGCC CCCCTGCCGG TTGTAACCAG CTTACGATT TTAGGCGACG
101 TAGCCAAACA AATCGGCGGA GAGCGCGTAT CCATACAAAG TTTGGTCGGA
151 GCCAACCAAG ATACGCACGC CTATCATATG ACCAGTGGCG ACATTAAAAA
201 AATCCGCAGT GCAAAACTCG TCCTGCTCAA CGGCTTAGGA CTTGAAGCTG
251 CCGATGTGCA ACGCGCCGTC AAACAAAGCA AAGTATCCTA TACCGAAGCG
301 ACCAAAGGCA TCCAACCCCT CAAAGCCGAA GAAGAAGGCG GACACCATCA
351 CGACCACGAT CATGACCACG AAGGACACCA CCATGACCAC GGCGAATATG
401 ACCCGCACGT CTGGAACGAC CCCGTCCTTA TGTCCGCTA TGCCCAAAAC
451 GTTGCCAAAG CCCTGATAAA GGCCGATCCC GAAGGCAAAG TTTATTATCA
501 ACAACGCTTG GGCAACTACC AAATGCAGCT CAAAAAAGT CACAGCGACG
551 CACAAGCCGC ATTTAATGCC GTCCCTGCTG CCAAACGCAA AGTCCTGACC
601 GGGCACGATG CCTTTTCCTA TATGGGCAA CGTTACCATA TCGAATTCAT
651 CGCCCCGCAA GGCGTGAGCA GCGAAGCCGA GCCTTCGGCC AAACAAGTCG
701 CCGCCATCAT CCGACAAATC AAACGCGAAG GCATCAAAGC CGTCTTTACC
751 GAAAACATCA AGGACACCCG TATGGTTGAC CGTATCGCCA AAGAAACCGG
801 TGTCAACGTC AGCGGCAAAC TGTATTCCGA CGCACTCGGC AACCGGCCCCG
851 CAGACACCTA CATCGGAATG TACCGCCACA ACATCAAAGC CTTGACCAAC
901 GCGATGAAGC AATAA

```

This corresponds to the amino acid sequence <SEQ ID 1154; ORF 280>:

m280.pep

```

1  MKHLKLTLIA ALLTASATAA PLPVVTSFSI LGDVAKQIGG ERVSIQSLVG
51  ANQDTHAYHM TSGDIKKIRS AKLVLLNGLG LEAADVQRAV QSKVSYTEA
101 TKGIQPLKAE EGGHHHDH HDHEGHHHDH GEYDPHVWND PVLMSAYAQN
151 VAKALIKADP EGKVYYQQL GNYQMQLKKL HSDAQAAFNA VPAKRKVL

```


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201 GHDAFSYMGK RYHIEFIAPQ GVSSEAEPSA KQVAAIIRQI KREGIKAVFT
 251 ENIKDTRMVD RIAKETGVNV SGKLYSDALG NAPADTYIGM YRHNKALTN
 301 AMKQ*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 280 shows 93.8% identity over a 308 aa overlap with a predicted ORF (ORF 280.ng)
 from *N. gonorrhoeae*:

m280/g280

	10	20	30	40	50	60
m280.pep	MKHLKLTLIAALLTASATAAPLPVVTFSILGDVAKQIGGERVSIQSLVGANQDTHAYHM					
	::					
g280	MKHLKLTLIAALLATAATAAPLPVVTFSILGDVAKQIGGERVAVQSLVGANQDTHAYHM					
	10	20	30	40	50	60
	70	80	90	100	110	119
m280.pep	TSGDIKKIRSAKLVLLNGLGLEAADVQRAVKQSKVSYTEATKGIQPLKAEEEGGHHHDH-					
	:					
g280	TSGDIKKIRSAKLVLLNGLGLEAADIQRAVKQSKVSYAEATKGIQPLKAEEEGGHHHDH					
	70	80	90	100	110	120
	120	130	140	150	160	170
m280.pep	---DHDHEGHHHDHGEYDPHVWNDPVLMSAYAQNVAKALIKADPEGKVYYQQLGNYQMQ					
	:					
g280	HDHDHDHEGHHHDHGEYDPHVWNDPVLMSDYAQNVAETLIKADPEGKVYYQQLGNYQMQ					
	130	140	150	160	170	180
	180	190	200	210	220	230
m280.pep	LKKLHSDAQAAFNAVPAAKRKVLTGHDAFSYMGKRYHIEFIAPQGVSSAEPSAKQVAAI					
	:					
g280	LKKLHSDAQAAFNAVPAAKRKVLTGHDAFSYMGNRYNISFIAPQGVSSAEPSAKQVAAI					
	190	200	210	220	230	240
	240	250	260	270	280	290
m280.pep	IRQIKREGIKAVFTENIKDTRMVDRIAKETGVNVSGKLYSDALGNAPADTYIGMYRHNK					
	:					
g280	IRQIKREGIKAVFTENIKDTRMVDRIAKETGVNVSGKLYSDALGNAPADTYIGMYRHNVE					
	250	260	270	280	290	300
	300					
m280.pep	ALTNAMKQX					
g280	ALTNAMKQX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1155>:

a280.seq

1	ATGAAACACC	CCAAACTCAC	CCTTATCGCC	GCATTGCTGA	CCACTGCCGC
51	AACTGCCGCC	CCCCTGCCGG	TTGTAACCAG	CTTCAGCATT	TTAGCGCAGC
101	TAGCCAAACA	AATCGGCGGA	GAGCGCGTAT	CCATACAAAG	TTTGGTCGGA
151	GCCAACCAAG	ATACGCACGC	CTATCATATG	ACCAGCGGCG	ACATTAAAAA
201	AATCCGCAGT	GCAAAACTCG	TCCTGATTAA	CGGCTTAGGA	CTTGAAGCTG
251	CCGACATCCA	ACGTGCCGTC	AAACAGAGCA	AAGTATCCTA	TGCCGAAGCG
301	ACCAAAGGCA	TCCAACCCCT	CAAAGCCGAA	GAAGAAGGCG	GACACCATCA
351	CGACCACGAT	CATGACCACG	ACCATGACCA	CGAAGGACAC	CACCACGACC
401	ACGGCGAATA	TGACCCCCAC	GTCTGGAACG	ACCCCGTCTT	TATGTCCGCC
451	TATGCCCAAA	ACGTGCGCGA	AGCCCTGATA	AAGGCCGACC	CCGAAGGCAA
501	AGTTTATTAT	CAACAACGCT	TGGGCAACTA	CCAAATGCAG	CTCAAAAAAC
551	TGCACAGTGA	CGCACAAGCC	GCATTTAATG	CCGTCCCTGC	CGCCAAACGC
601	AAAGTCCTGA	CCGGGCACGA	TGCCTTTTCC	TATATGGGCA	AACGTTACCA
651	TATCGAATTC	ATCGCCCCAC	AAGGTGTGAG	CAGCGAAGCC	GAGCCTTCAG
701	CCAAACAAGT	CGCCGCCATC	ATCCGACAAA	TCAAACGCGA	AGGCATCAAA
751	GCCGTATTTA	CCGAAAATAT	CAAAGACACC	CGCATGGTTG	ACCGCATCGC

638

801 CAAAGAAACC GGTGTCAACG TCAGCGGCAA ACTGTATTCC GACGCACTCG
 851 GCAACGCACC CGCAGACACC TACATCGGCA TGTACCGCCA CAACATCAAA
 901 GCCTTAACCA ACGCGATGAA GCAATAA

This corresponds to the amino acid sequence <SEQ ID 1156; ORF 280.a>:

a280.pep
 1 MKHKPLTLIA ALLTTAATAA PLPVVTSFSI LGDVAKQIGG ERVSIQSLVG
 51 ANQDTHAYHM TSGDIKKIRS AKLVLINGLG LEAADIQRAV KQSKVSYAEA
 101 TKGIQPLKAE EEGGHHHDHD HDHDHDEGH HHDHGEYDPH VWNDPVLMSA
 151 YAQNVAEALI KADPEGKVYY QORLGNYQMQ LKKLHSDAQA AFNAVPAAKR
 201 KVLTHGDAFS YMGKRYHIEF IAPQGSSEA EPSAKQVAAI IRQIKREGIK
 251 AVFTENIKDT RMVDRIAKET GVNVSGLKLYS DALGNAPADT YIGMYRHNK
 301 ALTNAMKQ*

m280/a280 96.4% identity in 308 aa overlap

m280.pep	10	20	30	40	50	60
	MKHLKLTLIAALLTASATAAPLPVVTFSISILGDVAKQIGGERVSIQSLVGANQDTHAYHM					
a280	MKHKPLTLIAALLTTAATAAPLPVVTFSISILGDVAKQIGGERVSIQSLVGANQDTHAYHM					
	10	20	30	40	50	60
m280.pep	70	80	90	100	110	120
	TSGDIKKIRS AKLVLLNGLGLEAADVQRAVKQSKVSYTEATKGIQPLKAE EGGHHHDHD					
a280	TSGDIKKIRS AKLVLLNGLGLEAADVQRAVKQSKVSYAEATKGIQPLKAE EGGHHHDHD					
	70	80	90	100	110	120
m280.pep	130	140	150	160	170	
	HDH---EGHHHDHGEYDPHVWNDPVLMSAYAQNVAKALIKADPEGKVYYQORLGNYQMQ					
a280	HDHDHDEGHHHDHGEYDPHVWNDPVLMSAYAQNVAEALIKADPEGKVYYQORLGNYQMQ					
	130	140	150	160	170	180
m280.pep	180	190	200	210	220	230
	LKKLHSDAQA AFNAVPAAKRKVLTHGDAFSYMGKRYHIEFIAPQGSSEA EPSAKQVAAI					
a280	LKKLHSDAQA AFNAVPAAKRKVLTHGDAFSYMGKRYHIEFIAPQGSSEA EPSAKQVAAI					
	190	200	210	220	230	240
m280.pep	240	250	260	270	280	290
	IRQIKREGIKAVFTENIKDTRMVDRIAKETGVNVSGKLYSDALGNAPADTYIGMYRHNK					
a280	IRQIKREGIKAVFTENIKDTRMVDRIAKETGVNVSGKLYSDALGNAPADTYIGMYRHNK					
	250	260	270	280	290	300
m280.pep	300					
	ALTNAMKQX					
a280	ALTNAMKQX					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1157>:

g281.seq
 1 atgcactacg ccctcgcatc cgtcttctgc ctgtccctca gcgcgcgacc
 51 cgctggcgta ttctcgta tgcgcgat gagcctgata ggcgacgcat
 101 tgagccacgc cgtcctgccc ggtgcccgcg tcggctacat gtttgccggc
 151 ttgagcctgc ccgctatggg tgtggcgagg tttgcccgcg gtatgctgat
 201 ggcgctgctt gccggactcg tcagccgctt taccaccctg aaagaagatg
 251 ccaactttgc cgccttttac ctgagcagcc tcgccatcgg cgtaatcctc
 301 atcagcaaaa acggcagcag cgtcgattta ctccacctcc ttttcggatc
 351 tgtgcttgcc gtcgatattc ccgcactgca actcatcgcc gccgtctccg
 401 gcctcacgct cattaccctt gccgtcatct accgccccct ggtgctagaa
 451 agcatagacc cccttttctt caagtccgct aacggcaaag gcgggctttg

```

501 gcacgtcatt ttcctcatcc tcgtcggtat gaacctcgta tccggtttcc
551 aagctctcgg catcctgatg tcggtcggaa ttatgatgct gcccgccatt
601 accgcccgtt tatgggcaag aaatatgggg acgctcattc tgttgccgt
651 cctcatcgcc cttttttgcg gtttgatcgg gctgctcatt tcctaccaca
701 tcgaaatccc ttccggcccc gccatcatcc tctgttgag cgctctttat
751 cttttttccg tcatactcgg caaagaaggc ggcattctgc ccaaattggtt
801 caaaaaccac cgccaccaca ccacctga

```

This corresponds to the amino acid sequence <SEQ ID 1158; ORF 281.ng>:

g281.pep

```

1  MHYALASVFC  LSLSAAPVGV  FLVMRRMSLI  GDALSHAVLP  GAAVGYMFAG
51  LSLPAMGVGG  FAAGMLMALL  AGLVSRFTTL  KEDANFAAFY  LSSLAIGVIL
101 ISKNGSSVDL  LHLLFGSVLA  VDIPALQLIA  AVSGLTLITL  AVIYRPLVLE
151 SIDPLFLKSV  NGKGGWLWHVI  FLVLVVMNLV  SGFQALGILM  SVGIMMLPAI
201 TARLWARNMG  TLILLSVLI  LFCGLIGLLI  SYHIEIPSGP  AIILCCSVLY
251 LFSVILGKEG  GILPKWFKNH  RHHTT*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1159>:

m281.seq (partial)

```

1  ATGCGCTACG  CCCTCGCATC  CGTCTTCTGC  CTGTCCCTCA  GTGCCGCACC
51  CGTCGGCGTA  TTCCTCGTCA  TGCGCCGTAT  GAGCCTGATA  GGCGACGCAT
101 TGAGCCACGC  CGTCCTGCCC  GGTGCCGCCG  TCGGCTACAT  GTTTGCCGGC
151 TTGAGCCTGC  CCGCCATGGG  TTTGGGCGGC  GTAGCCGAG  GCATGCTGAT
201 GGCACCTGCTT  GCCGGACTCG  TCAGCCGCTT  CACCACCCTG  AAAGAAGATG
251 CCAACTTTGC  CGCCTTTTAT  CTCAGCAGCC  TCGCCATCGG  CGTAGTCCTC
301 GTCAGCAAAA  ACGGGAGCAG  CGTCGATTG  CTCCACCTCC  TTTTCGGCTC
351 TGTACTTGCC  GTCGATATTC  CTGCCCTGCA  GCTCATCGCC  GCCGTCTCCA
401 GCCTCACGCT  CATTACCCTT  GCCGTCATCT  ACCGCCCGCT  CGTACTCGAA
451 AGCATCGACC  CCCTGTTTCT  CAAATCCGTC  GGCGGCAAAG  GCGGGCTTTG
501 GCACGCTCTC  TTTCTCGTCC  TGGTCGTCAT  GAACCTCGTA  TCCGGCTTTC
551 AAGCCCTCGG  CACACTCATG  TCCGTCGGAC  TCATGATGCT  GCCAGCCATT
601 ACCGCCCGCC  TGTGGGCGAA  GCATATGGGC  GCACTCATCC  TCCTATCCGT
651 TCTGACAGCC  CTGCTGTGCG  GCTTGAGCGG  ACTGCTCATT  TCCTACCACA
701 TCGAAATTCC  TTCCGGTCCC  GCCATCATCC  TCTGTTGCAG  CGTCTTTTAT
751 CTCTTTTCCG  TCATACTCGG  CAAAGAAGGC  GGCATTCTGA  CC..

```

This corresponds to the amino acid sequence <SEQ ID 1160; ORF 281>:

m281.pep (partial)

```

1  MRYALASVFC  LSLSAAPVGV  FLVMRRMSLI  GDALSHAVLP  GAAVGYMFAG
51  LSLPAMGLGG  VAAGMLMALL  AGLVSRFTTL  KEDANFAAFY  LSSLAIGVVL
101 VSKNGSSVDL  LHLLFGSVLA  VDIPALQLIA  AVSSLTLITL  AVIYRPLVLE
151 SIDPLFLKSV  GGKGGWLWHVL  FLVLVVMNLV  SGFQALGILM  SVGLMMLPAI
201 TARLWAKHMG  ALILLSVLTA  LLCGLSGLLI  SYHIEIPSGP  AIILCCSVLY
251 LFSVILGKEG  GILT..

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 281 shows 93.5% identity over a 263 aa overlap with a predicted ORF (ORF 281.ng) from *N. gonorrhoeae*:

m281/g281

```

          10          20          30          40          50          60
m281 . pep  MRYALASVFCLSLSAAPVGVFLVMRRMSLIGDALSHAVLPAAVGYMFAGLSLPAMGLGG
          | : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : ||
g281        MHYALASVFCLSLSAAPVGVFLVMRRMSLIGDALSHAVLPAAVGYMFAGLSLPAMGVGG
          10          20          30          40          50          60

          70          80          90          100         110         120
m281 . pep  VAAGMLMALLAGLVSRTTLKEDANFAAFYLSSLAIGVVLVSKNGSSVDLLHLLFGSVLA
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g281        FAAGMLMALLAGLVSRTTLKEDANFAAFYLSSLAIGVILISKNGSSVDLLHLLFGSVLA
          70          80          90          100         110         120

          130         140         150         160         170         180
m281 . pep  VDIPALQLIAAVSSLTLITLAVIYRPLVLESIDPLFLKSVGGKGGWLWHVLFLVLVVMNLV

```

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```

g281      |||||:|||||:|||||:|||||:|||||
          130      140      150      160      170      180
          190      200      210      220      230      240
m281.pep  SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP
          |||||:|||||:|||||:|||||:|||||:|||||
g281      SGFQALGILMSVGIMMLPAITARLWARNMGTLLILLSVLIALFCGLIGLLISYHIEIPSGP
          190      200      210      220      230      240
          250      260
m281.pep  AIILCCSVLYLFSVILGKEGGILT
          |||||:|||||:|||||:|||||
g281      AIILCCSVLYLFSVILGKEGGILPKWFKNHRHHTTX
          250      260      270

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1161>:

```

a281.seq
1   ATGCGCTACG CCCTCGCATC CGTCTTCTGC CTGTCCCTCA GTGCCGCACC
51  CGTCGGCGTA TTCCTCGTCA TGCGCCGTAT GAGCCTGATA GGCGACGCAT
101 TGAGCCACGC CGTCTGCCC GGTGCCGCCG TCGGCTACAT GTTTGCCGGC
151 TTAAGCCTGC CCGCCATGGG TTTGGGCGGC GTAGCCGCAG GTATGCTGAT
201 GGCACGTGCTT GCCGGACTCG TCAGCCGCTT CACCACCCTG AAAGAAGATG
251 CCAACTTTGC CGCCTTTTAT CTCAGCAGCC TCGCCATCGG TGTAGTCCTC
301 GTCAGCAAAA ACGGCAGCAG CGTCGATTG CTCCACCTCC TTTTCGGCTC
351 CGTACTTGCC GTCGATATTC CTGCCCTGCA ACTCATCGCC GCCGTATCCA
401 CCCTCACACT GCTTACCCTT GCCGTCATCT ACCGCCCGCT CGTACTCGAA
451 AGCATCGACC CCCTGTTTCT CAAATCTGTC GGCGGCAAAG GCGGGCTTTG
501 GCACGTCCTC TTTCTCGTCC TGGTCGTCAT GAACCTCGTA TCCGGCTTTC
551 AAGCCCTCGG CACACTCATG TCCGTCGGAC TTATGATGCT GCCAGCCATT
601 ACCGCCCGCC TATGGGCGAA GCACATGGGC GCACTCATCC TCCTATCCGT
651 TCTGACAGCC CTGCTGTGCG GCTTGAGCGG ACTGCTCATT TCCTACCACA
701 TCGAAATTCC TTCCGGTCCC GCCATCATCC TCTGTTGCAG CGTCCTTTAT
751 CTCTTTTCCG TCATACTCGG CAAAGAAGGC GGCATTCTGA CCAAATGGCT
801 CAAAACCAC  CGCCACCACA CCACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1162; ORF 281.a>:

```

a281.pep
1   MRYALASVFC LSLSAAPGV FLVMRRMSLI GDALSHAVLP GAAVGYMFAG
51  LSLPAMGLGG VAAGMLMALL AGLVSRFTTL KEDANFAAFY LSSLAIGVVL
101 VSKNGSSVDL LHLLFGSVLA VDIPALQLIA AVSTLTLLTL AVIYRPLVLE
151 SIDPLFLKSV GKGGLWHVL FLVLVVMNLV SGFQALGTLM SVGLMMLPAI
201 TARLWAKHMG ALILLSVLT LLCLSGLLI SYHIEIPSGP AIILCCSVLY
251 LFSVILGKEG GILTKWLNH RHHTT*

```

m281/a281 99.2% identity in 264 aa overlap

```

          10      20      30      40      50      60
m281.pep  MRYALASVFC LSLSAAPGV FLVMRRMSLI GDALSHAVLP GAAVGYMFAG LSLPAMGLGG
          |||||:|||||:|||||:|||||:|||||:|||||
a281      MRYALASVFC LSLSAAPGV FLVMRRMSLI GDALSHAVLP GAAVGYMFAG LSLPAMGLGG
          10      20      30      40      50      60
          70      80      90      100     110     120
m281.pep  VAAGMLMALL AGLVSRFTTL KEDANFAAFY LSSLAIGVVL VSKNGSSVDL LHLLFGSVLA
          |||||:|||||:|||||:|||||:|||||:|||||
a281      VAAGMLMALL AGLVSRFTTL KEDANFAAFY LSSLAIGVVL VSKNGSSVDL LHLLFGSVLA
          70      80      90      100     110     120
          130     140     150     160     170     180
m281.pep  VDIPALQLIA AVSSLT LITLAVIYRPLV LESIDPLFLK SVGGKGGLWHV LFLVLVVMNLV
          |||||:|||||:|||||:|||||:|||||:|||||
a281      VDIPALQLIA AVSTLT LLLTAVIYRPLV LESIDPLFLK SVGGKGGLWHV LFLVLVVMNLV
          130     140     150     160     170     180

```

641

	190	200	210	220	230	240
m281.pep	SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP					
a281	SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP					
	190	200	210	220	230	240
	250	260				
m281.pep	AIILCCSVLYLFSVILGKEGGILT					
a281	AIILCCSVLYLFSVILGKEGGILT		KWLKNHRHHTTX			
	250	260	270			

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1163>:

g282.seq

```

1  atgggattgg gtatggaaat cggcaagctg attgtggctc ttttgggtgct
51  gatcaatccg tttagcgcgt tgcgcttta cttgacctg accaacggac
101 acagcacgaa ggagcgcagg aaggtcgcgc ggacggccgc cgtcgccgtg
151 tttgccgtga ttgcggtatt tgcgctgac ggcggtgcgc tattgaaggt
201 tttgggcatc agcgtcggtt cgtttcaggt cggcggcggg attttgggtg
251 tgctgatcgc catttcgatg atgaacggca acgacaatcc cgccaagcag
301 aatctcggcg cgcagccgga aacggggcaa gcgcgccccg cccgcaatgc
351 aggggcgatt gccgtcgtgc ccatcgccat accgatcacc atcggtcggt
401 gcggtatttc gactgtgatt atttatgctt cggcagccaa aacgtacagc
451 gatatcgcgc tgattatcgc ggccggtttg gtggtcagtg cgatttggtt
501 tgccatttta atcggtgccc ggaaggctcag ccgcctgctg ggcgcgacgg
551 ggctgacgat tttaaaccgc attatgggta tgatgctggc ggcggtatcg
601 gtggagatta ttgtgtcggg actgaaaacg atattcccgc aactggcagg
651 ttga

```

This corresponds to the amino acid sequence <SEQ ID 1164; ORF 282.ng>:

g282.pep

```

1  MGLGMEIGKL IVALLVLINP FSALSLYLDL TNGHSTKERR KVARTAAVAV
51  FAVIAVFALI GGALLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKO
101 NLGAQPETGQ ARPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAAKTYS
151 DIALIIAAGL VVSAICYAIL IVAGKVSRLI GATGLTILNR IMGMMMLAAVS
201 VEIIVSGLKT IFPQLAG*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1165>:

m282.seq

```

1  ATGGGATTGG GCATGGAAAT CGGCAAGCTG ATTGTGGCTT TTTTGGTGCT
51  GATTAATCCG TTTAGCGCGT TGTCGCTTTA CCTTGACCTG ACCAACGGGC
101 ACAGCACGAA GGAGCGCAGG AAGGTCGCGC GGACGGCCGC CGTTGCCGTG
151 TTTGCCGTGA TTGCGGTATT TGCCTGATC GGCGGTACGC TGCTGAAGGT
201 TTTGGGCATC AGCGTCGGTT CGTTTCAGGT CGGCGGCGGG ATTTTGGTGC
251 TGCTGATCGC CATTTCGATG ATGAACGGCA ACGACAATCC CGCCAAGCAG
301 AATCTCGGCG CGCAGCCGGA AACGGGGCAG GCGCGCCCCG CCGCAATGC
351 CGGAGCGATT GCCGTCGTGC CCATCGCCAT ACCGATCACC ATCGGCCCCG
401 GCGGTATTTT GACCGTGATT ATTTACGCTT CGGCGGCTAA AACATACGGC
451 GACATCGCGT TGATTATCGC GGCCGGTTTG GTGGTCAGTG CGATTGTGTA
501 TGCCATTTTA ATCGTTGCCG GGAAGGTCAG CCGCCTGCTG GGCGCGACGG
551 GGCTGACGAT TTAAACCGC ATTATGGGTA TGATGCTGGC GGCGGTATCG
601 GTGGAGATTA TTGTGTCGGG ACTGAAAACG ATATTCCCGC AACTGGCAGG
651 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1166; ORF 282.ng>:

m282.pep

```

1  MGLGMEIGKL IVAFLVLINP FSALSLYLDL TNGHSTKERR KVARTAAVAV
51  FAVIAVFALI GGTLLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKO
101 NLGAQPETGQ ARPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAAKTYG
151 DIALIIAAGL VVSAICYAIL IVAGKVSRLI GATGLTILNR IMGMMMLAAVS
201 VEIIVSGLKT IFPQLAG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 282 shows 98.6 % identity over a 217 aa overlap with a predicted ORF (ORF 282.ng) from *N. gonorrhoeae*:

m282/g282

	10	20	30	40	50	60
m282.pep	MGLGMEIGKLIVAFVLINPFSALSPLYDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
	:					
g282	MGLGMEIGKLIVALLVLINPFSALSPLYDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m282.pep	GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQARPARNAGAI					
	:					
g282	GGALLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQARPARNAGAI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m282.pep	AVVPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL					
	:					
g282	AVVPIAIPITIGPGGISTVIIYASAAKTYSDIALIIAAGLVVSAICYAILIVAGKVSRL					
	130	140	150	160	170	180
	190	200	210			
m282.pep	GATGLTILNRIMGMMMLAAVSVEIIVSGLKTIFPQLAGX					
g282	GATGLTILNRIMGMMMLAAVSVEIIVSGLKTIFPQLAGX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1167>:

```
a282.seq
1  ATGGGATTGG GCATGGAAAT CGGCAAGCTG ATTGTGGCTT TTTTGGTGCT
51  GATTAATCCG TTTAGCGCGT TGTCGCTTTA CCTTGACCTG ACCAACGGGC
101 ACAGCACGAA GGAGCGCAGG AAGGTCGCGC GGACGGCCGC CGTTGCCGTG
151 TTTGCCGTGA TTGCGGTATT TGCGCTGATC GGCGGTACGC TGCTGAAGGT
201 TTTGGGCATC AGCGTCGGTT CGTTTCAGGT CGGCGGCGGA ATTTTGGTGT
251 TGCTGATTGC CATTTTCGATG ATGAACGGCA ACGACAATCC CGCCAAGCAG
301 AATCTCGGCG CGCAGCCGGA AACGGGGCAG GTGCGCCCCG CCCGCAATGC
351 CGGAGCGATT GCCGTCGTGC CCATCGCCAT ACCGATCACC ATCGGCCCGG
401 GCGGTATTTT GACCGTGATT ATTTACGCTT CGGCGGCTAA AACATACGGC
451 GACATCGCGT TGATTATCGC AGCCGTTTGT GTGGTCAGTG CGATTTGTTA
501 TGCCATTTTA ATCGTTGCCG GGAAGGTCAG CCGCCTGCTG GGTGCGACGG
551 GGCTGACGAT TTAAACCGT ATCATGGGTA TGATGCTGGC GCGGTATCG
601 GTGGAGATTA TTGTGTCGGG ACTGAAAATG ATATCCCGC AACTGCGAGG
651 TTGA
```

This corresponds to the amino acid sequence <SEQ ID 1168; ORF 282.a>:

```
a282.pep
1  MGLGMEIGKL IVAFLVLINP FSALSPLYDL TNGHSTKERR KVARTAAVAV
51  FAVIAVFALI GGTLLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKQ
101 NLGAQPETGQ VRPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAAKTYG
151 DIALIIAAGL VVSAICYAIL IVAGKVSRL GATGLTILNR IMGMMMLAAVS
201 VEIIVSGLKM IFPQLAG*
```

m282/a282 99.1% identity in 217 aa overlap

	10	20	30	40	50	60
m282.pep	MGLGMEIGKLIVAFVLINPFSALSPLYDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
a282	MGLGMEIGKLIVAFVLINPFSALSPLYDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m282.pep	GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGOARPARNAGAI					
a282	GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGOVRPARNAGAI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m282.pep	AVVPPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL					
a282	AVVPPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL					
	130	140	150	160	170	180
	190	200	210			
m282.pep	GATGLTILNRIMGMLAAVSVEIIVSGLKTIFFPQLAGX					
a282	GATGLTILNRIMGMLAAVSVEIIVSGLKMIFFPQLAGX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1169>:

g283.seq

1	atgaactttg	ctttatccgt	catcacattt	accctcgcct	ctttcctgcc
51	cgtcccgcc	gccggaaccg	ccgtctttac	ttggaaagac	ggcggcggca
101	acagctattc	ggatgtgccg	aaacagcttc	atcccgacca	gagccaaatc
151	ctcaacctgc	ggacgctcca	aaccaaaccg	gcggtcaagc	ccaaacctgc
201	cgtcgatacg	aatgctggaca	gtgcgaagga	aaacgaaaag	gatatcgccg
251	agaaaaacgg	gcagcttgag	gaagaaaaga	aaaaaattgc	cgaaaccgaa
301	cggcagaaca	aagaagaaaa	ctgccggatt	tcaaaaatga	acctgaaggc
351	ggtgggaaac	tcaaatgcga	aaaacaagga	tgatttgatc	cgtaaataca
401	ataacgccgt	aaacaaatac	tgccgttaa		

This corresponds to the amino acid sequence <SEQ ID 1170; ORF 283.ng>:

g283.pep

1	MNFALSVITF	TLASFLPVPP	AGTAVFTWKD	GGGNSYSDVP	KQLHPDQSQI
51	LNLRTLQTKP	AVKPKPAVDT	NADSAKENEK	DIAEKNGQLE	EEKKKIAETE
101	RQNKEENCRI	SKMNLKAVGN	SNAKNKDDLI	RKYNNAVNKY	CR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1171>:

m283.seq

1	ATGAACTTTG	CTTTATCCGT	CATTATGTTG	ACCCTCGCCT	CTTTCCTGCC
51	CGTCCCGCCT	GCCGGAGCCG	CCGTCTTTAC	TTGGAAGGAC	GGCGGCGGCA
101	ACAGCTATTC	GGATGTACCG	AAACAGCTTC	ATCCCGACCA	AAGCCAAATC
151	TTAAACCTGC	GGACGCGCCA	AACCAAACCG	GCGGTCAAAC	CCGCCCAAGC
201	CGACGCAGGG	AAGCGCACAG	ACGGCGCGGC	ACAGGAAAAC	AATCCCGACA
251	CTGCGGAGAA	AAACCGGCAG	CTTGAGGAAG	AAAAGAAAAG	AATTGCCGAA
301	ACCGAACGGC	AGAACAAGA	AGAAACTGC	CGGATTTCAA	AAATGAACCT
351	GAAGCGGTG	GGAAATTCAA	ATGCAAAAAA	CAAGGATGAT	TTGATTCGGA
401	AATACAATAA	CGCCGTAAAC	AAATACTGCC	GTAA	

This corresponds to the amino acid sequence <SEQ ID 1172; ORF 283>:

m283.pep

1	MNFALSVIML	TLASFLPVPP	AGAAVFTWKD	GGGNSYSDVP	KQLHPDQSQI
51	LNLRTRQTKP	AVKPAQADAG	KRTDGAAQEN	NPDTAEKNRQ	LEEEKKRIAE
101	TERQNKEENC	RISKMNLKAV	GNSNAKNKDD	LIRKYNNAVN	KYCR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m283/g283 86.1% identity in 144 aa overlap

	10	20	30	40	50	60
m283.pep	MNFALSVIMLTLASFLPVPPAGAAVFTWKDGGGNSYSDVPKQLHPDQSQILNLRTRQTKP					
g283	MNFALSVITFTLASFLPVPPAGTAVFTWKDGGGNSYSDVPKQLHPDQSQILNLRTLQTKP					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m283.pep	AVKPAQADAGKRTDGAAQENNPDTAEKNRQLEEEKKRIAETERQNKEENCRISKMNLKAV					
		:	:	:	:	
g283	AVKPKPA-VDTNAD-SAKENEKDIAEKNGQLEEEKKRIAETERQNKEENCRISKMNLKAV					
	70	80	90	100	110	
	130	140				
m283.pep	GNSNAKNKDDLIRKYNNNAVNKYCRX					
g283	GNSNAKNKDDLIRKYNNNAVNKYCRX					
	120	130	140			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1173>:

```
a283.seq
1  ATGAACTTTG CTTTATCCGT CATTATGTTG ACCCTCGCCT CTTTCCTGCG
51  CGTCCCGCCT GCCGGAGCCG CCGTCTTTAC TTGGAAGGAC GGCGGCGGCA
101 ACAGCTATTC GGATGTACCG AAACAGCTTC ATCCCGACCA AAGCCAAATC
151 TTAAACCTGC GGACGCGCCA AACCAAACCG GCGGTCAAAC CCGCCCAAGC
201 CGACGCAGGG AAGCGCACAG ACGGCGCGGC ACAGGAAAAC AATCCCGACA
251 CTGCCGAGAA AAACCGGCAG CTTGAGGAAG AAAAGAAAAG AATTGCCGAA
301 ACCGAACGGC AGAACAAAGA AGAAAAGTGC CGGATTTCAA AAATGAACCT
351 GAAAGCGGTG GGAAATTCAA ATGCAAAAAA CAAGGATGAT TTGATTCGGA
401 AATACAATAA CGCCGTAAAC AAATACTGCC GTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1174; ORF 283.a>:

```
a283.pep
1  MNFALSVIML TLASFLPVPP AGAAVFTWKD GGGNSYSVDP KQLHPDQSQI
51  LNLRTQTKP AVKPAQADAG KRTDGAAQEN NPDTAENRQ LEEKKRIAIE
101 TERQNKEENC RISKMNLKAV GNSNAKNKDD LIRKYNNAVN KYCR*
```

m283/a283 100.0% identity in 144 aa overlap

	10	20	30	40	50	60
m283.pep	MNFALSVIMLTLASFLPVPPAGAAVFTWKDGGGNSYSDVPKQLHPDQSQIILNLRTQTKP					
a283	MNFALSVIMLTLASFLPVPPAGAAVFTWKDGGGNSYSDVPKQLHPDQSQIILNLRTQTKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m283.pep	AVKPAQADAGKRTDGAAQENNPDTAEKNRQLEEEKKRIAETERQNKEENCRISKMNLKAV					
a283	AVKPAQADAGKRTDGAAQENNPDTAEKNRQLEEEKKRIAETERQNKEENCRISKMNLKAV					
	70	80	90	100	110	120
	130	140				
m283.pep	GNSNAKNKDDLIRKYNNNAVNKYCRX					
a283	GNSNAKNKDDLIRKYNNNAVNKYCRX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1175>:

```
g284.seq.
1  atgccgtctg aaactcgaaa tcggtttcag acggcattgg tttacgcggc
51  aggttggggc ttagcggctt ttgtaacggc attcgctttt gcctgcaaaa
101 gactgcgcgg ctttgcgttt gcctttgaag ccttcgcggg tttttttgaa
151 actgtctttc ttaaagcctt ctttcttgaa accttcgcgg cgcgttttgc
201 cgccgaagcc ttctttgccc ggtttatgat cgccgcgcgg gccgcgggat
251 ttcctatcgc ccagcgcggc ttgacctttc ggcttgccgc ctgcggattt
301 gcgtttgcgg gccggctcca tgccttcgat ggtcagttcg ggcagtttgc
351 ggttaatgta tttttcgatt ttgtggactt tgacgtattc gttcacttcg
401 gcaaacgtaa tcgcaatacc cgtgcggcct gcgcggccgg tgcgccgat
451 gcggtggacg tagtcttccg cctgtttcgg caggtcgtag tttatgacgt
```



```

501  gggtaatggt  cggtagctca  ataccgcgtg  cggcaacgtc  ggtggcaacc
551  aaaattttgc  agcggccttt  acgcaaattc  gtcagcgtgc  ggttgcgcca
601  gccctgcggc  atatcgccgt  gcaggcagtt  gccggcgaaa  cctttttcgt
651  acaattcatc  cgcgatgact  tcggatcatc  ctttggtgga  cgtgaaaatc
701  acacattggt  cgatgttggc  atcgcgcagg  atgtggtcga  gcaggcggtt
751  tttgtggcgc  atatcgtcgc  agtacaacaa  ctgctcttcg  attttgcctt
801  ggccgtccac  gcgttcgact  tcgataattt  cagagtcctt  ggtcagtttg
851  cgcgccagtt  tgccgactgc  gccgtcccaa  gtggcggaga  acaataa

```

This corresponds to the amino acid sequence <SEQ ID 1176; ORF 284.ng>:

g284.pep

```

1  MPSETRNRFO  TALVYAAGWG  LAVFVTAFAF  ACKRVAGFAF  AFEAFAGFFE
51  TVFLKAFFLE  TFAARFAAEA  FFARFMIAAP  AAGFPIAPAA  FAFRLAACGF
101 AFAGRLHAFD  GQFGQFAVNV  FFDFVDFDVF  VHFGKRRNNT  RAACAAGAPD
151 AVDVVFRLEF  QVVVDVGNNG  RYVNTACGNV  GGNQNFAAAF  TQIRQRAVAP
201 ALRHIAVQAV  GGETFFVQFI  RDDFGHRFGG  RENHTLVDVG  IAQDVVEQAV
251 FVAHIVAVQQ  LLFDFAALVH  AFDFDNFRVF  GQFARQFADC  AVPSGGEQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1177>:

m284.seq..

```

1  ATGCCGCTCTG  AAACCTCGAAA  TCGGTTTTCAG  ACGGCATTGG  TTTATGCGGC
51  AGGTTGGGGC  TTAGCGGTCT  TTGTAACGGC  GTTCGCCTTT  GCCTGCAAAA
101 GAATCGCCGG  CTTTGCCTTT  GCCTTTGAAG  CCTTCGCCGG  TTTTGTGAA
151 ACCGTCTCTC  TTAAAGCCTT  CTTTCTTGAA  ACCTTCGCCG  CGCGTTTGC
201 CGCCGAAGCC  TTCTTTGCTC  GGTTTATGAT  CGCCGCGCCA  ACCGCCGGAT
251 TTACGATCGC  CCCAGCCGCC  TTTGCCTTTC  GGCTTGCCGC  CTGCGGATTT
301 GCGTTTGCGG  GTCGGTTCCA  TGCCTTCGAT  GGTCAGTTTC  GGCAGTTTTC
351 GGTTAATGTA  TTTTTCGATT  TTGTGGACTT  TGACGTATTC  GTTCACTTCG
401 GCAAACGTAA  TCGCAATACC  CGTGCAGCCT  GCGCGGCCGG  TGCGCCCGAT
451 GCGGTGGACG  TAGTCTTCCG  CCTGTTTTCG  CAGGTCGTAG  TTGATAACGT
501 GGGTAATGGT  CGGTACGTCG  ATACCGCGTG  CGGCAACATC  GGTGGCAACC
551 AAAAATTTTG  AGCGGCCTTT  ACGCAAATCC  ATCAGCGTGC  GGTTCGCGCA
601 GCCTTGCGGC  ATATCGCCGT  GCAGGCAGTT  TGCGGCGAAA  CCTTTTTCGT
651 ACAGTTCATC  CGCAATGACT  TCGGTCATGG  CTTTGGTGGA  CGTGAAATC
701 ACGCATTGAT  CGATATTGGC  ATCGCGCAAG  ATATGATCGA  GCAGGCGGTT
751 TTTGTGGCGC  ATATCGTCGC  AGTACAGCAG  TTGTTCTTCG  ATTTTGCCTT
801 GATCGTCCAC  GCGTTCGACT  TCGATGATTT  CAGGGTCTTT  GGTTCGTTG
851 CGCGCCAGTT  TGCCGACCGC  GCCGTCCCAA  GTGGCGGAGA  ACAACAAAGT
901 CTGACGGTCG  CTCGCGGTTG  CTTCCACGAT  GGTTCGATG  TCGTCGATAA
951 AGCCCATATC  CAACATACGG  TCGGCTTCGT  CCAAATCAG  CACTTCCAAA
1001 CGTTCAAAAT  CAACTTTGCC  GCTTTGCATC  AGGTCCATCA  GACGGCCCCG
1051 CGTGGCGACA  ATCAGATCGA  CCGGTTTGCT  CAGGGCACGG  GTTTGGTAGC
1101 CGAAAGACGC  GCCGCCGACG  ATGCTGACGG  TGCGGAACCA  ACGCATATTT
1151 TTGGCATACG  CCAGCGCGTT  TTTCTCGACT  TGAGCCGCCA  GTTCGCGGGT
1201 CGGGGTCAAC  ACCAAAGCAC  GCGGGCCTTT  GCCCGGTTTT  TCGCTGCGTT
1251 TGGTCAGTTT  TTGCAAAGTC  GGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1178; ORF 284>:

m284.pep

```

1  MPSETRNRFO  TALVYAAGWG  LAVFVTAFAF  ACKRIAGFAF  AFEAFAGFFE
51  TVSLKAFFLE  TFAARFAAEA  FFARFMIAAP  TAGFTIAPAA  FAFRLAACGF
101 AFAGRFLHAFD  GQFGQFSVNV  FFDFVDFDVF  VHFGKRRNNT  RAACAAGAPD
151 AVDVVFRLEF  QVVVDVGNNG  RYVDTACGNI  GGNQNFAAAF  TQIRQRAVAP
201 ALRHIAVQAV  CGETFFVQFI  RNDFGHGFVG  RENHALIDIG  IAQDMIEQAV
251 FVAHIVAVQQ  LFFDFALIVH  AFDFDDFRVF  GQFARQFADR  AVPSGGEQQS
301 LTVARRCFHD  GFDVVDKAHI  QHTVGFVQNG  HFQTFKINFA  ALHQVHQATAR
351 RGDNQIDRFA  QGTGLVAERR  AADDADGAEP  THIFGIRQRV  FLDLSRQFAG
401 RGQHQSTRAF  ARFFAAFGQF  LQSR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m284/g284 92.3% identity in 298 aa overlap

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	10	20	30	40	50	60
m284.pep	MPSETRNRFTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE					
g284	MPSETRNRFTALVYAAGWGLAVFVTAFAFACKRVAGFAFAFEAFAGFFETVFLKAFFLE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m284.pep	TFAARFAAEAFFARFMIAAPTAGFTIAPAAFAFRLAACGFAGRFHAFDQGQFQFSVNV					
g284	TFAARFAAEAFFARFMIAAPAAGFPIAPAAFAFRLAACGFAGRLHAFDQGQFAVNV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m284.pep	FFDFVDFDVVHFGKRNTRACAAGAPDAVDVVFRLFRQVVVDVNGRNVDTACGNI					
g284	FFDFVDFDVVHFGKRNTRACAAGAPDAVDVVFRLFRQVVVDVNGRNVNTACGNV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m284.pep	GGNQNFAAFTQIHQRAVAPALRHIAVQAVCGETFFVQFIRNDFGHGFGGRENHALIDIG					
g284	GGNQNFAAFTQIRQRAVAPALRHIAVQAVGGETFFVQFIRDDFGHRRFGGRENHTLVGV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m284.pep	IAQDMIEQAVFVAHIVAVQQLFFDFALIVHAFDFDDFRVFGQFARQFADRAVPSGGEQQS					
g284	IAQDVVEQAVFVAHIVAVQQLFFDFALAVHAFDFDNFRVFGQFARQFADCAVPSGGEQX					
	250	260	270	280	290	
	310	320	330	340	350	360
m284.pep	LTVARRCFHDFDVVDKAHIQHTVGFVQNHQFQTFKINFALHQQVHTARRGDNQIDREA					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1179>:

```

a284.seq
1  ATGCCGCTCTG  AAACGCGAAA  TCGGTTTCAG  ACGGCATTGG  TTTATGCGGC
51  AGGTTGGGGC  TTAGCGGTCT  TTGTAACGGC  GTTCGCCTTT  GCCTGCAAAA
101  GAATCGCCGG  CTTTGCGTTC  GCCTTTGAAG  CCTTCGCCGG  TTTTGTGAA
151  ACCGCTCTCTC  TTAAAGCCTT  CTTTCTTGAA  ACCTTCGCCG  CGCGTTTTC
201  CGCCGAAGCC  TTCTTTGCTC  GGTATTATGAT  CGCCGCGCCA  ACCGCGCGAT
251  TTACGATCGC  CCCAGCCGCC  TTTGCCTTTC  GGCTTGCCGC  CTGCGGATTT
301  GCGTTTTCGG  GTCGTTTCCA  TGCCTTCGAT  GGTGAGTTTC  GGCAGTTTTC
351  GGTAAATGTA  TTTTTCGATT  TTGTGGACTT  TGACGTATTC  GTTCACTTCG
401  GCAAACGTAA  TCGCAATACC  CGTGCAGCCT  GCGCGGCCGG  TCGCGCCGAT
451  GCGGTGGACG  TAGTCTTCCG  CCTGTTTCGG  CAGGTCGTAG  TTGATAACGT
501  GGGTAATGGT  CGGTACGTCG  ATACCGCGTG  CGGCAACGTC  GGTGGCAACC
551  AAAATTTTGC  AGCGGCCTTT  GCGCAAATCC  ATCAGCGTGC  GGTGCGCCA
601  GCCTTGCGGC  ATATCGCCGT  GCAGGCAGTT  GCGGCGGAAA  CCTTTTTCGT
651  ACAATTCATC  CGCGATGACT  TCGGTCATGG  CTTTGGTGGA  CGTGAAATTC
701  ACGCATTGAT  CGATGTCGGC  ATCGCGCAAG  ATATGATCGA  GCAGGCGGTT
751  TTTGTGGCGC  ATATCGTCGC  AGTACAGCAG  TTGTTCTTCG  ATTTTGCCTT
801  GGTGCTCCAC  GCGTTCGACT  TCGATGATTT  CAGGGTCTTT  GGTGAGTTTG
851  CGCGCCAGTT  TGCCGACCGC  GCCGTCCCAA  GTGGCGGAGA  ACAACAAAGT
901  CTGACGGTCT  TCCGGCGTGG  CTTTCGACGAT  GGTTCGATG  TCGTCGATAA
951  AGCCCATATC  CAACATACGG  TCGGCTTCGT  CAAAATCAG  CACTTCCAAG
1001  CGGGCGAAAT  CGACTTTGCC  GCTTTGCATC  AAGTCCATCA  GACGCCCCGG
1051  CGTGGCGACA  ATCAGATCGA  CCGGTTTGCT  CAGGGCGCGG  GTTTGGTAGC
1101  CGAACGATGC  ACCACCGACG  ATGCTGACGG  TACGGAACCA  ACGCATATTT
1151  TTGGCATACG  CCAGCGCGTT  TTTCTCGACT  TGAGCCGCCA  ATTCGCGGGT
1201  CGGCGTCAAC  ACCAACGCGC  GCGGCGCTTT  GCCCGGTTTT  TCGCTGCGTT
1251  TGGTCAGTCG  CTGCAAAGTC  GGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1180; ORF 284.a>:

```

a284.pep
1  MPSETRNRFO  TALVYAAGWG  LAVFVTAFAF  ACKRIAGFAF  AFEAFAGFFE

```

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```

51 TVSLKAFFLE TFAARFAAEA FFAREFMIAAP TAGFTIAPAA FAFRLAACGF
101 AFAGRHFHAFD GQFGQFSVNV FFDFVDFDVF VHFGRNRNT RAACAAGAPD
151 AVDVVFRFLFR QVVVDNVGNG RYVDTACGNV GGNQNFAAAF AQIHQRAVAP
201 ALRHIAVQAV GGETFFVQFI RDDFGHGFGG RENHALIDVG IAQDMIEQAV
251 FVAHIVAVQQ LFFDFALVVH AFDFDDFRVF GQFARQFADR AVPSGGEQQS
301 LTVFRRGFDD GFDVVDKAHI QHTVGFVQNG HFQAGEIDFA ALHQVHQTAR
351 RGDNQIDRFA QGAGLVAERC TTDDADGTEP THIFGIRQRV FLDLSRQFAG
401 RRQHQRRARAF ARFFAAGQS LQSR*

```

m284/a284 94.8% identity in 424 aa overlap

```

              10      20      30      40      50      60
m284.pep      MPSETRNRFQTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE
              |||||
a284          MPSETRNRFQTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE
              10      20      30      40      50      60

              70      80      90      100     110     120
m284.pep      TFAARFAAEAFFARFMIAAPTAGFTIAPAAFAFRLAACGFAGRFHAFDGGQFGQFSVNV
              |||||
a284          TFAARFAAEAFFARFMIAAPTAGFTIAPAAFAFRLAACGFAGRFHAFDGGQFGQFSVNV
              70      80      90      100     110     120

              130     140     150     160     170     180
m284.pep      FFDFVDFDVFVHFGRNRNTRAACAAGAPDAVDVFRFLFRQVVVDNVGNRYVDTACGNI
              |||||
a284          FFDFVDFDVFVHFGRNRNTRAACAAGAPDAVDVFRFLFRQVVVDNVGNRYVDTACGNV
              130     140     150     160     170     180

              190     200     210     220     230     240
m284.pep      GGNQNFAAAFTQIHQRAVAPALRHIAVQAVCGETFFVQFIRNDFGHGFGGRENHALIDIG
              |||||
a284          GGNQNFAAAFAQIHQRAVAPALRHIAVQAVGGETFFVQFIRDDFGHGFGGRENHALIDVG
              190     200     210     220     230     240

              250     260     270     280     290     300
m284.pep      IAQDMIEQAVFVAHIVAVQQLFDFALIVHAFDFDDFRVFGQFARQFADRAVPSGGEQQS
              |||||
a284          IAQDMIEQAVFVAHIVAVQQLFDFALIVHAFDFDDFRVFGQFARQFADRAVPSGGEQQS
              250     260     270     280     290     300

              310     320     330     340     350     360
m284.pep      LTVARRCFHDGFDVVDKAHIQHTVGFVQNGHFQTFKINFAALHQVHQTARRGDNQIDRFA
              |||||
a284          LTVFRRGFDDGFDVVDKAHIQHTVGFVQNGHFQAGEIDFAALHQVHQTARRGDNQIDRFA
              310     320     330     340     350     360

              370     380     390     400     410     420
m284.pep      QGTGLVAERRAADDADGAEPHTHIFGIRQRVFLDLSRQFAGRGQHSTRAFARFFAAGQF
              |||||
a284          QGAGLVAERCTTDDADGTEPHTHIFGIRQRVFLDLSRQFAGRRQHQRRARAFARFFAAGQS
              370     380     390     400     410     420

m284.pep      LQSRX
              ||||
a284          LQSRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1181>:

```

g285.seq
1  atgaccgata ccacaccgac agataccgat ccgaccgaaa acggcacgcg
51 caaaatgccg tctgaacacc gccccgcccc gccggcaaaa aaacgccgcc
101 cgctgctgaa gctgtcggcg gcactgctgt ctgtcctgat tttggcagta

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151 tgtttcctcg gctggatcgc cggtagcgaa gcaggtttgc gcttcgggct
201 gtaccaaatac cgttcctggt tcggcgtaaa cttttcctcc caaaacctca
251 aaggcacact gctcgacggc ttcgacggcg acaactggtc gatagaaacc
301 gagggggcag accttaaaat cagccgcttc cgcttcgctg ggaaccgctc
351 cgaactgatg cgccgcagcc tgcacatcac cgacatctcc gccggcgaca
401 tcgccatcgt aaccaaaccg actccgccta aagaagaacg cccgcctcaa
451 ggcctgcccg acagcataga cctgcccgcc gctgtctatc tcgaccgctt
501 cgagacgggc aaaatcagca tgggcaaaac ctttgacaaa caaacctgtc
551 atctcgaacg cctcaacgcy gcataccgtt acgaccgtaa agggcaccgc
601 ctcgacctga aggccgcga cagcccgtyg agcagttcgt cggggtcagc
651 ctcggtcggc ttgaaaaaac cgtttgccct cgataccgcc atttacacca
701 aaggcggtat cgaaggcgaa accatacaca gtacggcgcg gctgagcggc
751 agcctgaagg atgtgcgcgc cgaactgacg atcgacggcg gcaatatccg
801 cctctcgga aaatccgtca tccaccggtt tgccgaatca ttggataaaa
851 cattggaaga agtactggtc aaaggattca acatcaatcc gtccgccttc
901 gtgccttccc tgcccgatgc cgggctgaat ttcgacctga ccgcatccc
951 gtcgttttca gacggcatcg cgttggaagg ctgctcgat ttgaaaaaca
1001 ccaaagccgg ctttgccgac cgcaacggca tccccgtccg tcaggttttg
1051 ggcggttttg tcatccggca ggacggcacg gtgcataatc gcaatacgtc
1101 cgccgccctg ctcgacggg gcggcatcag gctgtcgggc aaaaatcgaca
1151 ccgaaaaaga catccttgat ttaaatatag gcatcaactc cgtcggcgcg
1201 gaagacgtgc tgcaaacgc gttcaaaagg aggttgagc gcagcatcgg
1251 catcgggcgc acgaccgcct cgcccaaaat ctcttggaac ctcgaccgc
1301 gacggcacg cacggacggc agcctcccca tcgcaagcga ccccgcaaac
1351 gaacagcgga aactggtgtt cgacacggtc aacatctccg ccggggaagg
1401 cagcctgacc gcgcaaggct atctcgagct gtttaaagac cgctgtctca
1451 agctggacat ccgttcccgc gcattcgacc ctctcgcat cgatccgcaa
1501 tttccggcag gcaatatcaa cgttcgatt catcttgccg gtgaactggc
1551 aaaagagaaa ttacgggca aaatgcgttt tttgcccgtt acgttcaacg
1601 gcgtgccgat tgccggcagc gccgacattg tttacgagtc ccgccacct
1651 ccgcgcgccg ccgtcgattt gcggttgggg cggaacatcg tcaaaacaga
1701 cggcggtctc ggcaaaaaag gcgaccggct taacctcaat atcaccgcac
1751 ccgatttate ccgtttcggc ttcggactcg cggggtcttt aaatgtacgc
1801 ggacaccttt ccggcgattt ggacggcggc atccgaacct ttgaaaccga
1851 cctttccggc acggcgcgca acttacacat cggcaaaagc gcagacatcc
1901 gtctgctcga ttttaccctc aaaggctcac ccggcacaag ccgcccgatg
1951 cgcgccgata tcaagggcgg ccgcctttcc ctgtcgggcy gcgcgcggt
2001 tctcgatacc gccggcctga cgctggaagg tacgggcygc cagcaccgca
2051 tccgcacaca cgccgccatg acgctggacg gcaaacggtt caaactcgat
2101 ttggacgctt caggcgcat caacaggga cttaccgat ggaaggcag
2151 catcggtatc ctcgacatcg gcggcgcat caacctcaag ctgcaaaacc
2201 gtatgacgct cgaagccggt gcggaacacg tggcggaag tcgggcaaat
2251 tggcaggcaa tggggcgag cctcaacctg caacactttt cttgggacag
2301 gaaaaccggc atatcgga aaggcggcgc acgcgccctg cacatcgccg
2351 agttgcacaa tttcttcaaa ccgcccttcg aacacaatct ggttttaaac
2401 ggcgactggg atgtcgcta cgggcacaac gcgcgcygc acctcaatat
2451 cagccggcaa agcgcgatg ccgtattgcc cggcgggcag gctttgggtt
2501 tgaacgcat ttcctgaaa acgcgcttcc aaaacgaccg catcggaatc
2551 ctgcttgacg gcggcgcgcy tttcgacgg attaacgccc atttgggcat
2601 cggcaacgcc ttcggcgga atatggcaaa tacaccgctc ggcgcgaga
2651 ttacagcctc ctttccgac ttgggcgcgt tgaagccctt tctgcccgc
2701 gccgcgcaaa acattaccg cagcctgaat gcctccgcy aaatcgcgcy
2751 acgggtaggc tctccgtccg tcaatgccgc cgtcaacggt agcagcaact
2801 acgggaaaa caacggcaat atcaccgctg ggcaagccg ctccctcgat
2851 accgcacctt tggcgcgag gctcaacctg accgttgccg atgccgaagc
2901 attccgcaac ttcctaccg tcggacaaac cgtcaaaggc agcctgaatg
2951 ccgcccgaac cctcgcgcy agcatcgcc acccgcaact gggcgcgagt
3001 atcaacggcy acaagctcta ttaccgcaac caaacccaag gcatcatctt
3051 ggacaacggc tcgctgcgtt cgcatattgc aggcaggaaa tgggtaatcg
3101 acagcctgaa attccggcac gaagggacgg cggaactctc cggcacggtc
3151 agcatggaaa acagcgtgcc cgatgtcgat atcgcgcgcy tgttcgacaa
3201 ataccgcac ctgtcccgc ccaaccgcy cctgacggtt tccggcaaca
3251 cccgctgcy ctattcgcc caaaaaggca tatccgttac cggatgatt
3301 aaaactgat agggcggtt cggttcgca aaatcctcga tgccgtccgt
3351 cggcgacgat gtcgtcgat tgggcgaagt caagaaagag gcggcgcat
3401 cgctccccgt caatatgaac ctgactttag acctcaatga cggcatccgc

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3451 ttctccggct acggcgcgga cgttaccata ggccggcaaac tgaccctgac
3501 cgcgcaaccg ggccggaatg tgcgtggggg gggcacgggtc cgcgtcatca
3551 aaggcggtta caaagcatac gggcaggatt tagacattac caaaggcaca
3601 gtctcctttg tcggcccgtc caacgacccc aacctgaaca tccgcgcga
3651 acgcccgcct tccccgcgtg gtgcgggctg ggaaatattg ggcagcctca
3701 acagcccgcg cattacgctg acggcaaacg aaccgatgag tgaaaaagac
3751 aagctctcct ggctcatcct caaccgtgcc ggcagcggca gcagcggca
3801 caatgccgcc ctgtccgcag ccgcaggcgc gctgcttgcc gggcaaatca
3851 acgaccgcat cgggctggtg gatgatttgg gctttaccag caagcgagc
3901 cgcaacgcgc aaaccggcga actcaacccc gccgaacagg tgctgaccgt
3951 cggcaaacaa ctgaccggca aactctacat cggctacgaa tacggcatct
4001 ccagcgcgga acagtccgtc aaactgattt accggctgac ccgcgccata
4051 caggcggttg cccgtatcgg cagccgttcg tcgggcggcg agctgacata
4101 caccatacgt ttcgaccgcc tcttcggttc ggacaaaaaa gactccgcag
4151 gaaacggcaa agggaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1182; ORF 285.ng>:

g285.pep

```

1  MTDTPPTD TD PTENGTRKMP SEHRPAPPAK KRRPLLKLSA ALLSVLILAV
51  CFLGWIAGTE AGLRFGLYQI PSWFGVNISS QNLKGTLLDG FDGDNWSIET
101 EGADLKISR FFAWKPS ELM RRS LHITDIS AGDIAIVTKP TTPKEERPPQ
151 GLPDSIDLPA AVYLD RFETG KISMGT FDK QTVYLERLNA AYRYDRKGHR
201 LDLKAADTPW SSSSGSASVG LKKPFALDTA IYTKGGFEGE TIHSTARLSG
251 SLKDVR AELT IDGGNIRLSG KSVIHPFAES LDKTLEEV LV KGFNINPSAF
301 VPSLPDAGLN FDLTAIPSFS DGIALEGLSD LENTKAGFAD RNGIPVRQVL
351 GGFVIRQDGT VHIGNTSAAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
401 EDVLQTAFKG RLDGSIGIGG TTASPKISWQ LGTGTARTDG SLPIASDPAN
451 EQRKL VFDTV NISAGEGLT AQGYLELFKD RLLKLDIRSR AFDPSRIDPQ
501 FPAGNINGSI HLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL
551 PRAAVDLRLG RNIVKT DGGF GKKGDRNLN ITAPDL SRFG FGLAGSLNVR
601 GHLSGDL DGG IRTFETDLSG TARNLHIGKA ADIRSLDFTL KGSFGTSRPM
651 RADIKGGRLS LSGGA AVVDT AGLTLEGTGA QHRIRTHAAM TLDGKPFKLD
701 LDASGGINRE LTRWKG SIGI LDIGGA FNLK LQNRMTLEAG AEHVAASAAN
751 WQAMGGSLNL QHFSWDRKTG ISAKGGARGL HIAELHNFFK PFEHNLVLN
801 GDWDVAYGHN ARGYNISRQ SGDAVLPGGQ ALGLNAFSLK TRFQNDRIGI
851 LLDGGARFGR INADLGIGNA FGGNMANTPL GGRITASLPD LGALKPFLPA
901 AAQNITGSLN ASAQIGGRVG SPSVNA AVNG SSNYGKINGN ITVGQSR SFD
951 TAPLGGR LNL TVADAEAFRN FLPVGQTVKG SLNAAVTLGG SIADPHLGGS
1001 INGDKLYYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAELSGTV
1051 SMENSVPD VD IGA VFDKYRI LSRPNRRLTV SGNTRLRYSP QKGISVTGMI
1101 KTDQGLFGSQ KSSMP SVGDD VVVLGEVKKE AAASLPVN MN LTLDLNDGIR
1151 FSGYGADV TI GKKLT LTAQP GGNVRGVGT V RVIKGRYKAY GQDL DITKGT
1201 VSFVGPLNDP NLNIRAERRL SPVGAGVEIL GSLNSPRITL TANEFMSEKD
1251 KLSWLILNRA GSGSSGD NAA LSAAAGALLA GQINDRIGLV DDLGFTSKRS
1301 RNAQTGELNP AEQVLTVGKQ LTGKLYIGYE YGISSAEQSV KLIYRLTRAI
1351 QAVARIGSRS SGGELTYTIR FDR LFGSDKK DSAGNGK GK*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1183>:

m285.seq

```

1  ATGACCGATA CCGCACCGAC AGATACCGAT CCGACCGAAA ACGGCACGCG
51  CAAAATGCCG TCTGAACACC GCCCTACCCC GCCGGCAAAA AAACGCCGCC
101 CGTTGCTGAA GCTGTCGGCG GCACTGCTGT CTGTCCTGAT TTTGGCAGTA
151 TGTTTCCTCG GCTGGCTCGC CGGTACGGAA GCAGGTTTGC GCTTCGGGCT
201 GTACCAAATC CCGTCTTGGT TCGGCGTAAA CATTTCTCTC CAAAACCTCA
251 AAGGCACGCT GCTCGACGGC TTCGACGGCG ACAACTGGTC GATAGAAACC
301 GAGGGGGCAG ACCTTAAAAA CAGCCGCTTC CGCTTCGCGT GGAAACCGTC
351 CGAACTGATG CGCCGCAGCC TGCACATTAC CGAAATTTC GCCGCGGACA
401 TCGCCATCGT TACCAAACCG ACTCCGCCTA AAGAAGAACG CCCGCCGCTC
451 AGCCTTCCCG ACAGCATAGA CCTGCCTGCC GCCGTCTATC TCGACCGCTT
501 CGAGACGGGC AAAATCAGCA TGGGCAAAGC CTTTGACAAA CAAACCGTCT
551 ATCTCGAACG GCTGGATGCT TCATACCGTT ACGACCGCAA AGGACACCGC
601 CTTGACCTGA AGGCCGCCGA CACGCCGTGG AGCAGTTCGT CGGGGCGGCG
651 CTCGGTCGGC TTGAAAAAAC CGTTTGCCCT CGATACCGCC ATTTACACCA
701 AAGGCGGACT CGAAGGCAAA ACCATACACA GTACGGCTCG GCTGAGCGGC
751 AGCCTGAAGG ATGTGCGCGC CGAACTGGCG ATCGACGGCG GCAATATCCG

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801 CCTCTCGGGA AAATCCGTCA TCCACCCGTT TGCCGAATCA TTGGATAAAA
851 CATTGGAAGA AGTACTGGTC AAAGGGTTCA ACATCAATCC GGCCGCCTTC
901 GTGCCCTTCCC TGCCCGATGC CGGACTGAAT TTCGACCTGA CCGCCATCCC
951 GTCGTTTTTCA GACGGCATCG CGCTGGAAGG TTCGCTCGAT TTGGAAAACA
1001 CCAAAGCCGG CTTTGCCGAC CGCAACGGCA TCCCCGTCCG TCAGGTTTTTA
1051 GGCGGCTTTG TCATCCGGCA GGACGGCACG GTGCATATCG GCAATACGTC
1101 CGCCGCCCTG CTCGGACGGG GCGGCATCAG GCTGTCCGGC AAAATCGACA
1151 CCGAAAAAGA CATCTCGAT TTAATATAG GCATCAACTC CGTCGGCGCG
1201 GAAGACGTAC TGCAAAACCGC GTTCAAAGGC AGGTTGGACG GCAGCATCGG
1251 CATCGGTGGC ACGACCGCCT CGCCCAAAAT CTCTTGCAA CTCCGCATCG
1301 GCACGGCGCG CACGGACGGC AGCCTCGCCA TTGCAAGCGA CCCAGCAAAC
1351 GGACAGCGGA AACTGGTGCT CGACACCGTC AACATCGCCG CCGGGCAAGG
1401 CAGCCTGACC GCGCAAGGCT ATCTCGAGCT GTTTAAAGAC CGCCTGTCTCA
1451 AGCTGGACAT CCGTTCCCGC GCATTCGACC CTTCCGCGAT CGATCCGCAA
1501 CTTCCGGCAG GCAATATCAA CGGCTCAATA AACCTTGCCG GCGAACTGGC
1551 AAAAGAGAAA TTCACAGGCA AAATGCGGTT TTTACCCGGC ACGTTCAACG
1601 GCGTACCGAT TGCCGGCAGT GCCGACATTG TTTACGAGTC CCGCCACCTT
1651 CCGCGTGCCG CCGTCGATTT GCGGCTGGGG CGGAACATTA TTAACACAGA
1701 CGCGGGCTTC GCGAAAAAAG GCGACCGGCT TAACCTCAAT ATCACCACAC
1751 CCGATTTATC CCGTTTCGGT TTCGGAATCG CGGGGTCTTT AAATGTACGC
1801 GGACACCTTT CCGGTGATTT GGACGGCGGC ATCCGAACCT TTGAAACCGA
1851 CCTTTCGGGC GCGGCGCGCA ACCTGCACAT CGGCAAGGCG GCAGACATCC
1901 GTTCGCTCGA TTTCACGCTC AAAGGTTTCG CCGACACAAG CCGCCCGATA
1951 GCGCCCGACA TCAAAGGCAG CCGCCTTTCG CTGTCCGGCG GAGCGCGGT
2001 TGTCGATACC GCCGACCTGA TGCTGGACGG CACGGGCGTG CAGCACCGCA
2051 TCCGCACACA CGCCGCCATG ACGCTGGATG GCAAACCGTT CAAATTCGAT
2101 TTGGACGCTT CAGGCGGCAT CAACAGGGAA CTTACCCGAT GGAAGGCGAG
2151 CATCGGCATC CTCGACATCG GCGGCGCATT CAACCTCAAG CTGCAAAACC
2201 GTATGACGCT CGAAGCCGGT GCGGAACGCG TGCGGCAAG TGCGGCAAT
2251 TGGCAGGCAA TGGGCGGCAG CCTCAACCTG CAACACTTTT CTGGGATAA
2301 AAAAACCGGC ATATCGGCAA AAGGCGGCGC ACACGGTCTG CATATCGCCG
2351 AGTTGCACAA TTTCTTCAA CCGCCCTTCG AACACAATCT GGTTTTAAAC
2401 GCGGACTGGG ATGTGCGCTA CGGGCGCAAC GCGGCGGCT ACCTCAATAT
2451 CAGCCGCAAA AGCGGCGATG CCGTATTGCC CCGCGGGCAG GCTTTGGGTT
2501 TGAACGCATT TTCCCTGAAA ACGCGCTTTC AAAACGACCG CATCGGAATC
2551 CTGCTTGACG GCGGCGCGCG TTTCGGGCGG ATTAACGCCG ATTTGGGCAT
2601 CGCCAACGCC TTCGGCGGCA ATATGGCAA TGCACCGCTC GCGGCGAGGA
2651 TTACCGCCTC CCTTCCGAC TTGGGCGCAT TGAAGCCCTT TCTGCCCGCC
2701 GCGGCGCAAA ACATTACCGG CAGCCTGAAT GCCGCGCGC AAATCCGCGG
2751 ACGGGTAGGC TCTCCGTCCG TCAATGCCGC CGTCAACGGC AGCAGCAACT
2801 ACGGAAAAAT CAACGGCAAC ATCACCCTCG GGCAAAGCCG CTCTTTCGAT
2851 ACCGCGCCTT TGGGCGGCGAG GCTCAACCTG ACCGTTGCCG ATGCCGAAGT
2901 ATTCCGCAAC TTCCTACCGG TCGGACAAAC CGTCAAAGGC AGCCTGAATG
2951 CCGCCGTAAC CCTCGGCGGC AGCATCGCCG ATCCGCACTT GGGCGGACG
3001 ATCAACGGCG ACAAACTCTA TTACCGCAAC CAAACCCAAG GCATCATCTT
3051 GGACAACGGC TCGCTGCGTT CGCATATCGC GGGCAGGAAA TGGGTAATCG
3101 ACAGCCTGAA ATTCGGGCAC GAAGGGACGG CGGAACTCTC CCGTACGGTC
3151 GGTATGGAAA ACAGCGGACC CGATGTCGAT ATCGGCGCGG TGTTGCACAA
3201 ATACCGCATC CTGTCCCGCC CCAACCGCCG CCTGACGGTT TCCGGCAACA
3251 CCCGCTGCG CTATTGCGCG CAAAAAGGCA TATCCGTTAC CGGGATGATT
3301 AAAACGGATC AGGGGCTGTT CGGTTTCGAA AAATCCTCGA TGCCGTCCGT
3351 CGGCGACGAT GTCGTCGTAT TAGGCGAAGT CAAAAAGAG GCGGCGGCAC
3401 CGTCCCCGT CAATATGAAC CTGACTTTAG ACCTCAATGA CCGCATCCGC
3451 TTCGCGGCT ACGGCGCGGA CGTTACCATA GCGGCAAAAC TGACCTGAC
3501 CGCCAATCG GCGGAAGCG TACGGGCGGT GGGCACGGTC CGCGTCATCA
3551 AAGGGCGTTA TAAGGCATAC GGGCAGGATT TGGACATTAC CAAAGGCACG
3601 GTCTCCTTTG TCGGCCGCT CAACGATCCC AACCTCAACA TCCGCGCCGA
3651 ACGCGCCTT TCCCCGTCG GTGCGGGCGT GGAAATATG GGCAGCCTCA
3701 ACAGCCCGCG CATTACGCTG ACGGCAAAAC AACCGATGAG TGAAAAAGAC
3751 AAGCTCTCTT GGCTCATCCT CAACCGCGCC GGCAGCGGCA GCAGCGGCGA
3801 CAATGCCGCC CTGTCTGCAG CCGCAGGTGC GCTGCTTGCC GGGCAAATCA
3851 ACGACCGCAT CGGGCTGGTG GATGATTTGG GCTTTACCAG CAAGCGCAGC
3901 CGCAACGCGC AAACCGCGCA ACTCAACCCC GCCGAACAGG TGCTGACCGT
3951 CGGCAACAAA CTGACCGGCA AACTCTACAT CGGCTACGAA TACAGCATCT
4001 CCAGCGCGGA ACAGTCCGTC AAATGATTT ACCGGCTGAC CCGCGCCATA
4051 CAGGCGGTTG CCGTATCGG CAGCCGTTTCG TCGGCGGCG AGCTGACATA

4101 CACCATACGT TTCGACCGCT TCTCCGGTTC GGACAAAAA GACTCCGCCG
4151 GAAACGGCAA AGGAAATAA

This corresponds to the amino acid sequence <SEQ ID 1184; ORF 285>:

```
m285.pep
1  MTDAPTDTPTD PTENGTRKMP SEHRPTPPAK KRRPLLKLSA ALLSVLILAV
51  CFLGWLAGE AGLRFGLYQI PSWFGVNISS QNLKGTLLDG FDGDNWSIET
101 EGADLKISR FFAWKPSSELM RRLSHITEIS AGDIAIVTKP TPPKEERPPL
151 SLPDSIDLPA AVYLDRFETG KISMKGAFDK QTVYLERLDA SYRYDRKGHR
201 LDLKAADTPW SSSSGAASVG LKKPFALDTA IYTKGGLEGK TIHSTARLSG
251 SLKDVRAELA IDGGNIRLSG KSVIHPFAES LDKTLEEVLV KGFNINPAAF
301 VPSLPDAGLN FDLTAIPSF S DGIALEGLD LENTKAGFAD RNGIPVRQVL
351 GGFVIRQDGT VHIGNTSAAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
401 EDVLQTAFKG RLDGSIGIGG TTASPKISWQ LGIGTARTDG SLAIASDPAN
451 GQRKLVLDTV NIAAGQGS LT AQGYLELFKD RLLKLDIRSR AFDPSTRIDPQ
501 LPAGNINGSI NLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL
551 PRAAVDLRLG RNIKTG DGGF GKKGDRNLN ITAPDLSRFG FGLAGSLNVR
601 GHLSGDL DGG IRTFETDL SG AARNLHIGKA ADIRSLDFTL KGSPDTSRPI
651 RADIKSRLS LSGGA AVVD T ADLMLDGTGV QHRIRTHAAM TLDGKPFKFD
701 LDASGGINRE LTRWKSIGI LDIGGAFNLK LQNRMTLEAG AERVAASAAN
751 WQAMGGS LNL QHFSWDKKTG ISAKGGAHGL HIAELHNFFK PPFEHNLVLN
801 GDWDVAYGRN ARGYLNISRQ SGDAVLPGGQ ALGLNAFSLK TRFQNDRIGI
851 LLDGGARFGR INADLGIANA FGGNMANAPL GGRITASLPD LGALKPFPLPA
901 AAQNITGSLN AAAQIGGRVG SPSVNAAVNG SSNYGKINGN ITVGQSR SFD
951 TAPLGGR LNL TVADA EVFRN FLVPVQTVKG SLNAAVTLGG SIADPHLGGS
1001 INGDKLYYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAELSGTV
1051 GMENSGPDVD IGAVFDKYRI LSRPNRRLTV SGNTRLRYSP QKGISVTGMI
1101 KTDQGLFGSQ KSSMPSVGGD VVVLGEVKKE AAAPLPVNMN LTLDLNDGIR
1151 FAGYGADVTI GGKLTTLTAQS GGSVRGVGT V RVIKGRYKAY GQDL DITKGT
1201 VSFVGPLNDP NLNIRAERRL SPVGAGVEIL GSLNSPRITL TANEPMS EKD
1251 KLSWLILNRA GSGSSGD NAA LSAAAGALLA GQINDRIGLV DDLGFTSKRS
1301 RNAQTGELNP AEQVLTVGKQ LTGKLYIGYE YSISAEQSV KLIYRLTRAI
1351 QAVARIGSRS SGGELTYTIR FDRFSGS DKK DSAGNGK GK*
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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m285/g285 96.5% identity in 1389 aa overlap

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      10      20      30      40      50      60
m285.pep  MTDAPTDTPTDPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g285      MTDTTPTDPTDPTENGTRKMPSEHRPAPPKRRPLLKLSAALLSVLILAVCFLGWIAGE
          10      20      30      40      50      60

      70      80      90     100     110     120
m285.pep  AGLRFGLYQIPSWFGVNISSQNLKGTLLDGF DGDNWSIETEGADLKISRFRFAWKPSSELM
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g285      AGLRFGLYQIPSWFGVNISSQNLKGTLLDGF DGDNWSIETEGADLKISRFRFAWKPSSELM
          70      80      90     100     110     120

      130     140     150     160     170     180
m285.pep  RRLSHITEISAGDIAIVTKPTTPPKEERPPLSLPDSIDLPAAVYLD RFETGKISMKGAFDK
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g285      RRLSHITDISAGDIAIVTKPTTPPKEERP PQGLPDSIDLPAAVYLD RFETGKISMGT FDK
          130     140     150     160     170     180

      190     200     210     220     230     240
m285.pep  QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGAASVGLK KPFALDTAIYTKGGLEGK
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g285      QTVYLERLNAAARYDRKGHRDLKAADTPWSSSSGSASVGLK KPFALDTAIYTKGGFEGE
          190     200     210     220     230     240

      250     260     270     280     290     300
m285.pep  TIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIHPFAESLDKTLEEV LVKGFNINPAAF
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653

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g285      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
          AAQNITGSLNASAQIGGRVGSPSVNAAVNGSSNYKINGNITVGQSRSFDTAPLGGRNLN
          910      920      930      940      950      960

          970      980      990      1000     1010     1020
m285.pep  TVADAEVFRNFLPVGQTVKGSLNAAVTLGGSIADPHLGGSSINGDKLYYRNQTQGIILDNG
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g285      TVADAEAFRNFLPVGQTVKGSLNAAVTLGGSIADPHLGGSSINGDKLYYRNQTQGIILDNG
          970      980      990      1000     1010     1020

          1030     1040     1050     1060     1070     1080
m285.pep  SLRSHIAGRKWVIDSLKFRHEGTAELSGTVGMENSGPDVDIGAVFDKYRILSRPNRRLTV
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g285      SLRSHIAGRKWVIDSLKFRHEGTAELSGTVSMENSVDPVDIGAVFDKYRILSRPNRRLTV
          1030     1040     1050     1060     1070     1080

          1090     1100     1110     1120     1130     1140
m285.pep  SGNTRLRYSPQKGISVTGMIKTDQGLFGSQKSSMPVSGDDVVVLGEVKKEAAAPLPVNMN
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g285      SGNTRLRYSPQKGISVTGMIKTDQGLFGSQKSSMPVSGDDVVVLGEVKKEAAASLPVNMN
          1090     1100     1110     1120     1130     1140

          1150     1160     1170     1180     1190     1200
m285.pep  LTLDLNDGIRFAGYGADVTIGGKLTTLTAQSGGVRGVGTVRVIKGRYKAYQDLDITKGT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g285      LTLDLNDGIRFSGYGADVTIGGKLTTLTAQPGGNVRGVGTVRVIKGRYKAYQDLDITKGT
          1150     1160     1170     1180     1190     1200

          1210     1220     1230     1240     1250     1260
m285.pep  VSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNSPRITLTANEPMSEKDKLSWLILNRA
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g285      VSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNSPRITLTANEPMSEKDKLSWLILNRA
          1210     1220     1230     1240     1250     1260

          1270     1280     1290     1300     1310     1320
m285.pep  GSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGFSTSKRSRNAQTGELNPAEQVLTVGKQ
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g285      GSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGFSTSKRSRNAQTGELNPAEQVLTVGKQ
          1270     1280     1290     1300     1310     1320

          1330     1340     1350     1360     1370     1380
m285.pep  LTGKLYIGYEYSSISAEQSVKLIYRLTRAIQAVARIGSRSSGGELTYTIRFDRFGSDKK
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g285      LTGKLYIGYEYGISSAEQSVKLIYRLTRAIQAVARIGSRSSGGELTYTIRFDRFGSDKK
          1330     1340     1350     1360     1370     1380

          1390
m285.pep  DSAGNGKGKX
          |||||
g285      DSAGNGKGKX

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1185>:

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a285.seq
1  ATGACCGATA CCGCACCGAC AGATACCGAT CCGACCGAAA ACGGCACGCG
51  CAAAATGCCG TCTGAACACC GCCCTACCCC GCCGGCAAAA AAACGCCGCC
101 CGCTGCTGAA GCTGTCGGCG GCACTGCTGT CTGTTCTGAT TTTGGCAGTA
151 TGTTTCCTCG GCTGGCTCGC CGGCACGGAA GCGGGTTTGC GCTTCGGGCT
201 GTACCAAATC CCGTCTTGGT TCGGCGTAAA CATTTCTCTC CAAAACCTCA
251 AAGGCACGCT GCTCGACGGC TTCGACGGCG ACAACTGGTC GATAGAAACC
301 GAGGGGGCAG ACCTTAAAT CAGCCGCTTC CGCTTCGCGT GGAAACCGTC
351 CGAACTGATG CGCCGCAGCC TGCACATTAC CGAAATTTCC GCCGGCGACA
401 TCGCCATCGT TACCAAACCG ACTCCGCCTA AAGAAGAACG CCCGCCGCTC
451 AGCCTTCCCG ACAGCATAGA CCTGCCTGCC GCCGTCTATC TCGACCGCTT
501 CGAGACGGGC AAAATCAGCA TGGGCAAAGC CTTTGACAAA CAAACCGTCT
551 ATCTCGAACG GCTGGATGCT TCATACCGTT ACGACCGCAA AGGACACCGC
601 CTCGACCTGA AGGCTGCCGA CACGCCGTGG AGCAGTTCGT CGGGGTCAGC

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651 CTCGGTCGGC TTGAAAAAAC CGTTTGCCCT CGATACCGCC ATTTACACCA
701 AAGGCGGACT CGAAGGCAAA ACCATACACA GTACGGCTCG GCTGAGCGGC
751 AGCCTGAAGG ATGTGCGCGC CGAACTGGCG ATCGACGGCG GCAATATCCG
801 CCTCTCGGGA AAATCCGTCA TCCACCCGTT TGCCGAATCA TTGGATAAAA
851 CATTGGAAGA AGTACTGGTC AAAGGGTTCA ACATCAATCC GTCCGCTTC
901 GTGCCCTCCC TGCCCGATGC CGGGCTGAAT TTCGACCTGA CCGCCATCCC
951 GTCGTTTTCA GACGGCATCG CGCTGGAAGG CTCGCTCGAT TTGAAAAACA
1001 CCAAAGCCGG CTTTGCCGAC CGCAACGGCA TCCCGCTCCG TCAGGTTTAA
1051 GGCAGCTTTG TCATCCGGCA GGACGGCACG GTGCATATCG GCAATACGTC
1101 CGTCGCCCTG CTCGGACGGG GCGGCATCAG GCTGTGCGGC AAAATCGACA
1151 CCGAAAAAGA CATCCTCGAT TTAAATATAG GCATCAACTC CGTCGGCGCG
1201 GAAGACGTAC TGCAAACCGC GTTCAAAGGC AGGTTGGACG GCAGCATCGG
1251 CATCGGTGGC ACGACCGCCT CGCCAAAAT CTCTTGGCAA CTCGGCATCG
1301 GCACGGCGCG CACGGACGGC AGCCTCGCCA TTGCAAGCGA CCGCGCAAAC
1351 GGACAGCGGA AACTGGTGCT CGACACCGTC AACATCGCCG CCGGGCAAGG
1401 CAGCCTGACC GCGCAAGGCT ATCTCGAGCT GTTTAAAGAC CGCCTGCTCA
1451 AGCTGGACAT CCGTTCCCGC GCATTCGACC CTTCGCGCAT CGATCCGCAA
1501 CTTCGGGCAG GCAATATCAA CGGCTCAATA AACCTTGCCG GCGAACTGGC
1551 AAAAGAGAAA TTACAGGCA AAATGCGGTT TTTACCCGGC ACGTTCAACG
1601 GCGTACCGAT TGCCGGCAGT GCCGACATTG TTTACGAGTC CCGCCACCTT
1651 CCGCGTGCCG CCGTCGATTT GCGGCTGGGG CGGAACATTA TTAACACAGA
1701 CGGCGGCTTC GGCAAAAAAG GCGACCGGCT TAACCTCAAT ATCACCAGCA
1751 CCGATTATAT CCGTTTCGGT TTCGGACTCG CGGGGTCTTT AAATGTACGC
1801 GGACACCTTT CCGGCGATTT GGACGGTGGC ATCCGAACCT TTGAAACCGA
1851 CCTTTCGGC GCGGCGCGCA ACCTGCACAT CGGCAAGGCG GCAGACATCC
1901 GTTCGCTCGA TTTCACGCTC AAAGGTTGCG CCGACACAAG CCGCCCGATA
1951 CCGCGCGACA TCAAAGGCAG CCGCCTTTCG CTGTGCGGGC GAGCGGAGGT
2001 TGTGATACC GCCGACCTGA TGCTGGACGG CACGGGCGTG CAGCACCGCA
2051 TCCGCACACA CGCCGCCATG ACGCTGGATG GCAAACCGTT CAAATTCGAT
2101 TTGGACGCTT CAGGCGGCAT CAACAGGGAA CTTACCCGAT GGAAAGGCAG
2151 CATCGGCATC CTCGACATCG GCGGCGCATT CAACCTCAAG CTGCAAAACC
2201 GTATGACGCT CGAAGCCGGT GCGGAACGCG TGGCGGCAAG TGGCGCAAAAT
2251 TGGCAGGCAA TGGGCGGCAG CCTCAACCTG CAACACTTTT CTGGGATAA
2301 AAAAACCAGC ATATCGGCAA AAGGCGGCGC ACACGGTCTG CATATCGCCG
2351 AGTTGCACAA TTTCTTCAAA CCGCCCTTCG AACACAATCT GGTTTTAAAC
2401 GGCGACTGGG ATGTGCGCTA CCGGCGAAAC GCGCGCGGCT ACCTCAATAT
2451 CAGCGGCAA AGCGGCGATG CCGTATTGCC CCGCGGGCAG GCTTTGGGTT
2501 TGAACGCATT TTCCCTGAAA ACGCGCTTTC AAAACGACCG TATCGGAATC
2551 CTGCTTGACG GCGGCGCGCG TTTGCGGCGG ATTAACGCCG ATTTGGACAT
2601 CCGCAACGCC TTCGGCGGCA ATATGGCAA TGCACCGCTC GCGGCGAGGA
2651 TTACCGCCTC CTTTCCGAC TTGGGCACAT TGAAGCCCTT TCTGCCCACC
2701 GCCGCGCAA ACATTACCGG CAGCCTGAAT CCGCGCGCGC AAATCGGCGG
2751 ACGGGTCGGC TCTCCGTCCG TCAATGCCGC CGTCAACGGC AGCAGCAACT
2801 ACGGAAAAAT CAACGGCAAC ATCACCCTCG GGCAAAAGCG CTCTTTCGAT
2851 ACCGCGCCTT TGGGCGGCAG GCTCAACCTG ACCGTTGCCG ATGCCGAAGT
2901 ATTCCGCAAC TTCTACCGG TCGGACAAAC CGTCAAAGGC AGCCTGAATG
2951 CCGCGGTAAC CCTCGGCGGC AGCATCGCCG ATCCGCACTT GCGCGGCAGC
3001 ATCAACGGCG ACAAACCTTA TTACCGCAAC CAAACCCAAG GCATCATCTT
3051 GGACAACGGC TCGCTGCGTT CGCATATCGC GGGCAGGAAA TGGGTAATCG
3101 ACAGCCTGAA ATTCCGGCAC GAAGGGACGG CGGAACCTCT CCGTACGGTC
3151 GGTATGAAA ACAGCGGACC CGATGTCGAT ATCGGCGCGG TGTTGACAAA
3201 ATACCGCATC CTGTCCCGCC CCAACCGCCG CCTGACGGTT TCCGGCAACA
3251 CCCGCTGCG CTATTGCGCG CAAAAAGGCA TATCCGTTAC CGGGATGATT
3301 AAAACGGATC AGGGGCTGTT CGGTTTCGCAA AAATCCTCGA TGCCGTCCGT
3351 CCGCGACGAT GTCGTCGTAT TAGGCGAAGT CAAAAAGAG GCGGCGGCAC
3401 CGTCCCGGT CAATATGAAC CTGACTTTAG ACCTCAATGA CGGCATCCGC
3451 TTCGCGGCT ACGGCGCGGA CGTTACCATA GCGGCGAAAC TGACCCTGAC
3501 CGCCCAATCG GCGGGAAGCG TGCGGGGCGT GGGCACGGTC CGCGTCATCA
3551 AAGGCGGTTA TAAGGCATAC GGGCAGGATT TGGACATTAC CAAAGGCACG
3601 GTCTCCTTTG TCGGCCGCT CAACGACCCC AACCTCAACA TCCGCGCCGA
3651 ACGCGCCTT TCCCGGTCG GTGCGGGCGT GGAAATATTG GGCAGCCTCA
3701 ACAGTCCGCG CATTACGCTG ACGGCAAAC AACCGATGAG TGAAAAAGAC
3751 AAGTCTCCT GGCTCATCCT CAACCGCGCC GGCAGTGGCA GCAGCGGCGA
3801 CAATGCCGCC CTGTCCGCG CCGCGGCGCG GCTGCTTGCC GGGCAAAATCA
3851 ACGACCGCAT CCGGCTGGTG GATGATTTGG GCTTTACCAG CAAGCGCAGC
3901 CGCAACCGCG AAACCGGCGA ACTCAACCCC GCCGAACAGG TGCTGACCGT

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3951 CGGCAAACAA CTGACCGGCA AACTCTACAT CGGCTACGAA TACAGCATCT
4001 CCAGCGCGGA ACAGTCCGTC AAAGTATT ACCGGCTGAC CCGCGCCATA
4051 CAGGCGGTTG CCGTATCGG CAGCGGTCG TCGGGCGGCG AGCTGACATA
4101 CACCATACGT TTCGACCGCT TCTCCGGTTC GGACAAAAAA GACTCCGCCG
4151 GAAACAGCAA AGGAAATAA

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This corresponds to the amino acid sequence <SEQ ID 1186; ORF 285.a>:

```

a285.pep
  1  MTDAPTDTPTD PTENGTRKMP SEHRPTPPAK KRRPLLKLSA ALLSVLILAV
  51  CFLGWLAGTE AGLRFGLYQI PSWFGVNISS QNLKGTLLDG FDGDNWSIET
 101  EGADLKISRF RFAWKPELMM RRLSHITEIS AGDIAIVTKP TPPKEERPPL
 151  SLPDSIDLPA AVYLDRFETG KISMKGAFDK QTVYLERLDA SYRYDRKGHR
 201  LDLKAADTPW SSSSGSASVG LKKPFALDTA IYTKGGLEGK TIHSTARLSG
 251  SLKDVRAELA IDGGNIRLSG KSVIHPFAES LDKTLEEVLV KGFNINPSAF
 301  VPSLPDAGLN FDLTAIPFSF DGIALEGSLD LENTKAGFAD RNGIPVRQVL
 351  GSFVIRQDGT VHIGNTSVAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
 401  EDVLQTAFKG RLDGSIGIGG TTASPKISWQ LGIGTARTDG SLAIASDPAN
 451  GQRKLVLDTV NIAAGQGS LT AQGYLELFKD RLLKLDIRSR AFDPSRIDPQ
 501  LPAGNINGSI NLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL
 551  PRAAVDLRLG RNIKTGDFG GKKGDRNLNL ITAPDLRFRG FGLAGSLNVR
 601  GHLSGDLGG IRTFETDLG AARNLHIGKA ADIRSLDFTL KGSPDTSRPI
 651  RADIKSRLS LSGGAEVVD ADLMLDGTGV QHRIRTHAAM TLDGKPFKFD
 701  LDASGGINRE LTRWKGSI GI LDIGGAFNLK LQNRMTLEAG AERVAASAAN
 751  WQAMGGSNLN QHFSWDKKTG ISAKGGAHGL HIAELHNFFK PPFEHNLVLN
 801  GDWDVAYGRN ARGYLNISRQ SGDAVLPGGQ ALGLNAFSLK TRFQNDRIGI
 851  LLDGGARFGR INADLDIGNA FGGNMANAPL GGRITASLPD LGTLKPFLPA
 901  AAQNITGSLN AAAQIGRVG SPSVNAAVNG SSNYKINGN ITVGQSRFSD
 951  TAPLGGRLNL TVADA EVFRN FLPVGTQVKG SLNAAVTLGG SIADPHLGGS
1001  INGDKLYYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAELSGTV
1051  GMENSGPDVD IGAVFDKYRI LSRENRLTV SGNTRLYRSP QKGISVTGMI
1101  KTDQGLFGSQ KSSMPSVGDD VVVLGEVKKE AAAPLPVNMN LTLDLNDGIR
1151  FAGYGADVTI GCKLTTLTAQS GGSVRGVGTV RVIKGRYKAY QODLDITKGT
1201  VSFVGPLNDP NLNIRAERRL SPVAGVEIL GSLNSPRITL TANEPMSSEK
1251  KLSWLILNRA GSGSSGDNA LSAAAGALLA QINDRIGLV DDLGFTSKRS
1301  RNAQTGELNP AEQVLTVGKQ LTGKLYIGYE YSISAEQSV KLIYRLTRAI
1351  QAVARIGSRS SGGELTYTIR FDRFSGSDDK DSAGNSKKG*

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m285/a285 99.4% identity in 1389 aa overlap

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              10      20      30      40      50      60
m285.pep      MTDAPTDTPTDPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGTE
              |||
a285           MTDAPTDTPTDPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGTE
              10      20      30      40      50      60

              70      80      90      100     110     120
m285.pep      AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDGDNWSIETEGADLKISRFRAWKPELMM
              |||
a285           AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDGDNWSIETEGADLKISRFRAWKPELMM
              70      80      90      100     110     120

              130     140     150     160     170     180
m285.pep      RRLSHITEISAGDIAIVTKPTPPKEERPPLSLPDSIDLPAAYLDRFETGKISMKGAFDK
              |||
a285           RRLSHITEISAGDIAIVTKPTPPKEERPPLSLPDSIDLPAAYLDRFETGKISMKGAFDK
              130     140     150     160     170     180

              190     200     210     220     230     240
m285.pep      QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGAASVGLKKPFALDTAIYTKGGLEGK
              |||
a285           QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGSASVGLKKPFALDTAIYTKGGLEGK
              190     200     210     220     230     240

              250     260     270     280     290     300
m285.pep      TIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIHPFAESLDKTLEEVLVKGFNINPAAF
              |||

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a285 TIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIHPFAESLDKTL EEVLVKGFNINPSAF
 250 260 270 280 290 300

m285.pep 310 320 330 340 350 360
VPSLPDAGLNFDLTAIPSFSDGIALEGS LDLENTKAGFADRNGIPVRQVLGGFVIRQDGT
|||||:|||||

a285 VPSLPDAGLNFDLTAIPSFSDGIALEGS LDLENTKAGFADRNGIPVRQVLGSFVIRQDGT
 310 320 330 340 350 360

m285.pep 370 380 390 400 410 420
VHIGNTSAALLGRGGIRLSGKIDTEKDILD LNIGINSVGAEDVLQTAFKGRLDGSIGIGG
|||||:|||||

a285 VHIGNTSVALGRGGIRLSGKIDTEKDILD LNIGINSVGAEDVLQTAFKGRLDGSIGIGG
 370 380 390 400 410 420

m285.pep 430 440 450 460 470 480
TTASPKISWQLGIGTARTDGS LAIASDPANGQRKLVLDTVNIAAGQGS LTAQGYLELFKD
|||||:|||||

a285 TTASPKISWQLGIGTARTDGS LAIASDPANGQRKLVLDTVNIAAGQGS LTAQGYLELFKD
 430 440 450 460 470 480

m285.pep 490 500 510 520 530 540
RLLKLDIRSRAFDPSRIDPQLPAGNINGS INLAGELAKEKFTGKMRF LPGT FNGVPIAGS
|||||:|||||

a285 RLLKLDIRSRAFDPSRIDPQLPAGNINGS INLAGELAKEKFTGKMRF LPGT FNGVPIAGS
 490 500 510 520 530 540

m285.pep 550 560 570 580 590 600
ADIVYESRHLPRAAVDLRLGRNI IKT DGGFGKKGDRLNLNITAPDLSRFGFGLAGSLNVR
|||||:|||||

a285 ADIVYESRHLPRAAVDLRLGRNI IKT DGGFGKKGDRLNLNITAPDLSRFGFGLAGSLNVR
 550 560 570 580 590 600

m285.pep 610 620 630 640 650 660
GHLSGDL DGGIRTFFETDLSGAARNLHIGKAADIRSLDFTLKGSPDTSRPIRADIKGSRLS
|||||:|||||

a285 GHLSGDL DGGIRTFFETDLSGAARNLHIGKAADIRSLDFTLKGSPDTSRPIRADIKGSRLS
 610 620 630 640 650 660

m285.pep 670 680 690 700 710 720
LSGGA VVD TADLMLDGTGVQHRIRTHAAMTLDGKPFKFDLDASGGINRELTRWKSGSIGI
|||||:|||||

a285 LSGGA EVVD TADLMLDGTGVQHRIRTHAAMTLDGKPFKFDLDASGGINRELTRWKSGSIGI
 670 680 690 700 710 720

m285.pep 730 740 750 760 770 780
LDIGGAFNLKQLQNRMTLEAGAERVAAS AANWQAMGGS LNLQHFSWDKKTGISAKGGAHGL
|||||:|||||

a285 LDIGGAFNLKQLQNRMTLEAGAERVAAS AANWQAMGGS LNLQHFSWDKKTGISAKGGAHGL
 730 740 750 760 770 780

m285.pep 790 800 810 820 830 840
HIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYL NISRQSGDAVLPGGQALGLNAFSLK
|||||:|||||

a285 HIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYL NISRQSGDAVLPGGQALGLNAFSLK
 790 800 810 820 830 840

m285.pep 850 860 870 880 890 900
TRFQNDRIGILLDGGARFGRINADL GIANAFGGNMANAPLGGRITASLPDLGALKPFLPA
|||||:|||||

a285 TRFQNDRIGILLDGGARFGRINADL GIANAFGGNMANAPLGGRITASLPDLGALKPFLPA
 850 860 870 880 890 900

m285.pep 910 920 930 940 950 960
AAQNITGSLNAAAQIGGRVGS PSVNAAVNGSSNYGKINGNITV GQSRSFDTAPLGGRINL
|||||:|||||

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a285	AAQNITGSLNAAQIGGRVGS	SPSVNA	AVNGSS	NYGKING	NITVGQ	SRSFDTAP	LGGR	LNL
	910	920	930	940	950	960		
m285.pep	TVADAEVFRN	FLPVGQ	TVKGS	LNAAVT	LGGS	ADPH	LGGS	INGDKLYRNQTQGIILDNG
a285	TVADAEVFRN	FLPVGQ	TVKGS	LNAAVT	LGGS	ADPH	LGGS	INGDKLYRNQTQGIILDNG
	970	980	990	1000	1010	1020		
m285.pep	SLRSHIAGRK	WVIDSL	KFRHEG	TAE	LSGT	VMEN	SGPD	VDIGAVFDKYRILSRPNRLTV
a285	SLRSHIAGRK	WVIDSL	KFRHEG	TAE	LSGT	VMEN	SGPD	VDIGAVFDKYRILSRPNRLTV
	1030	1040	1050	1060	1070	1080		
m285.pep	SGNTRLRY	SPQKGI	SVTGM	IKTDQ	GLFG	SQKSS	MPSV	GDDVVVLGEVKKEAAAPLPVNMN
a285	SGNTRLRY	SPQKGI	SVTGM	IKTDQ	GLFG	SQKSS	MPSV	GDDVVVLGEVKKEAAAPLPVNMN
	1090	1100	1110	1120	1130	1140		
m285.pep	LTLDLNDG	IRFAGY	GADV	TIGG	KLTL	TAQSG	SVRG	VGTVRVIKGRYKAYGQDLITKGT
a285	LTLDLNDG	IRFAGY	GADV	TIGG	KLTL	TAQSG	SVRG	VGTVRVIKGRYKAYGQDLITKGT
	1150	1160	1170	1180	1190	1200		
m285.pep	VSVFVG	PLNDP	NLNIRA	ERRLS	SPV	GAGVE	ILGSL	NSPRITLTANEP
a285	VSVFVG	PLNDP	NLNIRA	ERRLS	SPV	GAGVE	ILGSL	NSPRITLTANEP
	1210	1220	1230	1240	1250	1260		
m285.pep	GSGSSG	DNAAL	SAAAG	ALLAG	QIND	RIGL	VDDL	LGFTSKRSR
a285	GSGSSG	DNAAL	SAAAG	ALLAG	QIND	RIGL	VDDL	LGFTSKRSR
	1270	1280	1290	1300	1310	1320		
m285.pep	LTGKLY	IGYEY	SISSAE	QSVK	LIYRL	TRAIQ	AVAR	IGSRSSG
a285	LTGKLY	IGYEY	SISSAE	QSVK	LIYRL	TRAIQ	AVAR	IGSRSSG
	1330	1340	1350	1360	1370	1380		
m285.pep	DSAGN	GK	GKX					
a285	DSAGN	GK	GKX					
	1390							

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1187>:

g285-1.seq

```

1   CTGAAGCTGT CGGCGGCACT GCTGTCTGTC CTGATTTTGG CAGTATGTTT
51  CCTCGGCTGG ATCGCCGCTA CGGAAGCAGG TTTGCGCTTC GGGCTGTACC
101 AAATCCCGTC CTGGTTCGGC GTAAACATTT CCTCCCAAAA CCTCAAAGGC
151 ACACTGCTCG ACGGCTTCGA CGGCGACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGGAAA CCGTCCGAAC
251 TGATGCGCCG CAGCCTGCAC ATCACCAGCA TCTCCGCCGG CGACATCGCC
301 ATCGTAACCA AACCGACTCC GCCTAAAGAA GAACGCCCGC CTCAAGGCCT
351 GCCCGACAGC ATAGACCTGC CCGCCGCCGT CTATCTCGAC CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAACCTTTG ACAAACAAAC CGTCTATCTC
451 GAACGCCTCA ACGCGGCATA CCGTTACGAC CGTAAAGGGC ACCGCCTCGA
501 CCTGAAGGCC GCCGACACGC CGTGGAGCAG TTCGTCGGGG TCAGCCTCGG

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551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGATTCGAAG GCGAAACCAT ACACAGTACG GCGCGGCTGA GCGGCAGCCT
651 GAAGGATGTG CCGGCCGAAC TGACGATCGA CCGCGGCAAT ATCCGCTCT
701 CGGGAAATC CGTCATCCAC CCGTTTGCCG AATCATTGGA TAAACATTG
751 GAAGAAGTAC TGGTCAAAGG ATTC AACATC AATCCGTCCG CCTTCGTGCC
801 TTCCCTGCCC GATGCCGGGC TGAATTTGGA CCTGACCGCC ATCCCGTCGT
851 TTTCAGACGG CATCGCGCTG GAAGGCTCGC TCGATTTGGA AAACACCAA
901 GCCGGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTGAGG TTTTGGGCGG
951 CTTTGTCTAT CGGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGCGG
1001 CCCTGCTCGG ACGGGGCGGC ATCAGGCTGT CCGGCAAAAT CGACACCGAA
1051 AAAGACATCC TTGATTTAAA TATAGGCATC AACTCCGTCG GCGCGGAAGA
1101 CGTGCTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GCGGCACGAC CGCTCGCCC AAAATCTCTT GGCAACTCGG CACCGGCACG
1201 GCACGCACGG ACGGCAGCCT cgcCATCGCA AGCGAcCCG CAAACGAACA
1251 GCGGAAACTG GTGTTTCGACA CCGTCAACAT CTCCGCCGGG GAAGGCAGCC
1301 TGACCGCGCA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCCGTT CCCGCGCATT CGACCTTCG CGCATCGATC CGCAATTTC
1401 GGCAGGCGat atCAACGTT CGATTCATCT TGCCGGTGAA CTGGCAAAAG
1451 AGAAATTTAC GGGCAAAATG CGTTTTTTGC CCGGTACGTT CAACGGCGTG
1501 CCGATTGCCG GCAGCGCCGA CATTGTTTAC GAGTCCGCGC ACCTTCCGCG
1551 CGCCGCCGTC GATTTGCGGT TGGGGCGGAA CATCGTCAAA ACAGACGGCG
1601 GCTTCGGCAA AAAAGCGGAC CGGCTTAACC TCAATATCAC CGCACCAGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA
1701 CCTTTCCGGG GATTTGAGCG GCGGCATCCG AACCTTTGAA ACCGACCTTT
1751 CCGGCACGGC GCGCAACTTA CACATCGGCA AAGCGGCAGA CATCCGTTTCG
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1851 CGATATCAAG GCGGCGCGCC TTTCCCTGTC GGGCGGCGCG GCGGTTGTCG
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2001 GCCTTCAGCG GGCATCAACA GGGAACTTAC CCGATGGAAA GGCAGCATCG
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2151 GCGAATGGGC GGCAGCCTCA ACCTGCAACA CTTTTCTTGG GACAGGAAAA
2201 CCGGCATATC GGCAAAAGGC GCGCACGCGG GCCTGCACAT CGCCGAGTTG
2251 CACAATTTCT TCAAACCGCC CTTGCAACAC AATCTGGTTT TAAACGGCGA
2301 CTGGGATGTC GCCTACGGGC ACAACGCGCG CCGCTACCTC AATATCAGCC
2351 GGCAAAGCGG CGATGCCGTA TTGCCGCGG GGCAGGCTTT GGGTTTGAAC
2401 GCATTTCCCG TGAAACGCG CTTTCAAAC GACCGCATCG GAATCTGCT
2451 TGACGGCGGC GCGCGTTTCG GACGGATTAA CGCCGATTTG GGCATCGGCA
2501 ACGCCTTCGG CGGCAATATG GCAATACAC CGCTCGGCGG CAGGATTACA
2551 GCCTCCCTTC CCGACTTGGG CGCATGGAAG CCCTTTCTGC CCGCGCGCGC
2601 GCAAAACATT ACCGGCAGCC TGAATGCCTC CGCGCAAATC GCGGACGGG
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3151 CTGCGCTATT CGCCGCAAAA AGGCATATCC GTTACCGGTA TGATTAAAAC
3201 TGATCAGGGG CTGTTGCGTT CGCAAAAATC CTCGATGCCG TCCGTGCGCG
3251 ACGATGTCTG CGTATTGGGC GAAGTCAAGA AAGAGGCGGC GGCATCGCTC
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3351 CCGCTACGGC GCGGACGTTA CCATAGGCGG CAAACTGACC CTGACCGCGC
3401 AACCAGGCGG AAATGTGCGT GGGTGGGCA CGGTCCGCGT CATCAAAGG
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3551 GCCTTTCCCC CGTCGGTGCG GCGGTGGAAA TATTGGGCG CCTCAACAGC
3601 CCGCGCATTA CGCTGACGGC AAACGAACCG ATGAGTGAAA AAGACAAGCT
3651 CTCCTGGCTC ATCTCAACG GTGCCGGCAG CCGCAGCAGC GCGGACAATG
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3751 CGCATCGGGC TGGTGGATGA TTTGGGCTTT ACCAGCAAGC GCAGCCGCAA
3801 CCGCGAAACC GGCGAACCTA ACCCGCGCGA ACAGGTGCTG ACCGTGCGCA
3851 AACAACGTAC CCGCAAACTC TACATCGGCT ACGAATACGG CATCTCCAGC
3901 CCGGAACAGT CCGTCAAACCT GATTACCGG CTGACCCGCG CCATACAGGC
3951 GGTGCCCCGT ATCGGCAGCC GTTCGTGCGG CGGCAGCTG ACATACACCA
4001 TACGTTTCGA CCGCTCTTC GGTTCGGACA AAAAAGACTC CGCAGGAAAC
4051 GGCAAGGGGA AATAA

```

This corresponds to the amino acid sequence <SEQ ID 1188; ORF 285-1.ng>:
g285-1.pep

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1  LKLSAALLSV LILAVCFLGW IAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51  TLLDGFDDGN WSIETEGADL KISRFRFAWK PSELMRRSLH ITDISAGDIA
101 IVTKPTPPKE ERPPQGLPDS IDLPAAYVLD RFETGKISMG KTFDKQTVYL
151 ERLNAYRYD RKGHRLDLKA ADTPWSSSSG SASVGLKKPF ALDTAIYTKG
201 GFEGETIHST ARLSGSLKDV RAELTIDGGN IRLSGKSVIH PFAESLDKTL
251 EEVLVKGfNI NPSAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK
301 AGFADRNGIP VRQVLGGFVI RQDGTVHIGN TSAALLGRGG IRLSGKIDTE
351 KDILDLNIGI NSVGAEDVLQ TAFKGRLDGS IGIGGTTASP KISWQLGTGT
401 ARTDGSIAIA SDPANEQRKL VFDTVNISAG EGSILTAQGYL ELFKDRLLKL
451 DIRSRAFDPS RIDPQFPAGD INGSIHLAGL LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIVK TDGGFGKKGD RLNLNITAPD
551 LSRFGFGLAG SLNVRGHLG DLDDGGIRTFE TDLSGTARNL HIGKAADIRS
601 LDFTLKGSFG TSRPMRADIK GGRLSLSGGA AVVDTAGLTL EGTGAQHRIR
651 THAAMTLDGK PFKLDDLASG GINRELTRWK GSIGILDIGG AFNLKLQNRM
701 TLEAGAEHVA ASAANWQAMG GSNLNLQHSW DRKTGISAKG GARGLHIAEL
751 HNFFKPPFEH NLVLNGDWDV AYGHNARGYL NISRQSGDAV LPGGQALGLN
801 AFSLLTRFQN DRIGILLDGG ARFGRINADL GIGNAFGNM ANTPLGGRIT
851 ASLPDLGALK PFLPAAQNI TGSLNLSAQI GGRVGSPSVN AAVNGSSNYG
901 KINGNITVGO SRSFDTAPLG GRLNLTVADA EAFRNFLPVG QTVKGSNLAA
951 VTLLGGSIA DP HLGGSSINGDK LYRNTQOGI ILDNGLSLRS IAGRKWVIDS
1001 LKFRHEGTAE LSGTVSMENS VPDVDIGAVF DKYRILSRPN RRLTVSGNTR
1051 LRYSPQKGIS VTGMIKTDQG LFGSQKSSMP SVGGDDVVVLG EVKKEAAASL
1101 FVNMNLTLDL NDGIRFSGYG ADVTIGGKLT LTAQPGGNVR GVGTVRVIK
1151 RYKAYGDLDP ITKGTVSFVG PLNDPNLNIR AERRLSVGA GVEILGSLNS
1201 PRITLTANEP MSEKDKLSWL ILNRAGSGSS GDNAALSAAA GALLAGQIND
1251 RIGLVDDLGF TSKRSRNAQT GELNPAEQVL TVGKQLTGKL YIGYEYGISS
1301 AEQSVKLIYR LTRAIQAVAR IGSRSSGGEL TYTIRFDRLF GSDKKDSAGN
1351 GK GK*
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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1189>:

m285-1.seq

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1  CTGAAGCTGT CGGCGGCACT GCTGTCTGTC CTGATTTTGG CAGTATGTTT
51  CCTCGGCTGG CTCGCCGCTA CGGAAGCAGG TTTGCGCTTC GGGCTGTACC
101 AAATCCCCTG TTGGTTCCGC GTAAACATTT CCTCCCAAAA CCTCAAAGGC
151 ACGTGCTCTG ACGGCTTCGA CGGCGACAAC TGCTCGTAGT AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGGAAA CCGTCCGAAC
251 TGATGCGCCG CAGCCTGCAC ATTACCGAAA TTTCCGCCGG CGACATCGCC
301 ATCGTTACCA AACCGACTCC GCCTAAAGAA GAACGCCCGC CGCTCAGCCT
351 TCCCGACAGC ATAGACCTGC CTGCCGCCGT CTATCTCGAC CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAGCCTTTG ACAACAACAC CGTCTATCTC
451 GAACGGCTGG ATGCTTCATA CCGTTACGAC CGCAAAGGAC ACCGCCTTGA
501 CCTGAAGGCC GCCGACACGC CGTGGAGCAG TTCGTCGGGG GCGGCCTCGG
551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGAATCGAAG GCAAAACCAT ACACAGTACG GCTCGGCTGA GCGGCAGCCT
651 GAAGGATGTG CGCGCCGAAC TGGCGATCGA CGGCGGCAAT ATCCGCCTCT
701 CGGGAATAAT CGTCATCCAC CCGTTTGCCG AATCATTTGA TAAACATTG
751 GAAGAAGTAC TGGTCAAAGG GTTCAACATC AATCCGGCCG CCTTCGTGCC
801 TTTCCCTGCC GATGCCGGAC TGAATTTCTG CCTGACCGCC ATCCCGTCGT
851 TTTGACAGCG CATCGCGCTG GAAGGTTTCG TCGATTGGA AAACACCAA
901 GCCGGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTCAGG TTTTAGGCGG
951 CTTTGTATC CGGCGAGGAC GCACGGTGCA TATCGCAAT ACGTCCGCCG
1001 CCCTGCTCGG ACGGGCGGCG ATCAGGCTGT CGGGCAAAAT CGACACCGAA
1051 AAAGACATCC TCGATTTAAA TATAGGCATC AACTCCGTCG GCGCGGAAGA
1101 CGTACTGCAA ACCGCTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GTGGCAGGAC CGCCTCGCCC AAAATCTCTT GGCAACTCGG CATCGGCAGC
1201 CCGCGCACGG ACGGCAGCCT CGCCATTGCA AGCGACCCAG CAAACGGACA
1251 GCGGAAACTG GTGCTCGACA CCGTCAACAT CGCCGCCGGG CAAGGCAGCC
1301 TGACCGCGCA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCGGTT CCCGCGCATT CGACCTTCG CGCATCGATC CGCAACTTCC
1401 GGCAGGCCAT ATCAACGGCT CAATAAACCT TGCCGGCGAA CTGGCAAAAG
1451 AGAAATTAC AGGCAAAATG CCGTTTTTAC CCGGCACGTT CAACGGCGTA
1501 CCGATTGCGG GCAGTGCCGA CATTGTTTAC GAGTCCCGCC ACCTTCCGCG
1551 TGCCGCCGTC GATTGCGGCG TGGGCGGAA CATTATTA AAACAGCGCG
1601 GCTTCGGCAA AAAAGGCGAC CGGCTTAACC TCAATATCAC CGCACCCGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA
1701 CCTTCCGGT GATTGACG GCGGCATCCG AACCTTGAA ACCGACCTT
1751 CCGGCGCGGC GCGCAACCTG CACATCGGCA AGCGGCGAGA CATCCGTTG
1801 CTCGATTTCG CGCTCAAAGG TTCGCCGAC ACAAGCCGCC CGATACGCGC
1851 CGACATCAAA GGCAGCCGCC TTTGCTGTC GGGCGGAGCG GCGGTTGTCG
1901 ATACCGCGCA CCGATGCTG GACGGCACGG CCGTGCAGCA CCGCATCCGC
1951 ACACACGCCG CATGACGCT GGATGGCAA CCGTCAAA TCGATTGGA
2001 GCCTTCAGGC GGCATCAACA GGGAACTTAC CCGATGGAAA GGCAGCATCG
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2101 ACGCTCGAAG CCGGTGCGGA ACGCGTGGCG GCAAGTCCGG CAAATTGGCA
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2301 CTGGGATGTC GCCTACGGGC GCAACGCGCG CGGCTACCTC AATATCAGCC
2351 GGCAAAGCGG CGATGCCGTA TTGCCCGGCG GGCAGGCTTT GGGTTTGAAC
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2551 GCCTCCCTTC CCGACTTGGG CGCATTGAAG CCCTTTCTGC CCGCCGCGGC
2601 GCAAAACATT ACCGGCAGCC TGAATGCCCG CGCGCAAATC GGCAGACGGG
2651 TAGGCTCTCC GTCCGTCAAT GCCGCCGTCA ACGGCAGCAG CAACTACGGG
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2851 GTAACCTTCG GCGGCAGCAT CGCCGATCCG CACTTGGGCG GCAGCATCAA
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2951 ACGGCTCGCT ATCGCTCGCAT ATCGCGGGCA GGAATGGGT AATCGACAGC
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3151 CTGCGCTATT CGCCGCAAAA AGGCATATCC GTTACCGGGA TGATTAA AAC
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3251 ACGATGTCGT CGTATTAGGC GAAGTCAAAA AAGAGCGGCG GGCACCGCTC
3301 CCGTCAATA TGAACCTGAC TTTAGACCTC AATGACGGCA TCCGCTTCGC
3351 CGGCTACGGC GCGGACGTTA CCATAGGCGG CAACTGACC CTGACCGCCC
3401 AATCGGGGCG AAGCGTACGG GGCGTGGGCA CGGTCCGCGT CATCAAAGGG
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3501 CTTTGTCCGC CCGCTCAACG ATCCCAACCT CAACATCCGC GCCGAACGCC
3551 GCCTTTCCCC CGTCGGTGGC GGCGTGGAAA TATTGGGCGC CCTCAACAGC
3601 CGCGCATTA CGCTGACGGC AAACGAACCG ATGAGTGAAG AAGACAAGCT
3651 CTCTTGGCTC ATCTCAACC GCGCCGGCAG CGGCAGCAGC GGCAGCAATG
3701 CCGCCCTGTC TGCAGCCGCA GGTGCGCTGC TTGCCGGGCA AATCAACGAC
3751 CGCATCGGGC TGGTGGATGA TTTGGGCTTT ACCAGCAAGC GCAGCCGCAA
3801 CGCGCAAACC GCGCAACTCA ACCCGCCGGA ACAGGTGCTG ACCGTCGGCA
3851 AACAACTGAC CGGCAAACTC TACATCGGCT ACGAATACAG CATCTCCAGC
3901 GCGGAACAGT CCGTCAAAC TATTACCGG CTGACCCGCG CCATACAGGC
3951 GGTGCCCCGT ATCGGCAGCC GTTCGTCGGG CGGCGAGCTG ACATACACCA
4001 TACGTTTCGA CCGCTTCTCC GGTTCGGACA AAAAAGACTC CGCCGGAAC
4051 GGCAAGGAA AATAA

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This corresponds to the amino acid sequence <SEQ ID 1190; ORF 285-1>:

m285-1.psp

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1 LKLSAALLSV LILAVCFLGW LAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51 TLLDGFDFGN WSIETEGADL KISRFRFAWK PSELMRRSLH ITEISAGDIA
101 IVTKPTPPKE ERPLSLPDS IDLPAAVYLD RFETGKISMG KAFDKQTVYL
151 ERLDASYRYD RKGHRLDLKA ADTPWSSSSG AASVGLKKPF ALDTAIYTKG
201 GLEGKTIHST ARLSGSLKDV RAELAIDGGN IRLSGKSVIH PFAESLDKTL
251 EEVLVKGFNI NPAAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK
301 AGFADRNGIP VROVLGGFVI RQDGTVHIGN TSAALLGRGG IRLSGKIDTE
351 KDILLDLNIGI NSVGAEDVLQ TAFKGRLDGS IGIGGTTASP KISWQLGIGT
401 ARTDGLSLAIA SDPANGQRKL VLDTVNIAAG QGSLTAQGYL ELFKDRLLKL
451 DIRSRAFDPS RIDPQLPAGN INGSINLAGE LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIIK TDGGFGKKGD RLNLNITAPD
551 LSRFGFGLAG SLNVRGHL SG DLDGGIRTFE TDLSGAARNL HIGKAADIRS
601 LDFTLKGSPD TSRPIRADIK GSRLSLSGGA AVVDATDML DGTGVQHRIR
651 THAAMTLDGK PFKFDLDASG GINRELTRWK GSGILDIGG AFNLKLQNRM
701 TLEAGAERVA ASANWQAMG GSLNLQHFSW DKKTGISAKG GAHGLHIAEL
751 HNFFKPPFEH NLVLNGDWDV AYGRNARGYL NISRQSGDAV LPGGQALGLN
801 AFSLKTRFQF DRIGILLDGG ARFGRINADL GIANAFGGNM ANAPLGGRIT
851 ASLPDLGALK PFLPAAQNI TGSLNAAQI GGRVGSPPSVN AAVNGSSNYG
901 KINGNITVGO SRSFDTAPLG GRLNLTVADA EVFRNFLPVG QTVKGS LNAA
951 VTLLGGSIA DP HLGGSINGDK LYRNRQTQGI ILDNGLSLRH IAGRKWVIDS
1001 LKFRHEGTAE LSGTVGMENS GPDVDIGAVF DKYRILSRPN RRLTVSGNTR
1051 LRYSPQKGIS VTGMIKTDQG LFGSQKSSMP SVGDDVVVLG EVKKEAAAPL
1101 PVMNMLTLDL NDGIRFAGYG ADVTIGGKLT LTAQSGGSVR GVGTVRVIKG
1151 RYKAYGQDLD ITKGTVSFVG PLNDPNLNIR AERRLSPVGA GVEILGSLNS
1201 PRITLTANEP MSEKDKLSWL ILNRAGSGSS GDNAALSAAA GALLAQIND
1251 RIGLVDDLGF TSKRSRNAQT GELNPAEQVL TVGKQLTGKL YIGYEYSISS
1301 AEQSVKLIYR LTRAIQAVAR IGSRSSGGEL TYTIRFDRFS GSDKKDSAGN
1351 GK GK*

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g285-1/m285-1 96.5% identity in 1354 aa overlap

10

20

30

40

50

60

662

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	790	800	810	820	830	840
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m285-1	NISRQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLGIANAFGGNM					
	790	800	810	820	830	840
	850	860	870	880	890	900
g285-1.pep	ANTPLGGRITASLPDLGALKPFLPAAQONITGSLNAAQIGGRVGSVNAAVNGSSNYG					
m285-1	ANAPLGGRITASLPDLGALKPFLPAAQONITGSLNAAQIGGRVGSVNAAVNGSSNYG					
	850	860	870	880	890	900
	910	920	930	940	950	960
g285-1.pep	KINGNITVGQSRSDTAPLGGRLNLTVADAEAFRNFLPVGQTVKGSLNAAVTLGGSIADP					
m285-1	KINGNITVGQSRSDTAPLGGRLNLTVADAEVFRNFLPVGQTVKGSLNAAVTLGGSIADP					
	910	920	930	940	950	960
	970	980	990	1000	1010	1020
g285-1.pep	HLGGSINGDKLYYRNQTQGIILDNGSLRSHIAGRKWVIDSLKFRHEGTAELSGTVSMENS					
m285-1	HLGGSINGDKLYYRNQTQGIILDNGSLRSHIAGRKWVIDSLKFRHEGTAELSGTVSMENS					
	970	980	990	1000	1010	1020
	1030	1040	1050	1060	1070	1080
g285-1.pep	VPDVIDGAVFDKYRILSRPNRRLTVSGNTRLRYSPQKGISVTGMIKTDQGLFGSQKSSMP					
m285-1	GPDVDIGAVFDKYRILSRPNRRLTVSGNTRLRYSPQKGISVTGMIKTDQGLFGSQKSSMP					
	1030	1040	1050	1060	1070	1080
	1090	1100	1110	1120	1130	1140
g285-1.pep	SVGDDVVVLGEVKKEAAASLPVNMNLTLDLNDGIRFSGYGADVTIGGKLTLTAPGGNVR					
m285-1	SVGDDVVVLGEVKKEAAAPLPVNMNLTLDLNDGIRFAGYGADVTIGGKLTLTQSGGSVR					
	1090	1100	1110	1120	1130	1140
	1150	1160	1170	1180	1190	1200
g285-1.pep	GVGTVRVIKGRYKAYGQDLDTKGTVSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS					
m285-1	GVGTVRVIKGRYKAYGQDLDTKGTVSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS					
	1150	1160	1170	1180	1190	1200
	1210	1220	1230	1240	1250	1260
g285-1.pep	PRITLTANEPMSEKDKLSWLILNRAGSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGF					
m285-1	PRITLTANEPMSEKDKLSWLILNRAGSGSGDNAALSAAAGALLAGQINDRIGLVDDLGF					
	1210	1220	1230	1240	1250	1260
	1270	1280	1290	1300	1310	1320
g285-1.pep	TSKRSRNAQTGELNPAEQVLTVGKQLTGKLYIGYEYGISSAEQSVKLIYRLTRAIQAVAR					
m285-1	TSKRSRNAQTGELNPAEQVLTVGKQLTGKLYIGYEYGISSAEQSVKLIYRLTRAIQAVAR					
	1270	1280	1290	1300	1310	1320
	1330	1340	1350			
g285-1.pep	IGSRSSGGELTYTIRFDRFLFGSDKKDSAGNGKGK					
m285-1	IGSRSSGGELTYTIRFDRFSGSDKKDSAGNGKGKX					
	1330	1340	1350			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1191>:

a285-1.seq

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1  CTGAAGCTGT  CGGCGGCACT  GCTGTCTGTT  CTGATTTTGG  CAGTATGTTT
51  CCTCGGCTGG  CTCGCCGCA  CGGAAGCGGG  TTTGCGCTTC  GGGCTGTACC
101  AAATCCCCTG  TTGGTTTCGC  GTAAACATT  CCTCCCAAAA  CCTCAAAGGC
151  ACGCTGCTCG  ACGGCTTCGA  CGGCGACAAC  TGGTCGATAG  AAACCGAGGG
201  GGCAGACCTT  AAAATCAGCC  GCTTCCGCTT  CGCGTGGAAA  CCGTCCGAAC
251  TGATGCCCGG  CAGCCTGCAC  ATTACCGAAA  TTTCCGCCGG  CGACATCGCC
301  ATCGTTACCA  AACCGACTCC  GCCTAAAGAA  GAACGCCCGC  CGCTCAGCCT
351  TCCCGACAGC  ATAGACCTGC  CTGCCGCCGT  CTATCTCGAC  CGCTTCGAGA
401  CGGGCAAAAT  CAGCATGGGC  AAAGCCTTTG  ACAACAAAC  CGTCTATCTC
451  GAACGGCTGG  ATGCTTCATA  CCGTTACGAC  CGCAAAGGAC  ACCGCCTCGA

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501 CCTGAAGGCT GCCGACACGC CGTGGAGCAG TTCGTCGGGG TCAGCCTCGG
551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAGGCG
601 GGACTCGAAG GCAAAACCAT ACACAGTACG GCTCGGCTGA GCGGCAGCCT
651 GAAGGATGTG CGCGCCGAAC TGGCGATCGA CGGCGGCAAT ATCCGCTCT
701 CGGGAAAAATC CGTCATCCAC CCGTTTGCCG AATCATTGGA TAAACATTG
751 GAAGAAGTAC TGGTCAAAGG GTTCAACATC AATCCGTCCG CCTTCGTGCC
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901 GCCGGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTCAGG TTTTAGGCAG
951 CTTTGTCAAT CGGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCGTCG
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1301 TGACCGCGCA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCCGTT CCCGCGCATT CGACCCCTTCG CGCATCGATC CGCAACTTCC
1401 GGCAGGCAAT ATCAACGGCT CAATAAACCT TGCCGGCGAA CTGGCAAAAG
1451 AGAAATTAC AGGCAAAATG CCGTTTTTAC CCGGCACGTT CAACGGCGTA
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1601 GCTTCGGCAA AAAAGGCGAC CGGCTTAACC TCAATATCAC CGCACCAGAT
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1801 CTCGATTTCA CGCTCAAAGG TTGCCCCGAC ACAAGCCGCC CGATACGCGC
1851 CGACATCAAA GGCAGCCGCC TTTCGCTGTC GGGCGGAGCG GAGGTTGTCT
1901 ATACCGCCGA CTTGATGCTG GACGGCACGG GCGTGCAGCA CCGCATCCGC
1951 ACACACGCCG CCATGACGCT GGATGGCAAA CCGTTCAAAT TCGATTTGGA
2001 CGCTTCAGGC GGCATCAACA GGGAACTTAC CCGATGGAAG GGCAGCATCG
2051 GCATCCTCGA CATCGGCGGC GCATTCAACC TCAAGCTGCA AAACCGTATG
2101 ACGCTCGAAG CCGGTGCGGA ACGCGTGGCG GCAAGTGGCG CAAATTGGCA
2151 GGCAATGGGC GGCAGCTCA ACCTGCAACA CTTTCTTGG GATAAAAAAA
2201 CCGGCATATC GGCAAAAGGC GCGCACACAG GTCTGCATAT CGCCGAGTTG
2251 CACAATTTCT TCAAACCGCC CTTCGAACAC AATCTGGTTT TAAACGGCGA
2301 CTGGGATGTC GCCTACGGGC GAAACGCGCG CGGCTACCTC AATATCAGCC
2351 GGCAAAAGCG CGATGCCGTA TTGCCCGGCG GGCAGGCTTT GGGTTTGAAC
2401 GCATTTTCCC TGAAAACGCG CTTTCAAAC GACCGTATCG GAATCCTGCT
2451 TGACGGCGCG GCGCGTTTCG GCGGGATTAA CGCCGATTTC GACATCGGCA
2501 ACGCTTCGG CGGCAATATG GCAAATGCAC CGCTCGGCGG CAGGATTACC
2551 CCCTCCCTTC CCGACTTGGG CACATTGAAG CCCTTTCTGC CCGCCGCCGC
2601 GCAAAACATT ACCGGCAGCC TGAATGCCGC CGCGCAAAAT GCGGGACGGG
2651 TCGGCTCTCT GTCCGTCAAT GCCGCCGTCA ACGGCAGCAG CAACTACGGG
2701 AAAATCAACG GCAACATCAC CGTCGGGCAA AGCCGCTCTT TCGATACCGC
2751 GCCTTTGGGC GGCAGGCTCA ACCTGACCGT TGCCGATGCC GAAGTATTCC
2801 GCAACTTCTC ACCGGTCGGA CAAACCGTCA AAGGCAGCCT GAATGCCGCC
2851 GTAACCTCTG GCGGCAGCAT CGCCGATCCG CACTTGGGCG GCAGCATCAA
2901 CCGCGACAAA CTCTATTACC GCAACCAAAC CCAAGGCATC ATCTTGGAAC
2951 ACGGCTCGCT GCGTTCGCAT ATCGCGGGCA GGAATGGGT AATCGACAGC
3001 CTGAAATTCC GGCACGAAGG GACGGCGGAA CTCTCCGGTA CGGTCGGTAT
3051 GGAAAACAGC GGACCCGATG TCGATATCGG CGCGGTGTTG GACAAATACC
3101 GCATCTGTCT CCGCCCCAAC CGCCGCTGTA CGGTTTCCGG CAACACCCGC
3151 CTGCGCTATT CGCCGCAAAA AGGCATATCC GTTACCGGGA TGATTAATAAC
3201 GGATCAGGGG CTGTTCCGTT CGCAAAAATC CTCGATGCCG TCCGTCGGCG
3251 ACGATGTCGT CGTATTAGGC GAAGTCAAAA AAGAGGCGGC GGCACCGCTC
3301 CCCGTCAATA TGAACCTGAC TTAGACCTC AATGACGGCA TCCGCTTCGC
3351 CCGCTACGGC GCGGACGTTA CCATAGCGCG CAAACTGACC CTGACCGCCC
3401 AATCGGGCGG AAGCGTGCGG GCGTGCGGCA CGGTCCGCGT CATCAAAGGG
3451 CGTTATAAGG CATAAGGGCA GGATTTGGAC ATTACCAAAG GCACGGTCTC
3501 CTTTGTGCGG CCGCTCAACG ACCCCAACCT CAACATCCGC GCCGAACGCC
3551 GCCTTTCCCC CGTCGGTGCG GCGTGGAATA TATTGGGCG CTTCAACAGT
3601 CCGCGCATTA CGCTGACGGC AAACGAACCG ATGAGTGAAA AAGACAAGCT
3651 CTCCTGGCTC ATCCTCAACC GCGCCGCGAG TGGCAGCAGC GCGGACAATG
3701 CCGCCCTGTC CGCAGCCGCC GCGCGCTGTC TTGCCGGGCA AATCAACGAC
3751 CGCATCGGGC TGGTGGATGA TTTGGGCTTT ACCAGCAAGC GCAGCCGCAA
3801 CGCGCAAACC GCGGAATCA ACCCCGCCGA ACAGGTGCTG ACCGTCGGCA
3851 AACAATGAC CGGCAAACTC TACATCGGCT ACGAATACAG CATCTCCAGC
3901 CGGGAACAGT CCGTCAAACT GATTACCGG CTGACCCGCG CCATACAGGC
3951 GGTGCCCCGT ATCGGCAGCC GTTCGTCGGG CCGCGAGCTG ACATACACCA
4001 TACGTTTCGA CCGCTTCTCC GGTTCGGACA AAAAAGACTC CGCCGGAAC
4051 AGCAAAGGAA AATAA

```

This corresponds to the amino acid sequence <SEQ ID 1192; ORF 285-1.a>:

a285-1.pep

1 LKLSAALLSV LILAVCFLGW LAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51 TLLDGFDDGN WSIETEGADL KISRFRFAWK PSELMRRSLH ITEISAGDIA
101 IVTKPTPPKE ERPPSLPDS IDLPAAVYLD RFETGKISMG KAFDKQTVYL
151 ERLDASYRYD RKGHRDLKA ADTPWSSSSG SASVGLKKPF ALDTAIYTKG
201 GLEGKTIHST ARLSGSLKDV RAELAIDGGN IRLSGKSVIH PFAESLDKTL
251 EEVLVKGFNI NPSAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK
301 AGFADRNGIP VRQVLGSFVI RQDGTVHIGN TSVALLGRGG IRLSGKIDTE
351 KDILDLNIGI NSVGAEDVLQ TAFKGRLDGS IGIGGTTASP KISWQLGIGT
401 ARTDGSIAIA SDPANGQRKL VLDTVNIAAG QGSLTAQGYL ELFKDRLLKL
451 DIRSRAFDPD RIDPQLPAGN INGSINLAGE LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIK TDGGFGKKGD RLNLNITAPD
551 LSRFGFGLAG SLNVRGHLGS DLDGGIRTFE TDLGGAARNL HIGKAADIRS
601 LDFTLKGSPD TSRPIRADIK GSRLSLSGGA EVVDTADLML DGTGVQHRIR
651 THAAMTLDGK PFKFDLDASG GINRELTRWK GSIGILDIGG AFNLKLQNRM
701 TLEAGAERVA ASAANWQAMG GSNLQHFWSV DKKTGISAKG GAHGLHIAEL
751 HNFFKPPFEH NLVLNGDWDV AYGRNARGYL NISRQSGDAV LPGAQALGLN
801 AFSLKTRFQN DRIGILLDGG ARFGRINADL DIGNAFGGNM ANAPLGGRIT
851 ASLPDLGTLK PFLPAAQNI TGSLNAAQI GGRVGSPSVN AAVNGSSNYG
901 KINGNITVGQ SRSFDTAPLG GRNLTVADA EVFRNFLPVG QTVKGSLNAA
951 VTLGGSADP HLGGSSINGDK LYRNQTQGI ILDNGLSRSH IAGRKWVIDS
1001 LKFRHEGTAE LSGTVGMENS GPDVDIGAVF DKYRILSRPN RRLTVSGNTR
1051 LRYSPQKGIS VTGMIKTDQG LFGSQKSSMP SVGDDVVVLG EVKKEAAAPL
1101 PVNMNLTLDL NDGIRFAGYG ADVTIGGKLT LTAQSGGSVR GVGTVRVIK
1151 RYKAYGQDLD ITKGTVSFVG PLNDPNLNIR AERRLSPVGA GVEILGSLNS
1201 PRITLTANEP MSEKDKLSQL ILNRAGSGSS GDNAALSAAG GALLAGQIND
1251 RIGLVDDLGF TSKRSRNAQT GELNPAEQVL TVGKQLTGKL YIGYEYSISS
1301 AEQSVKLIYR LTRAIQAVAR IGRSSSGGEL TYTIRDFRFS GSDKKDSAGN
1351 SKGK*

a285-1/m285-1 99.3% identity in 1354 aa overlap

	10	20	30	40	50	60
a285-1.pep	LKLSAALLSVLILAVCFLGWLAGTEAGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGN					
m285-1	LKLSAALLSVLILAVCFLGWLAGTEAGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGN					
	10	20	30	40	50	60
	70	80	90	100	110	120
a285-1.pep	WSIETEGADLKISRFRFAWKPSSELMRRSLHITEISAGDIAIVTKPTPPKEERPPSLPDS					
m285-1	WSIETEGADLKISRFRFAWKPSSELMRRSLHITEISAGDIAIVTKPTPPKEERPPSLPDS					
	70	80	90	100	110	120
	130	140	150	160	170	180
a285-1.pep	IDLPAAVYLDRLFETGKISMGKAFDKQTVYLERLDASYRYDRKGRHLDLKAADTPWSSSSG					
m285-1	IDLPAAVYLDRLFETGKISMGKAFDKQTVYLERLDASYRYDRKGRHLDLKAADTPWSSSSG					
	130	140	150	160	170	180
	190	200	210	220	230	240
a285-1.pep	SASVGLKKPFALDTAIYTKGGLEGKTIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIH					
m285-1	AASVGLKKPFALDTAIYTKGGLEGKTIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIH					
	190	200	210	220	230	240
	250	260	270	280	290	300
a285-1.pep	PFAESLDKTL EEVLVKGFNI NPSAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK					
m285-1	PFAESLDKTL EEVLVKGFNI NPSAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK					
	250	260	270	280	290	300
	310	320	330	340	350	360
a285-1.pep	AGFADRNGIPVRQVLGSFVIRQDGTVHIGNTSVALLGRGGIRLSGKIDTEKDILDLNIGI					
m285-1	AGFADRNGIPVRQVLGSFVIRQDGTVHIGNTSVALLGRGGIRLSGKIDTEKDILDLNIGI					
	310	320	330	340	350	360
	370	380	390	400	410	420
a285-1.pep	NSVGAEDVLQTAFKGRLDGSIGIGGTTASPKISWQLGIGTARTDGSIAIASDPANGQRKL					
m285-1	NSVGAEDVLQTAFKGRLDGSIGIGGTTASPKISWQLGIGTARTDGSIAIASDPANGQRKL					
	370	380	390	400	410	420
	430	440	450	460	470	480

a285-1.pep	VLDTVNIAAGQGS	SLTAQGYLE	LFKDRLLK	LDIRSF	AFDPSRID	PQLPAGNINGS	INLAGE
m285-1	VLDTVNIAAGQGS	SLTAQGYLE	LFKDRLLK	LDIRSF	AFDPSRID	PQLPAGNINGS	INLAGE
	430	440	450	460	470	480	
a285-1.pep	490	500	510	520	530	540	
a285-1.pep	LAKEKFTGKMR	FLPGTFNGV	PIAGSADIV	YESRHL	PRAAVDL	RLGRNII	KTDGGFGKKGD
m285-1	LAKEKFTGKMR	FLPGTFNGV	PIAGSADIV	YESRHL	PRAAVDL	RLGRNII	KTDGGFGKKGD
	490	500	510	520	530	540	
a285-1.pep	550	560	570	580	590	600	
a285-1.pep	RLNLNITAPDL	SRFGFLAG	SLNVRGHL	SGDLGG	IRTFTDL	SGAARNL	HIGKAADIRS
m285-1	RLNLNITAPDL	SRFGFLAG	SLNVRGHL	SGDLGG	IRTFTDL	SGAARNL	HIGKAADIRS
	550	560	570	580	590	600	
a285-1.pep	610	620	630	640	650	660	
a285-1.pep	LDFTLKGPS	PDTSRPI	RADIKGS	RSLSL	SGGA	AEVVD	TADLMLDGTGVQHRIRTHAAMTLDGK
m285-1	LDFTLKGPS	PDTSRPI	RADIKGS	RSLSL	SGGA	AEVVD	TADLMLDGTGVQHRIRTHAAMTLDGK
	610	620	630	640	650	660	
a285-1.pep	670	680	690	700	710	720	
a285-1.pep	PFKFDLDAS	GGINREL	TRWKGS	IGILD	IGGAF	NLKLQNR	MTLEAGAERVAASAANWQAMG
m285-1	PFKFDLDAS	GGINREL	TRWKGS	IGILD	IGGAF	NLKLQNR	MTLEAGAERVAASAANWQAMG
	670	680	690	700	710	720	
a285-1.pep	730	740	750	760	770	780	
a285-1.pep	GSLNLQHFS	WDKKTG	ISAKG	AHGLH	IAELHN	FFKPPF	FEHNLVLNGDWDVAYGRNARGYL
m285-1	GSLNLQHFS	WDKKTG	ISAKG	AHGLH	IAELHN	FFKPPF	FEHNLVLNGDWDVAYGRNARGYL
	730	740	750	760	770	780	
a285-1.pep	790	800	810	820	830	840	
a285-1.pep	NISRQSGDA	VLPGGQ	ALGLNA	FSLKTR	FQNDRI	GILLD	GGARFGRINADLDIGNAFGGNM
m285-1	NISRQSGDA	VLPGGQ	ALGLNA	FSLKTR	FQNDRI	GILLD	GGARFGRINADLDIGNAFGGNM
	790	800	810	820	830	840	
a285-1.pep	850	860	870	880	890	900	
a285-1.pep	ANAPLGGR	ITASLP	DLGTLK	PFPLP	AAAQNI	TGSLN	AAQIGGRVGS
m285-1	ANAPLGGR	ITASLP	DLGTLK	PFPLP	AAAQNI	TGSLN	AAQIGGRVGS
	850	860	870	880	890	900	
a285-1.pep	910	920	930	940	950	960	
a285-1.pep	KINGNITV	GQSR	SFDTAP	LGGRLN	LTVA	DAEVR	NFLPVGQTVKGS
m285-1	KINGNITV	GQSR	SFDTAP	LGGRLN	LTVA	DAEVR	NFLPVGQTVKGS
	910	920	930	940	950	960	
a285-1.pep	970	980	990	1000	1010	1020	
a285-1.pep	HLGGSING	DKLYRN	QTQGI	ILDN	GLRSH	IAGR	KWVIDSLKFRHEGTAELSGTVGMENS
m285-1	HLGGSING	DKLYRN	QTQGI	ILDN	GLRSH	IAGR	KWVIDSLKFRHEGTAELSGTVGMENS
	970	980	990	1000	1010	1020	
a285-1.pep	1030	1040	1050	1060	1070	1080	
a285-1.pep	GPDVDIG	AVFDKY	RILSR	PNRRL	TVSGN	TRLR	YSPQKGISVTGM
m285-1	GPDVDIG	AVFDKY	RILSR	PNRRL	TVSGN	TRLR	YSPQKGISVTGM
	1030	1040	1050	1060	1070	1080	
a285-1.pep	1090	1100	1110	1120	1130	1140	
a285-1.pep	SVGDDVV	VLGEV	KKAAAP	LPVNM	NLTLD	NDGIR	FAGYGADV
m285-1	SVGDDVV	VLGEV	KKAAAP	LPVNM	NLTLD	NDGIR	FAGYGADV
	1090	1100	1110	1120	1130	1140	
a285-1.pep	1150	1160	1170	1180	1190	1200	
a285-1.pep	GVGTVR	VIKGRY	KAYQD	LDITK	GTVS	FGPLN	DPNLNIRAERRLSPVGAGVEILGSLNS
m285-1	GVGTVR	VIKGRY	KAYQD	LDITK	GTVS	FGPLN	DPNLNIRAERRLSPVGAGVEILGSLNS

666

	1150	1160	1170	1180	1190	1200
	1210	1220	1230	1240	1250	1260
a285-1.pep	PRITLTANEPMSSEKDKLSWLILNRAGSGSSGDNAALSAAGALLAGQINDRIGLVDDLGF					
m285-1	PRITLTANEPMSSEKDKLSWLILNRAGSGSSGDNAALSAAGALLAGQINDRIGLVDDLGF					
	1210	1220	1230	1240	1250	1260
	1270	1280	1290	1300	1310	1320
a285-1.pep	TSKRSRNAQTGELNPAEQVLTGKQLTGKLYIGYEYSISSAEQSVKLIYRLTRAIQAVAR					
m285-1	TSKRSRNAQTGELNPAEQVLTGKQLTGKLYIGYEYSISSAEQSVKLIYRLTRAIQAVAR					
	1270	1280	1290	1300	1310	1320
	1330	1340	1350			
a285-1.pep	IGSRSSGGELTYTIRFDRFSGSDKKDSAGNSKGKX					
m285-1	IGSRSSGGELTYTIRFDRFSGSDKKDSAGNGKGKX					
	1330	1340	1350			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1193>:

g286.seq

1	atgcagaaca	ccggtaccat	gatgatcaaa	ccgaccgccc	tgctcctgcc
51	ggcttttatt	ttctttccgc	acgcatacgc	gcctgccgcc	gacctttccg
101	aaaacaaggc	ggcggttttc	gcattgttca	aaagcaaaag	ccccgacacc
151	gaatcagtca	aattaaaacc	caaattcccc	gtccgcatcg	acacgcagga
201	cagtgaatc	aaagatatgg	tcgaagaaca	cctgccgctc	atcacgcagc
251	agcaggaaga	ggttttggat	aaggaacaga	cggtattcct	tgccgaagaa
301	gcaccggaca	acgttaaaac	aatgctccgc	agcaaaggct	atctcagcag
351	caaggtcagc	ctgacggaaa	aagacggagc	ttatacggtg	cacatcacac
401	cgggcccgcg	cacaaaatc	gccaacgtcg	gcgtcgccat	cctcggcgac
451	atcctttcag	acggcaacct	cgccgaatac	taccgcaacg	cgctggaaaa
501	ctggcagcag	ccggtaggca	gcgatttcga	tcaggacagt	tgggaaaaa
551	gcaaaaactc	cgctctcggc	gcggtaacgc	gcaaaaggct	cccgtttgcc
601	aagctcggca	acacccgggc	ggcgtcaaac	cccgtataccg	ccaccgccga
651	tttgaacgtc	gtcgtggaca	gcggccgccc	cattgccttc	ggcgactttg
701	aaatcaccgg	cacacagcgt	taccccgaac	aaaccgtctc	cggcctggcg
751	cgcttccaac	cgggcacgcc	ctacgacctc	gacctgtctc	tcgacttcca
801	acaggcgctc	gaacaaaacg	ggcattatct	cggcgcgtcc	gtacaagccg
851	acttcgaccg	cctcccaagg	ggaccgcgtc	cccgtcaaaag	tcagcgtaaac
901	cgaggtcaaa	cgccacaaac	tcgaaaccgg	catccgcctc	gattcgggaat
951	acggtttggg	cggcacaaatc	gcctacgact	attacaacct	cttcaacaaa
1001	ggctatatcg	gctcgggtcgt	ctgggatatg	gacaaatacg	aaaccacgct
1051	tgccgcgggc	atcagccagc	cgcgcaacta	tcggggcaac	tactggacaa
1101	gcaacgtttc	ctacaaccgt	tcgaccaccc	aaaacctcga	aaaacgcgcc
1151	ttctccggcg	gcattctgga	tgtgcgcgac	cgcgcgggca	tcgatgccag
1201	gctggggcg	gaatttctcg	cagaaggccg	gaaaatcccc	ggctcggatg
1251	tcgatttggg	caacagccac	gccacgatgc	tgaccgcctc	ttggaacgc
1301	cagctgtcga	acaacgtgct	gcaccccgaa	aacggccatt	acctcgacgg
1351	caaaatcggg	acgactttgg	gcacattcct	gtcctccacc	gcgtaattcc
1401	gcacctctgc	ccgcgcaggt	tatttcttca	cgcccgaata	caaaaaactc
1451	ggcacgttca	tcatacgcg	acaagcgggt	tacaccgttg	cacgcgacaa
1501	tgccgatgtc	ccctcggggc	tgatgttccg	cagcggcggc	gcgtcttccg
1551	tgcgcggtta	cgaacttga			

This corresponds to the amino acid sequence <SEQ ID 1194; ORF 286.ng>:

g286.pep

1	MQNTGTMMIK	PTALLLPALF	FFPHAYAPAA	DLSENKAAGF	ALFKSKSPDT
51	ESVKLKPFP	VRIDTQDSEI	KDMVEEHLPL	ITQQQEEVLD	KEQTGFLAEE
101	APDNVKTMLR	SKGYFSSKVS	LTEKDGYTV	HITPGPRTKI	ANVGVAIGLD
151	ILSDGNLAIEY	YRNALENWQQ	PVGSDFDQDS	WENSKTSVLG	AVTRKGYPLA
201	KLGNTRAAVN	PDTATADLNV	VVDSGRPIAF	GDFEITGTQR	YPEQTVSGLA
251	RFQPGTPYDL	DLLLDFQQAL	EQNGHYS GAS	VQADFDR LPR	GPRPRQSQRN
301	RGQTPQTRNR	HPFRFGIRFG	RQNRRLRLQP	LQQRLYRLGR	LGYGQIRNHA
351	CRRHQPAQQL	SGQLLDKQRF	LQPFDPKPR	KTRLLRRHLV	CARPRGRHRCQ
401	AGGGISRRRP	ENPRLGCRFG	QQPRHDADRL	LETPAAQQRA	APRKRFLPRR

451 QNRDDFGHIP VLHRANPHLC PRRLEFLHARK QKTRHVHHTR TSGLHRCTRQ
 501 CRCPLGADVQ QRRRVFRARL RT*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1195>:

m286.seq
 1 ATGCACGACA CCCGTACCAT GATGATCAAA CCGACCGCCC TGCTCCTGCC
 51 GGCTTTATTT TTCTTTCCGC ACGCATACGC GCCTGCCGCC GACCTTTCCG
 101 AAAACAAGGC GGCGGGTTTC GCATTGTTCA AAAACAAAAG CCCCACACACC
 151 GAATCAGTCA AATTAACACC CAAATTCCTC GTCCTCATCG ACACGCAGGA
 201 CAGTGAATC AAAGATATGG TCGAAGAACA CCTGCCGCTC ATCAGCAGC
 251 AGCAGGAAGA AGTATTGGAC AAGGAACAGA CGGGCTTCCT CGCCGAAGAA
 301 GCGCCGGACA ACGTTAAAC GATGCTCCGC AGCAAAGGCT ATTTACAGCAG
 351 CAAAGTCAGC CTGACGAAA AAGACGGAGC TTATACGGTA CACATCACAC
 401 CGGGCCCCGC CACCAAATC GCCAACGTCG GCGTCGCCAT CCTCGGCGAC
 451 ATCCTTTTCA ACGGCAACCT CGCCGAATAC TACCGCAACG CGCTGGAAAA
 501 CTGGCAGCAG CCGGTAGGCA GCGATTTCGA TCAGGACAGT TGGGAAAAACA
 551 GCAAACTTTC CGTCCTCGGC GCGGTAACGC GCAAAGCCTA CCCGCTTGCC
 601 AAGCTCGGCA ATACGCAGGC GGCCGTCAAC CCGGATACCG CCACCGCCGA
 651 TTTGAACGTC GTCGTGGACA GCGGCCGCC CATCGCCTTC GGCAGCTTTG
 701 AAATCACCGG CACACAGCGT TACCCCGAAC AAATCGTCTC CGGCCTTGCG
 751 CGTTTTCCAG CCGGTATGCC GTACGACCTC GACCTGCTGC TCGACTTCCA
 801 ACAGGCGCTC GAACAAAACG GGCATTATTC CGGCGCGTCC GTACAAGCCG
 851 ACTTCGACCG CCTCCAAGGC GACCGCGTCC CCGTCAAAGT CAGCGTAACC
 901 GAGGTCAAAC GCCACAACT CGAAACCGGC ATCCGCCTCG ATTCCGGAATA
 951 CGGTTTGGGC GGCAAAATCG CCTACGACTA TTACAACCTC TTCAACAAAG
 1001 GCTATATCGG TTCGGTCGTC TGGGATATGG ACAATAACGA AACACGCTT
 1051 GCCGCCGGCA TCAGCCAGCC GCGCAACTAT CGGGGCAACT ACTGGACAAG
 1101 CAACGTTTCC TACAACCGTT CGACCACCCA AAACCTCGAA AAACGCGCCT
 1151 TCTCCGGCGG CGTCTGGTAT GTGCGCGACC GCGCGGGCAT CGATGCCAGG
 1201 CTGGGGGCGG AATTTCTCGC AGAAGGCCGG AAAATCCCCG GCTCGGCTGT
 1251 CGATTTGGGC AACAGCCACG CCACGATGCT GACCGCCTCT TGGAAACGCC
 1301 AGCTGCTCAA CAACGTGCTG CATCCCGAAA ACGGCCATTA CCTCGACGGC
 1351 AAAATCGGTA CGACTTTGGG CACATTCTCT TCCTCCACCG CGCTGATCCG
 1401 CACCTCTGCC CGTGCAGGTT ATTTCTTCAC GCCGAAAAC AAAAACTCG
 1451 GCACGTTTCA CATACGCGGA CAAGCGGGTT ACACCGTTGC CCGCGACAAT
 1501 CCGGACGTTT CTTACGGGCT GATGTTCCGC AGCGGCGGCG CGTCTTCGCT
 1551 GCGCGGTTAC GAACTCGACA GCATCGGACT TGCCGGCCCC AACGGATCGG
 1601 TCCTGCCCGA ACGCGCCCTC CTGGTGGGCA GCCTGGAATA CCAACTGCCG
 1651 TTTACGCGCA CCCTTTCCGG CGCGGTGTTT CACGATATGG GCGATGCCCG
 1701 GCGCAATTTT AAACGTATGA AGCTGAAACA CGGTTCCGGA CTGGGCGTGC
 1751 CTGTGTTTCA CCGGCTTGGC CCGTTTTCCT TCGACATCGC CTACGGGCAC
 1801 AGCGATAAGA AAATCCGCTG GCACATCAGC TTGGGAACGC GCTTCTAA

This corresponds to the amino acid sequence <SEQ ID 1196; ORF 286>:

m286.pep
 1 MHDTRTMMIK PTALLLPALF FFPHAYAPAA DLSENKAAGF ALFKNKSPDT
 51 ESVKLPKFP VLIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGFALAE
 101 APDNVKTMLR SKGYFSSKVS LTEKDGAAYTV HITPGPRTKI ANVGVAIIGD
 151 ILSDGNLAAY YRNALENWQQ PVGSDFDQDS WENSKTSVLG AVTRKAYPLA
 201 KLGNTQAAVN PDTATADLNV VVDSGRPIAF GDFEITGTQR YPEQIVSGLA
 251 RFQPGMPYDL DLLLDFQQAL EQNGHYSYGAS VQADFDRLQG DRVPVKVSVT
 301 EVKRHKLETG IRLDSEYGLG GKIAIDYDYNL FNKGYSVSV WMDKYETTL
 351 AAGISQPRNY RGNWYTSNVS YNRSTQNLK KRAFSGGVWY VRDRAGIDAR
 401 LGAEFLAEGR KIPGSAVDLG NSHATMLTAS WKRLNNVL HPENGHYLDG
 451 KIGTTLGTFL SSTALIRTS RAGYFFTPEN KKLGTFIIRG QAGYTVARDN
 501 ADVPSGLMFR SGGASSVRGY ELDSIGLAGP NGSVLPERAL LVGSLEYQLP
 551 FTRTLGAVF HDMGDAAANF KRMKLKHGSG LGVRWFSPLA PFSFDIAYGH
 601 SDKKIRWHIS LGTRF*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m286/g286 95.9% identity in 293 aa overlap

668

	10	20	30	40	50	60
m286.pep	MHDTRTMMIKPTALLLPALFFFP	HAYAPAADLSENKAAGFALFKN	KSPDTE	SVKLKPKFP		
g286	MQNTGTMMIKPTALLLPALFFFP	HAYAPAADLSENKAAGFALFKS	KSPDTE	SVKLKPKFP		
	10	20	30	40	50	60
m286.pep	VLIDTQDSEIKDMVEEHLPLITQ	QEEVL	DKEQTGFLAEE	APDNVKTMLRSKGYFSSKVS		
g286	VRIDTQDSEIKDMVEEHLPLITQ	QEEVL	DKEQTGFLAEE	APDNVKTMLRSKGYFSSKVS		
	70	80	90	100	110	120
m286.pep	LTEKDGAYTVHITPGPRTKIANV	GVAILGDI	LSDGNLAEYYRNALENWQQPV	GSDFDQDS		
g286	LTEKDGAYTVHITPGPRTKIANV	GVAILGDI	LSDGNLAEYYRNALENWQQPV	GSDFDQDS		
	130	140	150	160	170	180
m286.pep	WENSKTSVLGAVTRKAYPLAKLG	NTQAAVN	PDATADLN	VVVD	SGRPIAFGDFEITGTQR	
g286	WENSKTSVLGAVTRKGYPLAKLG	NTRAAVN	PDATADLN	VVVD	SGRPIAFGDFEITGTQR	
	190	200	210	220	230	240
m286.pep	YPEQIVSGLARFQPGMPYDLDL	LLDFQQA	LEQNGHYS	GSASVQAD	FDRL-QGDRVPVKVSV	
g286	YPEQTVSGLARFQPGTPYDLDL	LLDFQQA	LEQNGHYS	GSASVQAD	FDRLPRGPRPRQSQRN	
	250	260	270	280	290	299
m286.pep	300	310	320	330	340	359
g286	TEV	KRHKLETGIRLDSEYGLGGK	IAVDYNNLFN	KGYIGSVVWMD	KYETTLAAGISQPRN	
	310	320	330	340	350	360
m286.pep	RGQTPQTRNRHPPRFGIRFGR	QNRRLRL	LQPLQORLYRLGR	LGYGQIRNHACRRHQ	PAAQL	

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 1197>:

a286.seq	1	51	101	151	201	251	301	351	401	451	501	551	601	651	701	751	801	851	901	951	1001	1051	1101	1151	1201	1251	1301
	ATGCACGACA	GGCTTTTATTT	AAAAC AAGGC	GAATCAGTTA	TAGTGAATC	AGCAGGAAGA	GCACCGGACA	CAAAGTCAGC	CGGGCCCCGGC	ATCCTTTTCAG	CTGGCAGCAG	GCAAAACTTC	AAGCTCGGCA	TTTGAACGTC	AAATTACCGG	CGCTTCCAAC	ACAGGCGCTC	ACTTCGACCG	GAGGTC AAAC	CGGTTTGGGG	GCTATATCGG	GCCGCGCGCA	CAACGTTTCC	TCTCCGGCGG	CTGGGGGCGG	CGATTTGGGC	AGCTGCTCAA
	CCCGTACCAT	TTCTTTCCGC	GGCGGGTTTC	AATTA AAAC	AAGATATGG	AGTATTGGAC	ACGTTAA AAC	CTGACGGAAA	CACCAAAATC	ACGGCAACCT	CCGGTAGGCA	CGTCCTCGGC	ACACCCGGGC	GTCGTGGACA	CACGCAGCGT	CGGGACGCGC	GAACAAACG	CCTCCAAGGC	GCCACAAGCT	GGCAAAATCG	TTCGGTCTG	TTCAGCCAGCC	TACAACCGTT	CATCTGGTAT	AGTTTCTCGC	AACAGCCACG	AACAGTGCTG
	GATGATTAAA	ACGCATACGC	GCATTGTTCA	CAAATTC C	TCAAGAACA	AAGGAACAGA	AATGCTCCGC	AAGACGGAGC	GCCAACGTGC	CGCCGAATAC	GTGATTT CGA	GCGGTAACGC	GGCCGTCAAC	GCGGCCGCCC	TACCCCGAAC	CTACGACCTC	GGCATTATTC	GACCGCGTCC	CGAAACCGGC	CCTACGACTA	TGGGATATGG	CGCGAACTAT	CGACCACCCA	GTGCGCGACC	AGAAGGCCGG	CCACGATGCT	CATCCCGAAA
	CCGACCGCCC	GCCTGCCGCC	AAAACA AAG	CTCCGCTACG	GTCGCCCTC	CGGGCTTCCT	AGCAAAGGCT	TTATACGGTA	CGCTCGCCAT	TACCGCAACG	TCAGGACAGT	GCAAAGCCTA	CCCGATACCG	CATCGCCTTC	AAATCGTCTC	GACCTGTCTG	CGGCGCGTCC	CCGTCAAAGT	ATCCGCCTCG	TTACAACCTC	ACAAATACGA	CGGGGCAACT	AAACCTCGAA	GCGCGGGCAT	AAAATCCCCG	GACCGCCTCT	ACGGCCATTA
	TGCTCCTGCC	GACCTTTCCG	CCCCGACACC	ACACGCAGGA	ATCACGCAGC	CGCCGAAGAA	ATTTCAGCAG	CACATCACAC	CCTCGGCGAC	CGTGGAAAAA	TGGGAAAAACA	CCCGCTTGCC	CCACGCGCGA	GGCGACTTTG	CGGCTTGGCG	TCGACTTCCA	GTACAAGCCG	CAGCGTAACC	ATTCCGAATA	TTCAACAAG	AACCACGCTT	ACTGGACAAG	AAACGCGCCT	CGATGCCAGG	GCTCGGATAT	TGGAAACGCC	TCTGCACGGG

669

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1351 AAAATCGGTA CGACTTTGGG CGCATTCCTG TCCTCCACCG CGCTGATCCG
1401 CACCTCTGCC CGCGCAGGTT ATTTCTTCAC GCCCGAAAAC AAAAAACTCG
1451 GCACGTTTAT CATACGCGGA CAAGCGGGTT ACACCGTTGC CCGCGACAAT
1501 GCCAACGTTT CTTCAGGGCT GATGTTCCGC AGCGGCGGCG CGTCTTCCGT
1551 GCGCGGTTAC GAACTCGACA GCATCGGGCT TGCCGGCCCG AACGGATCGG
1601 TCCTGCCCGA ACGCGCCCTC TTGGTGGGCA GCCTGGAATA CCAACTGCCG
1651 TTTACGCGCA CCCTTCCCGG CGCGGTGTTT CACGATATGG GCGACGCCGC
1701 CGCCAATTTT AAACGTATGA AGCTGAAACA CGGTTGCGGA CTGGGCGTGC
1751 GCTGGTTCAG CCCGCTCGCG CCGTTTCCCT TCGACATCGC CTACGGGCAC
1801 AGCGACAAGA AAATCCGCTG GCACATCAGC TTGGGAACGC GCTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 1198; ORF 286.a>:

a286.pep

```

1  MHDTRTMMIK PTALLLPALF FFPHAYAPAA DLSENKAAGF ALFKNKSPDT
51  ESVKLKPKFP VRIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGFLAEE
101 APDNVKTMLR SKGYFSSKVS LTEKDGAITV HITPGPRTKI ANVGVAAILGD
151 ILSDGNLAIE YRNALENWQQ PVGSDFDQDS WENKTSVLG AVTRKAYPLA
201 KLGNTAAVN PDATADLNV VVDSGRPIAF GDFEITGTQR YPEQIVSGLA
251 RFQPGTPYDL DLLLDFQQA EQNGHYS GASVQADFDR LQDRVPVKVSVT
301 EVKRHKLETG IRLDSEYGLG GKIAIDYYNL FNKGYIGSVV WMDKYETTL
351 AAGISQPRNY RGNWTSNVS YNRSTQNL KRAFSGGIWY VRDRAGIDAR
401 LGAEFLAAGR KIPGSDIDL NSHATMLTAS WKRLNNVL HPENGYLDG
451 KIGTTLGAFL SSTALIRTS RAGYFTFEN KKLGTFLIRG QAGYTVARDN
501 ANVPSGLMFR SGGASSVRGY ELSIGLAGP NGSVLPERAL LVGSLEYQLP
551 FTRLTGAVF HDMGDAAANF KRMKLKHGSG LGVRWFSPLA PFSFDIAYGH
601 SDKKIRWHIS LGTRF*

```

m286/a286 98.7% identity in 615 aa overlap

m286.pep	10	20	30	40	50	60
a286	10	20	30	40	50	60
m286.pep	70	80	90	100	110	120
a286	70	80	90	100	110	120
m286.pep	130	140	150	160	170	180
a286	130	140	150	160	170	180
m286.pep	190	200	210	220	230	240
a286	190	200	210	220	230	240
m286.pep	250	260	270	280	290	300
a286	250	260	270	280	290	300
m286.pep	310	320	330	340	350	360
a286	310	320	330	340	350	360
	370	380	390	400	410	420

670

```

m286.pep  RGNYWTSNVSYNRSTTQNLEKRAFSGGVWYVRDRAGIDARLGAEF LAEGRKIPGSAVDLG
          |||||||||||||||||||||||||||||:|||||||||||||||||||:||||
a286      RGNYWTSNVSYNRSTTQNLEKRAFSGGIWIYVRDRAGIDARLGAEF LAEGRKIPGSDIDLG
          370      380      390      400      410      420

          430      440      450      460      470      480
m286.pep  NSHATMLTASWKROLNNVLHPENGHYLDGKIGTTLGTFLSSTALIRTSARAGYFFTPEN
          |||||||||||||||||||||||||||||:|||||||||||||||||||
a286      NSHATMLTASWKROLNNVLHPENGHYLDGKIGTTLGAFLSSTALIRTSARAGYFFTPEN
          430      440      450      460      470      480

          490      500      510      520      530      540
m286.pep  KKLGTFIIRGQAGYTVARDNADVP SGLMFRSGGASSVRGYELDSIGLAGPN GSVLPERAL
          |||||||||||||||||||||||||||||:|||||||||||||||||||
a286      KKLGTFIIRGQAGYTVARDNANVP SGLMFRSGGASSVRGYELDSIGLAGPN GSVLPERAL
          490      500      510      520      530      540

          550      560      570      580      590      600
m286.pep  LVGSLEYQLPFTRTL SGAVFHDMDGAAANFKRMK LKHGSLGVRWFSPLAPFSFDIAYGH
          |||||||||||||||||||||||||||||:|||||||||||||||||||
a286      LVGSLEYQLPFTRTL SGAVFHDMDGAAANFKRMK LKHGSLGVRWFSPLAPFSFDIAYGH
          550      560      570      580      590      600

          610
m286.pep  SDKKIRWHISLGTRFX
          ||||||||||||||||
a286      SDKKIRWHISLGTRFX
          610

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1199>:

```

g287.seq
1  atgtttaaac gcagtgtgat tgcaatggct tgtatttttc ccctttcagc
51  ctgtgggggc ggcggtggcg gatcgcccga tgtcaagtcg gcggaacacg
101 cgtcaaaaacc ggcgcggccc gttgtgtctg aaaatgccg ggaaggggtg
151 ctgccgaaag aaaagaaaga tgaggaggca gcgggcggtg cgccgcaagc
201 cgatacgag gacgcaaccg ccggagaagg cagccaagat atggcggcag
251 ttctggcaga aaatacaggc aatggcggtg cggaacaac ggacaacccc
301 aaaaatgaag acgcgggggc gcaaaatgat atgccgcaa atgccgcga
351 atccgcaaat caaacaggga acaaccaacc cgccggttct tcagattccg
401 ccccgcgctc aaaccctgcc cctgcgaatg gcggtagcga ttttggaagg
451 acgaacgtgg gcaattctgt tgtgattgac ggaccgtcgc aaaatataac
501 gttgacccac tgtaaaaggcg attcttgtaa tggtgataat ttattggatg
551 aagaagcacc gtcaaaatca gaatttgaaa aattaagtga tgaagaaaaa
601 attaacgat ataaaaaaga cgagcaacgg gagaattttg tcggtttggt
651 tctgacagg gtaaaaaagg atggaactaa caaatatata atcttctata
701 cggacaaacc acctactcgt tctgcacggt cgaggaggtc gcttcgggcc
751 gagattccgc tgattcccg tcaatcaggcc gatacgctga ttgtggatgg
801 ggaagcggtc agcctgacgg ggcattccgg caatatcttc gcgcccgaag
851 ggaattaccg gtatctgact tacggggcgg aaaaattgcc cggcggatcg
901 tatgccctcc gtgtgcaagg cgaaccggca aaaggcgaaa tgcttggttg
951 cacggcggcg tacaacggcg aagtgtgca tttccatatg gaaaacggcc
1001 gtccgtaccc gtccggaggc aggtttgccc caaaagtcga ttccggcagc
1051 aaatctgtgg acggcattat cgacagcggc gatgatttgc atatgggtac
1101 gcaaaaattc aaagccgcca tcgatggaag cggctttaag gggacttgga
1151 cggaaaatgg cggcggggat gtttccggaa ggttttacgg cccggccggc
1201 gaggaagtgg cgggaaaata cagctatcgc ccgacagatg ctgaaaaggg
1251 cggattcggc gtgtttgccg gcaaaaaaga tcgggattga

```

This corresponds to the amino acid sequence <SEQ ID 1200; ORF 287.ng>:

```

g287.pep
1  MFKRSVIAMA CIFPLSACGG GGGGSPDVKS ADTPSKPAAP VVAENAGEGV
51  LPKEKKDEEA AGGAPQADTQ DATAGEGSQD MAAVSAENTG NGGAATTDNP
101 KNEDAGAQN DMPQNAAESAN QTGNNQPAGS SDSAPASNPA PANGGSDFGR

```

```

151  TNVGNVSVID  GPSQNLTLTH  CKGDSCNGDN  LLDEEAPSKS  EFEKLSDEEK
201  IKRYKKDEQR  ENFVGLVADR  VKKDGTKNYI  IFYTDKPPTR  SARSRRSLPA
251  EIPLIPVNQA  DTLIVDGEAV  SLTGHSGNIF  APEGNYRYLT  YGAEKLPGGS
301  YALRVQGEPA  KGEMLVGTAV  YNGEVLHFHM  ENGRPYPSGG  RFAAKVDFGS
351  KSVDDGIIDSG  DDLHMGTOKF  KAAIDGNGFK  GTWTENGSGD  VSGRFYGPAG
401  EEVAGKYSYR  PTDAEKGGFG  VFAGKKDRD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1201>:

```

m287.seq
  1  ATGTTTAAAC  GCAGCGTAAT  CGCAATGGCT  TGTATTTTTC  CCCTTTCAGC
 51  CTGCGGGGGC  GGCGGTGGCG  GATCGCCCGA  TGTCAAGTCG  GCGGACACGC
101  TGTCAAACCC  TGCCGCCCTT  GTTGTTCCTG  AAAAAGAGAC  AGAGGCAAAG
151  GAAGATGCGC  CACAGGCAGG  TTCTCAAGGA  CAGGGCGCGC  CATCCGCACA
201  AGGCAGTCAA  GATATGGCGG  CGGTTTCGGA  AGAAAATACA  GGCAATGGCG
251  GTGCGGTAAC  AGCGGATAAT  CCCAAAATG  AAGACGAGGT  GGCACAAAAT
301  GATATGCCGC  AAAATGCCGC  CGGTACAGAT  AGTTCGACAC  CGAATCACAC
351  CCCGGATCCG  AATATGCTTG  CCGGAAATAT  GGAAAATCAA  GCAACGGATG
401  CCGGGGAATC  GTCTCAGCCG  GCAAACCAAC  CGGATATGGC  AAATGCGGCG
451  GACGGAATGC  AGGGGGACGA  TCCGTCGGCA  GGCGGGGCAA  ATGCCGGCAA
501  TACGGCTGCC  CAAGGTGCAA  ATCAAGCCGG  AAACAATCAA  GCCGCCGGTT
551  CTTCAGATCC  CATCCCCGCG  TCAAACCCGT  CACCTGCGAA  TGGCGGTAGC
601  AATTTTGGA  GGGTTGATTT  GGCTAATGGC  GTTTTGATTG  ACGGGCCGTC
651  GCAAAATATA  ACGTTGACCC  ACTGTAAAGG  CGATTCTTGT  AGTGGCAATA
701  ATTTCTTGA  TGAAGAAGTA  CAGCTAAAAT  CAGAATTGTA  AAAATTAAGT
751  GATGCAGACA  AAATAAGTAA  TTACAAGAAA  GATGGGAAGA  ATGATAAATT
801  TGTGCGTTTG  GTTGCCGATA  GTGTGCAGAT  GAAGGGAATC  AATCAATATA
851  TTATCTTTTA  TAAACCTAAA  CCCACTTCAT  TTGCGCGATT  TAGGCGTTCT
901  GCACGGTCGA  GGCGGTGCGT  TCCGCGCGAG  ATGCCGCTGA  TTCCCGTCAA
951  TCAGGCGGAT  ACGCTGATTG  TCGATGGGGA  AGCGGTGAGC  CTGACGGGGC
1001  ATTCCGGCAA  TATCTTCGCG  CCCGAAGGGA  ATTACCGGTA  TCTGACTTAC
1051  GGGGCGGAAA  AATTGCCCGG  CGGATCGTAT  GCCCTTCGTG  TTCAAGGCGA
1101  ACCGGCAAAA  GGCGAAATGC  TTGCGGGCGC  GGCCGTGTAC  AACGGCGAAG
1151  TACTGCATTT  CCATACGGAA  AACGGCCGTC  CGTACCCGAC  CAGGGGCAGG
1201  TTTGCCGCAA  AAGTCGATTT  CGGCAGCAAA  TCTGTGGACG  GCATTATCGA
1251  CAGCGGCGAT  GATTTCGATA  TGGGTACGCA  AAAATCATA  GCCGCCATCG
1301  ATGGAAACGG  CTTTAAGGGG  ACTTGGACGG  AAAATGGCAG  CGGGGATGTT
1351  TCCGGAAAGT  TTTACGGCCC  GGCCGGCGAG  GAAGTGGCGG  GAAAATACAG
1401  CTATCGCCCG  ACAGATGCGG  AAAAGGGCGG  ATTCGGCGTG  TTTGCCGGCA
1451  AAAAAGAGCA  GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1202; ORF 287>:

```

m287.pep
  1  MFKRSVIAMA  CIFALSACGG  GGGGSPDVKS  ADTLSPKPAAP  VVSEKETEAK
 51  EDAPQAGSQ  QGAPSAQGSQ  DMAAVSEENT  GNGGAVTADN  PKNEDEVAQN
101  DMPQNAAGTD  SSTPNHTPDP  NMLAGNMENQ  ATDAGESSQP  ANQPDMANAA
151  DGMQDDPSA  GGQNAAGTAA  QGANQAGNNQ  AAGSSDPIPA  SNPAPANGGS
201  NFRVLDLANG  VLIDGPSQNI  TLTHCKGDSC  SGNNFLDEEV  QLKSEFEKLS
251  DADKISNYKK  DGKNDKFVGL  VADSVQMKGI  NQYIIFYKPK  PTSFARFRRS
301  ARSRRLPAE  MPLIPVNQAD  TLIVDGEAVS  LTGHSGNIFA  PEGNYRYLTY
351  GAEKLPGGSY  ALRVQGEPAK  GEMLAGAAVY  NGEVLHFHTE  NGRPYPTGRG
401  FAAKVDFGSK  SVDGIIDSGD  DLHMGTOKF  AAIDGNGFKG  TWTENGSGDV
451  SGKFYGPAGE  EVAGKYSYRP  TDAEKGGFGV  FAGKKEQD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m287/g287 70.1% identity in 499 aa overlap

```

          10      20      30      40      49
m287.pep  MFKRSVIAMACIFALSACGGGGGSPDVKSADTLSPKPAAPVVSE-----KETEAK
          |||||
g287       MFKRSVIAMACIFPLSACGGGGGSPDVKSADTPSKPAAPVVAENAGEGVLPKEKKDEEA
          10      20      30      40      50      60

```

	50	60	70	80	90	100	109
m287.pep	KEDAPQAGSQGGAPSAQGSQDMAAVSEENTGNGGAVTADNPKNEDEVAQN	DMPQNAAGT					
g287	AGGAPQADTQD--ATAGEGSQDMAAVSAENTGNGGAATTDNPKNEDAGAQN	DMPQNA--					
	70	80	90	100	110		
m287.pep	110	120	130	140	150	160	169
g287	DSSTPNHTPDPNMLAGNMENQATDAGESSQPANQPDMANAA	DGMQGD	DPSAGGQ	NAGNTA			
	170	180	190	200	210	220	229
m287.pep	AQGANQAGNNQAAGSSDPIPASNPAPANGGSNFRV	DLANGVLIDGPSQ	NITLTHCKGDS				
g287	-ESANQTGNNQPAGSSDSAPASNPAPANGGSDFGR	TNVGNSVVIDGPSQ	NITLTHCKGDS				
	120	130	140	150	160	170	
m287.pep	230	240	250	260	270	280	289
g287	CSGNNFLDEEVQLKSEFEKLS	DADKISNYKKD	GKNDKFVGLVADSVQ	MKGINQYII	IFYKP		
	180	190	200	210	220	230	
m287.pep	290	300	310	320	330	340	349
g287	KPTS	FAFRRSARSRRSLPAEMPLIPV	NQADTLIVDGEAVSLTGHSGNIF	AFEGNYRYLT			
	240	250	260	270	280	290	
m287.pep	350	360	370	380	390	400	409
g287	YGAEKLP	GGSYALRVQGEPAKGEMLAGA	AVYNGEVLHFHTENGRPYPTRGR	FAAKVD	FGS		
	300	310	320	330	340	350	
m287.pep	410	420	430	440	450	460	469
g287	KSV	DGIIDSGDDLHMG	TQKFKA	AIDGNGFKGTWTENGSGD	VSGKFYGPAGEE	VAGKYSYR	
	360	370	380	390	400	410	
m287.pep	470	480	489				
g287	PTDAEKGGFGVFAGKKEQDX						
	420	430					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1203>:

```
a287.seq
1  ATGTTTAAAC  GCAGTGTGAT  TGCAATGGCT  TGTATTGTTG  CCCTTTCAGC
51  CTGTGGGGGC  GGCGGTGGCG  GATCGCCCGA  TGTTAAGTCG  GCGGACACGC
101 TGTCAAAACC  TGCCGCCCTT  GTTGTACTG  AAGATGTCGG  GGAAGAGGTG
151 CTGCCGAAAG  AAAAGAAAGA  TCGAGAGCG  GTGAGTGGTG  GCCCCGCAAGC
201 CGATACGCAG  GACGCAACCG  CCGGAAAGG  CGGTCAAGAT  ATGGCGCGAG
251 TTTCCGCGAGA  AAATACAGGC  AATGGCGGTG  CGGCAACAAC  GGATAATCCC
301 GAAAATAAAG  ACGAGGGACC  GCAAAATGAT  ATGCCGCAAA  ATGCCGCCGA
351 TACAGATAGT  TCGACACCGA  ATCACACCCC  TGCACCCGAA  ATGCCAACCA
401 GAGATATGGG  AAACCAAGCA  CCGGATCCCG  GGAATCGGC  ACAACCGGCA
451 AACCAACCGG  ATATGGCAAA  TCGCGCGGAC  GGAATGCAGG  GCGAGCATCC
501 GTCGGCAGGG  GAAAATGCCG  GCAATACGGC  AGATCAAGCT  GCAAATCAAG
551 CTGAAAACAA  TCAAGTCGGC  GGCTCTCAA  ATCCTGCCTC  TTCAACCAAT
601 CCTAACGCCA  CGAATGGCGG  CAGCGATTTT  GGAAGGATAA  ATGTAGCTAA
651 TGGCATCAAG  CTTGACAGCG  GTTCGGAAAA  TGTAACGTTG  ACACATTGTA
701 AAGACAAAGT  ATGCGATAGA  GATTCTTAG  ATGAAGAAGC  ACCACCTAAA
751 TCAGAATTGT  AAAAATTAAG  TGATGAAGAA  AAAATTAATA  AATATAAAAA
```

a287.pep

1	MFKRSVIAMA	CIVALSACGG	GGGGSPDVKS	ADTLSPAAP	VVTEDVGEEV
51	LPKEKKDEEA	VSGAPQADTQ	DATAGKGGQD	MAAVSAENTG	NGGAATTDNP
101	ENKDEGPQND	MPQNAADTDS	STPNHTPAPN	MPTRDMGNQA	PDAGESAQPA
151	NQPDMANAAD	GMQGDPSAG	ENAGNTADQA	ANQAENNQVG	GSQNPASSTN
201	PNATNGSGDSF	GRINVANGIK	LDGSGSENVTL	THCKDKVCDR	DFLDEEAPPK
251	SEFEKLSDEE	KINKYKKDEQ	RENFVGLVAD	RVEKNGTNKY	VIIYKDKSAS
301	SSSARFRRSA	RSRRSLPAEM	PLIPVNQADT	LIVDGEAVSL	TGHSGNIFAP
351	EGNYRYLTYG	AEKLSGGSYA	LSVQGEPAKG	EMLAGTAVYN	GEVLHFHMEN
401	GRPSPSGGRF	AAKVDFGSKS	VDGIIDSGDD	LHMGTKQFKA	VIDNGFVKGT
451	WTENGGGDVS	GRFYGPAGEE	VAGKYSYRPT	DAEKGGEVGF	AGKKEOD*

m287/a287 77.2% identity in 501 aa overlap

```
m287.pep      MFKRSVIAMACIFALSACGGGGGSPDVKSADTL SKPAAPV VSE-----KETEA
               ||||| | ||||||| ||||||| ||||||| : |          |: ||
a287           MFKRSVIAMACIVALSACGGGGGSPDVKSADTL SKPAAPVV TEDVGEEVL PKEKKDEEA
               10       20       30       40                50       60
```

```

50      60      70      80      90      100      109
m287.pep KEDAPQAGSQGGAPSAQGSQDMAAVSEENTGNGGAVTADNPKNEDEVAQNMPQNAAGT
          |||| :| |:::||||| |||||:::|||:::||| |||||
a287      VSGAPQADTQ--DATAGKGGQDMAAVSAENTGNGGAATTNPNKDEGPQNDMPQNAADT
          70      80      90      100      110

```

```
m287.pep      110       120       130       140       150       160       169
               DSSTPNHTPDPNMLAGNMENQATDAGESSQPANQPDMANAADGMQGDDPSAGGQNAGNTA
               |||||:||| : :| || | ||| : ||||| : ||||| : |||||
a287          120       130       140       150       160       170
               DSSTPNHTPAPNMPTRDMGNQAFDAGESAQPANQPDMANAADGMQGDDPSAG-ENAGNTA
```

```

      170          180          190          200          210          220          229
m287.pep    AQGANQAGNNQAAGSSDPIPASNPAPANGGSNFRGVDLANGVLIDGPSQNITLTHCKGDS
             |:||||| ||::||::|| ::|| :||||:||||:::||: |: |::| |||||
a287        DQAAANQAEENNQGGSQNFASSTNPATNGGSDFGIRINVANGIKLDSGSENVTLTHCKDKV
             180          190          200          210          220          230

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```

      230      240      250      260      270      280      289
m287.pep  CSGNNFLDEEVQLKSEFEKLSADAKISNYKKDGKNDKFVGLVADSVQMKGINQYIIIFYKP
          |:  :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
a287      CD-RDFLDEEAPPKSEFEKLSDEEKINKYKKDEQRFVGLVADRVEKNGTNKYVIIYKD
          240      250      260      270      280      290

```

```

290      300      310      320      330      340
m287.pép  KP--TSFARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRY
          | : | | | | | | | | | | | | | | | | | | | | | | | | | |
a287      KSASSSSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRY
          300      310      320      330      340      350

```

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	350	360	370	380	390	400
m287.pep	LTYGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDF					
a287	LTYGAEKLSGGSYALSVQGEPAKGEMLAGTAVYNGEVLHFHMENGRPSPSGGRFAAKVDF					
	360	370	380	390	400	410
	410	420	430	440	450	460
m287.pep	GSKSVLDGIIDSGDDLHMGTQKFKAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYS					
a287	GSKSVLDGIIDSGDDLHMGTQKFKAIDGNGFKGTWTENGSGDVSGRFYGPAGEEVAGKYS					
	420	430	440	450	460	470
	470	480	489			
m287.pep	YRPTDAEKGFGVVFAGKKEQDX					
a287	YRPTDAEKGFGVVFAGKKEQDX					
	480	490				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1205>:

```

g288.seq
1   atgcacaccg gacaggcggt aagccggggt ctgtctcgga cagtcattcc
51  tctaggcata ccgttgccgg tatgctcaag caacctaccc gaacgctcgg
101 cgggcagcgt cattgcgttc tgtttggtct tgctccgaat ggggtttggc
151 ctgccgcata ttggttacaa atgcgcggtg cgcccttacc gcaccttttc
201 acccttgccg gtgctgccaa agcagccatc ggcggttttg ctttctgttc
251 cactttccgt cgcgttaccg cgcccgcccg ttaaccggca ttctaccctg
301 cggagcccgg actttcctcc ccgtatgcct tacgcgatac gcggcgactg
351 tctgcccgtc ccgtgtgcgg cgcggttat aacacgaaac gcaaaaatgc
401 cgtctgaaac ggtacaggtt tcagacggca tacagcctaa actacacacc
451 ctgtttcagg ctggcttcga tgaagccgct caagtcgccg tccaatacgg
501 ctttgtggtt gccgacttcg tagcctgtac gcaagtcttt gatgcgtga

```

This corresponds to the amino acid sequence <SEQ ID 1206; ORF 288.ng>:

```

g288.pep
1   MHTGQAVSRV LSRTVIPLGI PLPVCSSNLP ERSAGSVIAF CLVLLRMGFG
51  LPHIVTKCAV RPYRTFSPPL VLPKQPSAVL LSVPLSVALP RPAVNRHSTL
101 RSPDFPPRMP YAIRGDCLPV PCAARIITRN AKMPSETVQV SDGIQPKLHT
151 LFQAGFDEAV QVAVQYGFVV ADFVACTQVF DA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1207>:

```

m288.seq
1   ATGCACACCG GACAGGCGGT AAGCCGGGTT CTGTCTCGGA CAGTCATTCC
51  TCTAGGCATA CCGTTACCGG TATGCTCAAG CAACCTACCC GAACGCTCGG
101 CGGGCAGCGT CATTGCGTTC TGTTTGGTCT TGCTCCGAAT GGGGTTTGGC
151 CTGCCGCATA TTGTTACCAA ATGCGCGGTG CGCCCTTACC GCACCTTTTC
201 ACCCTTACCT GTGCTGCCAA AGCAGCCATC GGCGGTTTTG CTTTCTGTTC
251 CACTTTCCGT CGCGTTACCG CGCCCGGCCG TTAACCGGCA TTCTACCCTG
301 CGGAGCCCGG ACTTTCCTCC CCGTATGCCT TACGCGATAC GCGGCGACTG
351 TCTGCCCGTC CCGTGTGCGG CGCGGATTAT AACACGAAAC ACAAAAATGC
401 CGTCTGAAAC GGTACAGGTT TCAGACGGCA TACAGCCTAA ACTACACGCC
451 CTGTTTCAGG CTGGCTTCGA TGAAGCCGTC CAAGTCGCCA TCCAATACGG
501 CTTTGGTGTT GCCGACTTCG TAGCCTGTAC GCAAGTCTTT GATACGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1208; ORF 288>:

```

m288.pep
1   MHTGQAVSRV LSRTVIPLGI PLPVCSSNLP ERSAGSVIAF CLVLLRMGFG
51  LPHIVTKCAV RPYRTFSPPL VLPKQPSAVL LSVPLSVALP RPAVNRHSTL
101 RSPDFPPRMP YAIRGDCLPV PCAARIITRN TKMPSETVQV SDGIQPKLHA
151 LFQAGFDEAV QVAIQYGFVV ADFVACTQVF DT*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m288/g288 97.8% identity in 181 aa overlap

	10	20	30	40	50	60
m288.pep	MHTGQAVSRVLSRTVIPLGIPLVCSSNLPERSAGSVIAFCLVLLRMGFGLPHIVTKCAV					
g288	MHTGQAVSRVLSRTVIPLGIPLVCSSNLPERSAGSVIAFCLVLLRMGFGLPHIVTKCAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m288.pep	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
g288	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m288.pep	PCAARIITRNTKMPSETVQVSDGIQPKLHALFQAGFDEAVQVAIQYGFVADVFVACTQVF					
	: : : :					
g288	PCAARIITRNAKMPSETVQVSDGIQPKLHTLFQAGFDEAVQVAVQYGFVADVFVACTQVF					
	130	140	150	160	170	180
m288.pep	DTX					
	:					
g288	DAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1209>:

```

a288.seq
1  ATGCACACCG GACAGGCGGT AAGCCGGGTT CTGTCTCGGA CAGTCATTCC
51  TCTAGGCATA CCGTTGCCGG TATGCTCAAG CAACCTACCC GAACGCTCGG
101 CGGGCAGCGT CATTGCGTTC TGTGTTGGTCT TGCTCCGAAT GGGGTTTGGC
151 CTGCCGCATA TTGTTACCAA ATGCGCGGTG CGCCCTTACC GCACCTTTTC
201 ACCCTTGCTT GTGCTGCCAA AGCAGCCATC GCGGTTTTG CTTTCTGTTC
251 CACTTTCCGT CGCGTTACCG CGCCCGGCCG TTAACCGGCA TTCTACCCTG
301 CGGAGCCCGG ACTTTCCTCC CCGTATGCCT TACGCGATAC GCGGCGACTG
351 TCTGCCCGTC CCGTGTGCGG CGCGGATTAT AACACGAAAC GCAAAAATGC
401 CGTCTGAAAC GGTACAGGTT TCAGACGGCA TACAGCCTAA ACTACACGCC
451 CTGTTTCAGG CTGGCTTCGA TAAAGCCGTC CAAGTCGCCG TCCAATACGG
501 CTTTGGTGTT GCCGACTTCG TAGCCTGTGC GCAAGTCTTT AATGCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1210; ORF 288.a>:

```

a288.pep
1  MHTGQAVSRV LSRTVIPLGI PLPVCSSNLP ERSAGSVIAF CLVLLRMGFG
51  LPHIVTKCAV RPYRTFSPLP VLPKQPSAVL LSVPLSVALP RPAVNRHSTL
101 RSPDFPPRMP YAIRGDCLPV PCAARIITRN AKMPSETVQV SDGIQPKLHA
151 LFQAGFDKAV QVAVQYGFV ADFVACAQVF NA*

```

m288/a288 97.2% identity in 181 aa overlap

	10	20	30	40	50	60
m288.pep	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGLPHIVTKCAV					
a288	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGLPHIVTKCAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m288.pep	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
a288	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m288.pep	PCAARIITRNTKMPSETVQVSDGIQPKLHALFQAGFDEAVQVAIQYGFVADVFVACTQVF					
	: : : :					

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a288 PCAARIITRNAKMPSETVQVSDGIQPKLHALFQAGFDKAVQVAVQYGFVADFVACAQVF
 130 140 150 160 170 180

m288.pep DTX
 ::
 a288 NAX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1211>:

g290.seq

```

1 atggcaaaaa tgatgaaatg ggcggctgtt gcggcggtcg cggcggcagc
51 ggtttggggc ggatggtctt atctgaagcc cgaaccgcag gctgcttata
101 ttacggaagc ggtcaggcgc ggcgatatca gccggacggt ttccgcgacg
151 ggcgagattt cgcggtccaa cctggtatcg gtcggcgcg caggcttcggg
201 gcagattaaa aagctttatg tcaaactcgg gcaacagggt aaaaaggcgc
251 atttgattgc ggaaatcaat tcgaccacgc agaccaacac gatcgatatg
301 gaaaaatcca aattggaaac gtatcaggcg aagctggtgt ccgcacagat
351 tgcattgggc agcgcggaaa aaaaatataa gcgtcaggcg gcgttgtgga
401 aggatgatgc gacctctaaa gaagatttgg aaagcgcgca ggatgcgctt
451 gccgccgcca aagccaatgt tgccgagttg aagcctttaa tcagacagag
501 caaaatttcc atcaataccg ccgagtcgga tttgggctac acgcgcatta
551 ccgcgacgat ggacggcacg gtggtggcga ttcccggtga agaggggcag
601 actgtgaacg cggcgagtc tacgccgacg attgtccaat tggcgaatct
651 ggatatgatg ttgaacaaaa tgcagattgc cgagggcgat attaccaagg
701 tgaaggcggg gcaggatatt tcgtttacga ttttgtccga accggatacg
751 ccgattaagg cgaagctcga cagcgtcgac cccgggctga ccacgatgtc
801 tgcgggcggc tacaacagca gtacggatac ggcttccaat gcggtctatt
851 attatgcccg ttcgtttgtg ccgaatccgg acggcaaaact cgccacgggg
901 atgacgacgc agaatacggg tgaatcgcg ggtgtgaaaa atgtgttgct
951 tattccgctc ctgaccgtga aaaatcgcg cggcaaggcg ttcgtacgcg
1001 tgttgggtgc ggacggcaag gcagtggaac gcgaaatccg gaccggtatg
1051 aaagacagta tgaataccga agtgaaaagc gggttgaaag agggggacaa
1101 agtgggtcatc tccgaaataa ccgccgccga gcagcaggaa agcggcgaac
1151 gcgccctagg cggcccgccg cgccgataa
  
```

This corresponds to the amino acid sequence <SEQ ID 1212; ORF 290.ng>:

g290.pep

```

1 MAKMMKWA AVAAVAWVG GWSYLKPEPQ AAYITEAVRR GDISRTVSAT
51 GEISPSNLVS VQAQASGQIK KLYVKLGQQV KKGDLIAEIN STTQNTIDM
101 EKSLETYQA KLVSAQIALG SAEKKYKRQA ALWKDDATSK EDLESAQDAL
151 AAKANVAEL KALIRQSKIS INTAESDLGY TRITATMDGT VVAIPVEEGQ
201 TVNAAQSTPT IVQLANLDM LNKMQIAEGD ITKVKAGQDI SFTILSEPDT
251 PIKAKLDSVD PGLTTMSSGG YNSSTDASN AVYYYARFV PNPDGKLTATG
301 MTTQNTVEID GVKNVLLIPS LTVKNRGGKA FVRVLGADGK AVEREIRTGM
351 KDSMNTEVKS GLKEGDKVVI SEITAAEQQE SGERALGGPP RR*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1213>:

m290.seq (partial)

```

1 ..GTATCGGTCG GCGCGCAGGC ATCGGGGCAG ATTAAGATAC TTTATGTCAA
51 ACTCGGGCAA CAGGTTAAAA AGGGCGATTG GATTGCGGAA ATCAATTCTGA
101 CCTCGCAGAC CAATACGCTC AATACGGAAA AATCCAAGTT GGAACGTAT
151 CAGGCGAAGC TGGTGTGCGC ACAGATTGCA TTGGGCAGCG CGGAGAAGAA
201 ATATAAGCGT CAGGCGGCGT TATGGAAGGA AAACGCGACT TCCAAAGAGG
251 ATTTGGAAGG CGCGCAGGAT GCGTTTGCCG CCGCCAAAGC CAATGTTGCC
301 GAGCTGAAGG CTTTAATCAG ACAGAGCAAA ATTTCCATCA ATACCGCCGA
351 GTCGGAATTG GGCTACACGC GCATTACCGC AACGATGGAC GGCACGGTGG
401 TGGCGATTCT CGTGAAGAG GGCAGACTG TGAACGCGGC GCAGTCTACG
451 CCGACGATTG TCCAATTGGC GAATCTGGAT ATGATGTTGA ACAAATGCA
501 GATTGCCGAG GCGGATATTA CCAAGGTGAA GGCGGGGCAG GATATTTCTG
551 TTACGATTTT GTCCGAACCG GATACGCCGA TTAAGGCGAA GCTCGACAGC
601 GTCGACCCCG GGCTGACCAC GATGTCGTCG GGCGGTTACA ACAGCAGTAC
651 GGATACGGCT TCCAATGCGG TCTACTATTA TGCCCGTTTC TTTGTGCCGA
  
```


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```

701 ATCCGGACGG CAAACTCGCC ACGGGGATGA CGACGCAGAA TACGGTTGAA
751 ATCGACGGCG TGAAAAATGT GCTGATTATT CCGTCGCTGA CCGTGAAAAA
801 TCGCGGCGGC AAGGCGTTTG TCGCGGTGTT GGGTGC GGCAAGGCGG
851 CGGAACGCGA AATCCGGACC GGTATGAGAG ACAGTATGAA TACCGAAGTA
901 AAAAGCGGGT TGAAAGAGGG GGACAAAGTG GTCATCTCCG AAATAACCGC
951 CGCCGAGCAA CAGGAAAGCG GCGAACGCGC CCTAGGCGGC CCGCCGCGCC
1001 GATAA

```

This corresponds to the amino acid sequence <SEQ ID 1214; ORF 290>:

```

m290.pep (partial)
  1 ..VSVGAQASGQ IKILYVKLGQ QVKKGDLIAE INSTSQNTL NTEKSKLETY
 51 QAKLVSAQIA LGSAEKKYKR QAALWKENAT SKEDLESAQD AFAAAKANVA
101 ELKALIRQSK ISINTAESEL GYTRITATMD GTVVAILVEE GQTVNAAQST
151 PTIVQLANLD MMLNKMQIAE GDITKVKAGQ DISFTILSEP DTPIKAKLDS
201 VDPGLTTMSS GGYNSSTDTA SNAVYYARS FVPNPDGKLA TGMTTQNTVE
251 IDGVKNVLII PSLTVKNRGG KAFVRVLGAD GKAAEREIRT GMRDSMNTEV
301 KSGLKEGDKV VISEITAAEQ QESGERALGG PPRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m290/g290 96.1% identity in 334 aa overlap

```

                                10      20      30
m290.pep                      VSVGAQASGQIKILYVKLGQVKKGDLIAE
                                |||||
g290      PQAAYITEAVRRGDISRTVSATGEISPSNLVSVGAQASGQIKKLYVKLGQVKKGDLIAE
          30      40      50      60      70      80

                                40      50      60      70      80      90
m290.pep      INSTSQNTLNTEKSKLETYQAKLVSAQIALGSAEKKYKRAALWKENATSKEDLESAQD
          |||:||||: |||||
g290      INSTTQTNTIDMEKSKLETYQAKLVSAQIALGSAEKKYKRAALWKDDATSKEDLESAQD
          90      100     110     120     130     140

                                100     110     120     130     140     150
m290.pep      AFAAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST
          |:|||||
g290      ALAAAKANVAELKALIRQSKISINTAESDLGYTRITATMDGTVVAIPVEEGQTVNAAQST
          150     160     170     180     190     200

                                160     170     180     190     200     210
m290.pep      PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS
          |||||
g290      PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS
          210     220     230     240     250     260

                                220     230     240     250     260     270
m290.pep      GGYNSSTDASNAVYYARSFVPNPDGKLATGMTTQNTVEIDGVKNVLIIIPSLTVKNRGG
          |||||
g290      GGYNSSTDASNAVYYARSFVPNPDGKLATGMTTQNTVEIDGVKNVLLIPSLTVKNRGG
          270     280     290     300     310     320

                                280     290     300     310     320     330
m290.pep      KAFVRVLGADGKAAEREIRTGMRDSMNTEVKSGLKEGDKVVISEITAAEQQESGERALGG
          |||||
g290      KAFVRVLGADGKAVEREIRTGMKDSMNTEVKSGLKEGDKVVISEITAAEQQESGERALGG
          330     340     350     360     370     380

m290.pep      PPRRX
          ||||
g290      PPRRX
          390

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1215>:

```
a290.seq
1   ATGGCAAAAA TGATGAAATG GGCGGCTGTT GCGGCGGTCG CGGCGGCAGC
51  GGT TTGGGGC GGATGGTCTT ATCTGAAGCC CGAGCCGCAG GCTGCTTATA
101 TTACGGAAC GGT CAGGCGC GCGGACATCA GCCGGACGGT TTCTGCAACA
151 GGGGAGATTT CGCCGTCCAA CCTGGTATCG GTCGGCGCGC AGGCATCGGG
201 GCAGATTAAG AAAC TTTATG TCAAAC TCGG GCAACAGGTT AAAAAGGGCG
251 ATTTGATTGC GGAAATCAAT TCGACCTCGC AGACCAATAC GCTCAATACG
301 GAAAAATCCA AATTGGAAC GTATCAGGCG AAGCTGGTGT CGGCACAGAT
351 TGCATTGGGC AGCGCGGAGA AGAAATATAA GCGTCAGGCG GCGTTGTGGA
401 AGGATGATGC GACCGCTAAA GAAGATTTGG AAAGCGCACA GGATGCGCTT
451 GCCGCCGCCA AAGCCAATGT TGCCGAGCTG AAGGCTCTAA TCAGACAGAG
501 CAAAATTTCC ATCAATACCG CCGAGTCGGA ATTGGGCTAC ACGCGCATT
551 CCGCAACGAT GGACGGCAGC GTGGTGGCGA TTCTCGTGGA AGAGGGGCAG
601 ACTGTGAACG CGGCGCAGTC TACGCCGACG ATTGTCCAAT TGGCGAATCT
651 GGATATGATG TTGAACAAAA TGCAGATTGC CGAGGGCGAT ATTACCAAGG
701 TGAAGGCGGG GCAGGATATT TCGTTTACGA TTTTGTCCGA ACCGGATACG
751 CCGATTAAGG CGAAGCTCGA CAGCGTCGAC CCCGGGCTGA CCACGATGTC
801 GTCGGGCGGC TACAACAGCA GTACGGATAC GGCTTCCAAT GCGGTCTACT
851 ATTATGCCCG TCGTTTGTG CCGAATCCGG ACGGCAAACG CGCCACGGGG
901 ATGACGACGC AGAATACGGT TGAATTCGAC GGTGTGAAAA ATGTGCTGAT
951 TATTCCGTCG CTGACCGTGA AAAATCGCGG CGGCAGGGCG TTTGTGCGCG
1001 TGTTGGGTGC AGACGGCAAG GCGGCGGAAC GCGAAATCCG GACCGGTATG
1051 AGAGACAGTA TGAATACCGA AGTAAAAAGC GGGTTGAAAG AGGGGGACAA
1101 AGTGGTCATC TCCGAAATAA CCGCCGCCGA GCAGCAGGAA AGCGGCGAAC
1151 GCGCCCTAGG CGGCCGCCG CGCCGATAA
```

This corresponds to the amino acid sequence <SEQ ID 1216; ORF 290.a>:

```
a290.pep
1   MAKMMKWA AV AAVAAA AVWG GWSYLKPEPQ AAYITETVRR GDISRTVSAT
51  GEISPSNLVS VQAQASGQIK KLYVKLGQOV KKGDLIAEIN STSQTNTLNT
101 EKSKLETYQA KLVSAQIALG SAEKKYKRQA ALWKDDATAK EDLESAQDAL
151 AAAKANVAEL KALIRQSKIS INTAESELGY TRITATMDGT VVAILVEEGQ
201 TVNAAQSTPT IVQLANLDM LNKMQIAEGD ITKVKAGQDI SFTILSEPDT
251 PIKAKLDSVD PGLTTMSSGG YNSSTDASN AVYYYARSFV PNPDGKLATG
301 MTTQNTVEID GVKNVLIIPS LTVKNRGGRA FVRVLGADGK AAEREIRTGM
351 RDSMNTVEKS GLKEGDKVVI SEITAAEQQE SGERALGGPP RR*
```

m290/a290 98.2% identity in 334 aa overlap

```
m290.pep
10 20 30
VSVGAQASGQIKILYVKLGQOVKKGDLIAE
|||||
a290
30 40 50 60 70 80
PQAAYITETVRRGDISRTVSATGEISPSNLVS VSVGAQASGQIKKLYVKLGQOVKKGDLIAE

40 50 60 70 80 90
INSTSQTNTLNTEKSKLETYQAKLVSAQIALGSAEKKYKRQAALWKENATSKEDLESAQD
|||||
a290
90 100 110 120 130 140
INSTSQTNTLNTEKSKLETYQAKLVSAQIALGSAEKKYKRQAALWKDDATAKEDLESAQD

100 110 120 130 140 150
AFAAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST
|:|||||
a290
150 160 170 180 190 200
ALAAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST

160 170 180 190 200 210
PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS
|||||
a290
210 220 230 240 250 260
PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS

220 230 240 250 260 270
```

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```

m290.pep      GGYNSSTDASNAVYYYARSFVNPDPGKLATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
               |||||||||||||||||||||||||||||||||||||||||||||||||||
a290          GGYNSSTDASNAVYYYARSFVNPDPGKLATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
               270      280      290      300      310      320

               280      290      300      310      320      330
m290.pep      KAFVRVLGADGKAAEREIRTGMRDSMNTTEVKSGLKEGDKVVI SEITAAEQQESGERALGG
               :|||||||||||||||||||||||||||||||||||||||||||||||||
a290          RAFVRVLGADGKAAEREIRTGMRDSMNTTEVKSGLKEGDKVVI SEITAAEQQESGERALGG
               330      340      350      360      370      380

m290.pep      PPRRX
               |||||
a290          PPRRX
               390

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1217>:

```

g292.seq
1   atgaaaacca agttaatcaa aatcttgacc ccctttaccg tcctgccgct
51  gctggccttg gggcaaacgc ccgtttccaa tgccaacgcc gaatccgccg
101 tcaaagccga atccgccggc aaatccgttg ccgcttcttt gaaagcgcgt
151 ttggaaaaaa cctattccgc ccaagatttg aaagtgttga gcgtcagcga
201 aacaccggtc aaaggcattt acgaagtcgt cgtcagcggc aggcagatta
251 tctacaccga tgccgaaggc ggctatatgt tcgtcggcga actcatcaac
301 atcgacacgc gcaaaaacct gaccgaagaa cgcgccgccg atttgaacaa
351 aatcgacttc gcctccctgc ctttgacaaa agccatcaaa gaagtacgcg
401 gcaacggcaa gctgaaagtc gccgtcttct ccgaccccca ttgtccgttc
451 tgcaaacgct tggaacatga gtttgaaaaa atgaccgacg tgacggttta
501 cagctttatg atgcccattg ccggcctgca cccagatgcc gcgcgcaagg
551 cgcaaattct atggtgtcag cccgaccgtg ccaaagcggtg gacggattgg
601 atgcgtaaa gcaaattccc ggtcggcggc agcatctgcg acaatcccgt
651 cgcggaacc acttccttgg gcgaacagtt cggcttcaac ggacgcccga
701 cccttcgtct tccccaacgg gcgcacccaa agcggttaca gcccgatgcc
751 ccaactggag gaaatcatcc gcaaaaacca gcagtaaacc cgcaatga

```

This corresponds to the amino acid sequence <SEQ ID 1218; ORF 292.ng>:

```

g292.pep
1   MKTKLIKILT PFTVLPLLAC GQTPVSNANA ESAVKAESAG KSVAAASKAR
51  LEKTYSAQDL KVLVSVETPV KGIYEVVVSQ RQIIYTDAEG GYMFGELIN
101 IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRGNGKLKV AVFSDPDCPF
151 CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201 MRKGKFPVGG SICDNPVAET TSLGEQGFN GTPTLRLPQR AHPKRLQPD
251 PTGGNHPQKP AVNPQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1219>:

```

m292.seq
1   ATGAAAACCA AGTTAATCAA AATCTTGACC CCCTTTACCG TCCTCCCGCT
51  GCTGGCTTGC GGGCAAACGC CCGTTTCCAA TGCCAACGCC GAACCCGCCG
101 TCAAAGCCGA GTCCGCCGGC AAATCCGTTG CCGCTCTTTT GAAAGCGCGT
151 TTGGAAAAAA CCTATTCCGC CCAAGATTTG AAAGTGTTGA GCGTCAGCGA
201 AACACCGGTC AAAGGCATTT ACGAAGTCGT CGTCAGCGGC AGGCAGATTA
251 TCTACACCGA TGCCGAAGGC GGCTATATGT TCGTCGGCGA ACTCATCAAC
301 ATCGACACGC GCAAAAACCT GACCGAAGAA CGCGCCGCCG ATTTGAACAA
351 AATCGACTTC GCCTCCCTGC CTTTGGACAA AGCCATCAAA GAAGTGCGCG
401 GCAACGGCAA GCTGAAAGTC GCCGTCTTCT CCGACCCCGA TTGTCCGTTC
451 TGCAAACGCT TGGAACACGA GTTTGAAAAA ATGACCGACG TGACGGTTTA
501 CAGCTTTATG ATGCCCATTG CCGGCCTGCA CCCGATGCC GCGCGCAAGG
551 CGCAAATCTT ATGGTGTCTAG CCCGACCGCG CCAAAGCGTG GACGGATTGG
601 ATCGGTAAG GCAAATTCCC GGTGCGCGGC AGCATCTGCG ACAATCCCGT
651 CGCGGAAACC ACTTCCTTGG GCGAACAATT CGGCTTCAAC GGCACGCCGA
701 CCCTCGTCTT CCCCACGGG GCGAGCCAAA GCGGCTACAG CCCGATGCC

```

680

751 CAACTGGAGG AAATCATCCG CAAAATCAA TAA

This corresponds to the amino acid sequence <SEQ ID 1220; ORF 292>:

```

m292.pep
  1 MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSVASLKR
 51 LEKTYSAQDL KVLVSSETPV KGIYEVVVSQ RQIIYTDAEG GYMFVGELIN
101 IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRGNGKLKV AVFSDPDCPF
151 CKRLEHEFEK MTDVTYSEFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201 MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLVFPNG RSQSGYSPMP
251 QLEEIIRKNQ *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m292/g292 98.7% identity in 238 aa overlap

	10	20	30	40	50	60
m292.pep	MKTKLIKILTPFTVLPLLACGQTPVSNANAEPVKAESAGKSVASLKRLEKTYSAQDL					
g292	MKTKLIKILTPFTVLPLLACGQTPVSNANAESAVKAESAGKSVASLKRLEKTYSAQDL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m292.pep	KVLVSSETPVKGIYEVVVSQRQIIYTDAEGGYMFVGELINIDTRKNLTEERAADLNKIDF					
g292	KVLVSSETPVKGIYEVVVSQRQIIYTDAEGGYMFVGELINIDTRKNLTEERAADLNKIDF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m292.pep	ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCKRLEHEFEKMTDVTYSEFMPIAGLHPDA					
g292	ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCKRLEHEFEKMTDVTYSEFMPIAGLHPDA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m292.pep	ARKAQILWCQPDRAKAWTDWMRKGKFPVGGISICDNPVAETTSLSGEQFGFNGTPTLVFPNG					
g292	ARKAQILWCQPDRAKAWTDWMRKGKFPVGGISICDNPVAETTSLSGEQFGFNGTPTLRLPQR					
	190	200	210	220	230	240
	250	260				
m292.pep	RSQSGYSPMPQLEEIIRKNQX					
g292	AHPKRLQPDAPTGGNHPQKPAVNPQX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1221>:

```

a292.seq
  1 ATGAAAACCA AGTTAATCAA AATCTTGACC CCCTTTACCG TCCTCCCGCT
 51 GCTGGCTTGC GGGCAAACGC CCGTTTCCAA TGCCAACGCC GAACCCGCCG
101 TCAAAGCCGA GTCCGCCGGC AAATCCGTTG CCGCTCTTT GAAAGCGCGT
151 TTGGAAAAAA CCTATTCCGC CCAAGATTG AAAGTGTGA GCGTCAGCGA
201 AACACCGGTC AAAGGCATTT ACGAAGTCGT CGTCAGCGGC AGGCAGATTA
251 TCTACACCGA TGCCGAAGGC GGCTATATGT TCGTCGGCGA ACTCATCAAC
301 ATCGACACGC GCAAAAACCT GACCGAAGAA CGCGCCGCCG ATTTGAACAA
351 AATCGACTTC GCCTCCCTGC CTTTGGACAA AGCCATCAA GAAGTCCGCG
401 GCAACGGCAA GCTGAAAGTC GCCGTCTTCT CCGACCCCGA TTGTCCGTTT
451 TGCAAACGCT TGGAACACGA GTTTGAAAAA ATGACCGACG TGACGGTTTA
501 CAGCTTTATG ATGCCCATG CCGGCCTGCA CCCCAGATGC GCGCGCAAGG
551 CGCAAATCTT ATGGTGTCAG CCCGACCGCG CCAAAGCGTG GACGGATTGG
601 ATGCGTAAAG GCAAATTCCC GGTCCGGCGC AGCATCTGCG ACAATCCCGT
651 CGCGGAAACC ACTTCCTTGG GCGAACAATT CGGCTTCAAC GGCACGCCGA
701 CCCTCGTCTT CCCAACGGG CGCAGCCAAA GCGGCTACAG CCCGATGCCC
751 CAACTGGAGG AAATCATCCG CAAAATCAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1222; ORF 292.a>:

```

a292.pep
1  MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSPAASLKAR
51  LEKTYSAQDL KVLSVSETPV KGIYEVVVSQ RQIIYTDAEG GYMFVGELIN
101 IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRGNGKLKV AVFSDPDCPF
151 CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201 MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLVFPNG RSQSGYSPMP
251 QLEEIIRKNQ *

m292/a292 100.0% identity in 260 aa overlap

              10      20      30      40      50      60
m292.pep    MKTKLIKILTPFTVLPLLACGQTPVSNANAEPAVKAESAGKSPAASLKARLEKTYSAQDL
              |||||
a292        MKTKLIKILTPFTVLPLLACGQTPVSNANAEPAVKAESAGKSPAASLKARLEKTYSAQDL
              10      20      30      40      50      60

              70      80      90     100     110     120
m292.pep    KVLSVSETPVKGIYEVVVSQ RQIIYTDAEGGYMFVGELINIDTRKNLTEERAADLNKIDF
              |||||
a292        KVLSVSETPVKGIYEVVVSQ RQIIYTDAEGGYMFVGELINIDTRKNLTEERAADLNKIDF
              70      80      90     100     110     120

              130     140     150     160     170     180
m292.pep    ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCKRLEHEFEKMTDVTVYSFMMPIAGLHPDA
              |||||
a292        ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCKRLEHEFEKMTDVTVYSFMMPIAGLHPDA
              130     140     150     160     170     180

              190     200     210     220     230     240
m292.pep    ARKAQILWCQPDRAKAWTDWMRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLVFPNG
              |||||
a292        ARKAQILWCQPDRAKAWTDWMRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLVFPNG
              190     200     210     220     230     240

              250     260
m292.pep    RSQSGYSPMPQLEEIIRKNQX
              |||||
a292        RSQSGYSPMPQLEEIIRKNQX
              250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1223>:

```

g294.seq (partial)
1  atgcgtatta cctgtgcgcc gatgtcgctt ttgtcggcgg cagtctggtc
51  ggttcgggct gtcagaacat catcgaaccg ctttcctcgc gcgttacgac
101 gatattcggc ttttcgacct acaatttttc cgaagcctgc cggcacgcct
151 tggcatcggg tgcggcggtt caagtcgaat cggcgagacg gtggcgtgaa
201 gccgttgaaa aaaccttatc tggcgagggg ggcggaatgc agatgcaggc
251 gcgcgtggac ggctttatcg cacaacatcg cggagcgggc gcgagaatcg
301 ccgaggcggt gcgggaagcg gtatgcggac atcgggggcg atagtatac
351 aatccgtatc cgagttttcc ggttgagca tcgtatgagt atttatgccg
401 tcgcgcacat catccacctg tattgcgcca ccgccttgt cggcgcggtg
451 ttttttgaag tgctggtttt gtccgtcctg catacgggac ggggtgcgcg
501 cgaggcgcgg cgcggaagtg aaaaggcaat gtcttaccgc gccgtcaggg
551 tgatgccgtt tgcggtcgga ctgctgttcg ccagggaac tctagagtcg
601 actgcagcag catgccctc...

```

This corresponds to the amino acid sequence <SEQ ID 1224; ORF 294.ng>:

```

g294.pep (partial)
1  MRITCAPMSL LSAAVWSVRA VRTSSNRFP A LRRYSAFRP TIFPKPAGTP
51  WHRVRRFKSN RRTRGVKPLK KPYLARGAEC RCRRRAWTALS HNIAERARES
101 PRRCGKRYAD IGGDSDTIRI RVFRLEHRMS IYAVAHIIHL YCATAFVGGV
151 FFEVLVLSVL HTGRVSREAR REVEKAMSYR AVRVMFPAVG LLFARGTLES
201 TAAACP...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1225>:

m294.seq

```

1  ATGCGTATTA CCTGTGCGCC GATGTCGCTT TTGTCGGCGG CAGTCTGGTC
51  GATTCGGGTT GTCAGAACAT CATCGAACCG CTTTCCTGCG GCGTTCCGAC
101 GATATTCGGC TTTTCAACCT ACAATTTTTC CGAAGCCTGC CGACACGCCT
151 TGGCATCGGG TGCGGCGGTT CAAGTCGAAT CGGCGGATGC GTGGCGGGAA
201 GCCGTTGAAA AAACCTTATC GTCCGAGGGG GGGGGGATGC AGATGCAGGC
251 GCGCGTGGAC GGCTTTATCG CACAACATCG CGGAGCGGGC GCGAGAATCG
301 CCGAGGCGGT GCGGGAAGCG GTATGCGGAT ATCGGGGGCG ATAGTGATAC
351 AATCCGTATC CGAGTTTTC GTTTGGAGCA TCGTATGAGT ATTTATGCCG
401 TCGCGCACAT CGTTCATCTG TATTGCGCTA TTGCCCTTGT CGGCGGCGTG
451 TTTTTTGAAG TGCTGGTTTT GTCCGTCCTG CATAACGGAC GGGTGTGCGG
501 CGAGGCGCGG CGCGAAGTGG AAAAGGCAAT GTCTTACCGC GCCGTCAGGG
551 TGATGCCGTT TGTGGTCGGA CTGCTGTTTC CCAGCGGCAT CGTGATGGCG
601 GCAAACCGCT ATCTTTCTAT ATTGGGCGAA CCGTTTGCCA CTTCTTCGG
651 TACGATGCTG ACGCTGAAAA TCCTGTTGGC GTTCAGCGTA TTGGCGCACT
701 TCGCCATCGC CGTCGTCAA ATGGCGCGTT CCACACTGAC GGTCGGTTGG
751 TCGAAATACA TACACGCCGT CGTCTTACC CATATGcTGC TGATTGTCTT
801 TTTGCAAAA GCGATGTTTT ATATCAGCTG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 1226; ORF 294>:

m294.pep

```

1  MRITCAPMSL LSAAVWSIRV VRTSSNRFFA AFRRYSAFQP TIFPKPADTP
51  WHRVRRFKSN RRMRGKPLK KPYRPRGGG RCRRRAWTALS HNIAERARES
101 PRRCGKRYAD IGGDSDTIRI RVFRLEHRMS IYAVAHIVHL YCAIAFVGGV
151 FFEVLVLSVL HTGRVSREAR REVEKAMSYR AVRVMFVVG LLFASGIVMA
201 ANRYLSILGE PFATSFGTML TLKILLAFSV LAHFIAIVVK MARSTLTVGW
251 SKYIHAVVFT HMLLIVFLAK AMFYISW*

```

g294/m294 92.3% identity in 196 aa overlap

	10	20	30	40	50	60
g294.pep	MRITCAPMSLLSAAVWSVRAVRTSSNRFFAALRRYSAFRPTIFPKPAGTPWHRVRRFKSN					
m294	MRITCAPMSLLSAAVWSIRVVRTSSNRFFAALRRYSAFRPTIFPKPADTPWHRVRRFKSN					
	10	20	30	40	50	60
	70	80	90	100	110	120
g294.pep	RRTRGVKPLKKPYLARGAECRCRRRAWTALSHNIAERARESPPRCGKRYADIGGDSDTIRI					
m294	RRMRGGKPLKKPYRPRGGCRRRAWTALSHNIAERARESPPRCGKRYADIGGDSDTIRI					
	70	80	90	100	110	120
	130	140	150	160	170	180
g294.pep	RVFRLEHRMSIYAVAHIIHLYCATAFVGGVFFEVVLVLSVLHTGRVSREARREVEKAMSYR					
m294	RVFRLEHRMSIYAVAHIVHLYCAIAFVGGVFFEVVLVLSVLHTGRVSREARREVEKAMSYR					
	130	140	150	160	170	180
	190	200				
g294.pep	AVRVMFPAVGLLFARGTLESTAAACP					
m294	AVRVMFVVGLLFASGIVMAANRYLSILGEPFATSFGTMLTLKILLAFSVLAHFIAIVVK					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1227>:

a294.seq

```

1  ATGCGTATTA CCTGTGCGCC GATGTCGCTT TTGTCGGCGG CAGTCTGGTC
51  GATTCGGGCT GTCAGAACAT CATCGAACCG CTTTCCTGCG GCGTTCCGAC
101 GATATTCGGC TTTTCGACCT ACAATTTTTC CGAAGCCTGC CGGCACGCCT
151 TGGCATCGGG TGCGGCGGTT CAAGTCGAAT CGGCGGACGC GTGGCGGGAA
201 GCCGTTGAAA AAAACTTATC GTCCGAGGAG GCGGGAATGC AGATGCAGGC
251 GCGCGCGGAC GGCTTTATCG CACAACATCG CGGAGCGGGC GCGAGAATCG
301 CCGAGGCGGT ACGGGAAGCG GTATGCGGAC ATCGGGGACG ATAGTGATAC
351 AATCCGTATC CGAGTTTTC GGTGGAGTA CCGTATGAGT ATTTATGCCG
401 TCGCGCACAT CGTCCACCTG TATTGCGCCA TCGCCTTGTG CGGCGGCGTG
451 TTTTTTGAAG TGCTGGTTTT GTCCGTCCTG CATAACGGAC GGGTGTGCGG
501 CGAGGCGCGG CGCGAAGTGG AAAAGGCAAT GTCTTACCGC GCCGTCAGGG
551 TGATGCCGTT TGTGGTCGGA CTGCTGTTTC CCAGCGGCAT CGTGATGGCG
601 GCAAACCGCT ATCTTTCTAT ATTGGGCGAA CCGTTTGCCA CTTCTTCGG
651 TACGATGCTG ACGCTGAAAA TCCTGTTGGC GTTCAGCGTG TTGGCGCACT

```

683

701 TCGCCATCGC CGTCGTCAA ATGGCGCGTT CCACACTGAC CGTCGGCTGG
 751 TCGAAATACA TACACACCGT CGTCTTTACC CATATGCTGC TGATTGTCTT
 801 TTTGGCAAAA GCGATGTTTT ATATCAGCTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1228; ORF 294.a>:

a294.pep
 1 MRITCAPMSL LSAAVWSIRA VRTSSNRFP AFRYSAFRP TIFPKPAGTP
 51 WHRVRFKSN RRTRGGKPLK KTYRPRRAEC RCRARTALS HNIAERARES
 101 PRRYGKRYAD IGDDSDTIRI RVFRLEYRMS IYAVAHIVHL YCAIAFVGGV
 151 FFEVLVLSVL HTGRVSCEAR REVEKAMSYR AVRMPFVVG LLFASGIVMA
 201 ANRYSILGE PFATSFGTML TLKILLAFSV LAHFAIAVVK MARSTLTVGW
 251 SKYIHTVVFT HMLLIVFLAK AMFYISW*

m294/a294 94.9% identity in 277 aa overlap

	10	20	30	40	50	60
m294.pep	MRITCAPMSLLSA	AVWSIRVVRTSS	NRFPAAFRYSA	FQPTIFPKPAD	TPWHRVRRF	KSN
a294	MRITCAPMSLLSA	AVWSIRAVRTSS	NRFPAAFRYSA	FRPTIFPKPAG	TPWHRVRRF	KSN
	10	20	30	40	50	60
m294.pep	RRMRGGKPLKK	PYRPRGGGCR	CRRRAWTALSH	NIAERARESP	PRCGKRYAD	IGGDSDTIRI
a294	RRTRGGKPLKK	TYRPRRAECR	CRRARTALSH	NIAERARESP	RRYGKRYAD	IGGDSDTIRI
	70	80	90	100	110	120
m294.pep	RVFRLEHRMSI	YAVAHIVHLY	CAIAFVGGV	FEVLVLSVL	HTGRVSREAR	REVEKAMSYR
a294	RVFRLEHRMSI	YAVAHIVHLY	CAIAFVGGV	FEVLVLSVL	HTGRVSCEAR	REVEKAMSYR
	130	140	150	160	170	180
m294.pep	AVRMPFVVG	LLFASGIVMA	ANRYSILGE	PFATSFGTML	TLKILLAFSV	LAHFAIAVVK
a294	AVRMPFVVG	LLFASGIVMA	ANRYSILGE	PFATSFGTML	TLKILLAFSV	LAHFAIAVVK
	190	200	210	220	230	240
m294.pep	MARSTLTVGW	SKYIHAVVFT	HMLLIVFLAK	AMFYISWX		
a294	MARSTLTVGW	SKYIHTVVFT	HMLLIVFLAK	AMFYISWX		
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1229>:

g295.seq
 1 atgctcggga tggcgcggca cgacggccag cagggcatcg ccgcgatatt
 51 gttgccacgc cgccagcagt tttccgcct cgtcttcgcc ccgataaacg
 101 cgcgtgctgc cgcacacggc aaccggccgg cctccgatgc gtttttcaaa
 151 ctgcccgcgc agcgttttca tgtcttcaga cggcatcagg tcgtatttgg
 201 tattgccga cactgcacg gatgccgcgc ccaatttcgc caaccgcgcc
 251 gcatccgcct ccgtctgcgc cagacagccc gtcagcgaag cggctgcggg
 301 acggatcagg cggcggactt tcagataacc gttcagcgat tttccgcaca
 351 gccgcgcatt cgccaaaaac agcggcacac ccgctcgcgc gcattccttc
 401 atcagattgg gccagatttc ggtttccatc aaaatgccga acatcgggcg
 451 gtgttcgcgc aaaaactgcc gtaccacagt tttttgtca tacggaagat
 501 agcggcattg cgcacggga aacagaactt gcgcgggttc ccgtcccgtc
 551 ggggtcatct ggtcatcag cagcggcgca tcgggaaaac gccgccgcaa
 601 ctgcgctatc aagggctggg cggcacgcgt ttctccgacc gaaacggcgt
 651 gtatccaaac cgcgcgggta acgggattcg gatcgggctt gccgaaacgc
 701 tcgtccctat gcgcccggta tgccggggca cttccggagc gttgtccaa
 751 ataacgcgt atccatatcg gcgaagcag ccacaataca tcataaagcc
 801 attggaacat ctttctattt cctgcaaaac aaatgccgtc cgaacgggtc
 851 ggacggcatt tcggcaacgg aatcaaatat cgtag

This corresponds to the amino acid sequence <SEQ ID 1230; ORF 295.ng>:

g295.pep

```
1 MLGMARHDDGQ QGIAAAILLPR RQOFFRLVFA PINARAAAHG NRPASDAFFK
51 LPRQRFHVFR RHQVVFGLAA HLHGCRAQFR QPRRIRLRLR QTARQSRGCG
101 TDQAADFQIT VQRFRRQPRI RQKQRHTRSP AFLHQIGPDF GFHQNAEHRA
151 VFAQKLPYPR FFVIRKIAAL RIGKQNLGRF PSRRGHLRHQ QRRIGKTPPQ
201 LAYQGLGGTR FSDRNGVYPN RAGNGIRMRL AETLVPMRPV CRGTSGAFVQ
251 ITPYPYRRKQ PQYIIKPLEH LSISCKTNAV RTVRTAFRQR NQIS*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1231>:

m295.seq

```
1 ATGCTCGGGA TGGCGCGGCA CGACGACCAG CAGCGCATCG CCGCGATATT
51 GTTGCCACGC CGCCAGCAGT TTTCCGCCT CGTCTTCACC CCGATAAACG
101 CGCGTGCTGC CGCACACGGC AACCGGCCGG CCTCCGATGC GTTTTTCAAA
151 CTGCCCCGCC AGCGTTTCA TCTGTTCCGA CGGTATGATG TCGTATTTGG
201 TATTGCCGCA CACCTGCACG GATGCCGCGC CCAATTTTCG CAACCGCGCC
251 GCATCCGCCT CTGTCTGCGC CAGACACCCC GTCAGCGAAG CGGCGGCAGG
301 ACGGATCAGG CGGCGGACTT TCAGATAACC GTTCAACGAT TTTTCCGACA
351 GCCGCGCATT CGCCAAAAC AGCGGCACAC CCGCGCGCGG GCATTCCCTC
401 ATCAGGTTGG GCCAGATTTC GGTTCATC AAAATGCCGA ACATCGGGCG
451 GTGTTCCGCG AAAAAGTCCC GTACCCACGT TTTTGTGCA TACGGAAGAT
501 AGCGGCATTG CGCATCGGGA AACAGAACTT GCGCGGTTTC CCGCCCCGTC
551 GGGGTCATCT GCGTCATCAG CAGCGGCGCA TCGGGAAGAA GCCGCGCGCA
601 CTCGCGTATC AAGGACTGGG CGGCACGCGT TTCTCCGACC GAAACGGCGT
651 GTATCCAAAC CGGCGCGGTA ACGGGATTCG GATACGGCTT GCCGAAACGC
701 TCGTCCCGAT GCGCCCGATA TGCCGGGGCA CTCCGGAGC GTTGTGTCGA
751 ATAACGCCGT ATCCATATCG GCGCAAGCAG CCACAATACA TCATAAGGCC
801 ATTGGAACAT CTTTCTATT CTGCAAAAC AAATGCCGTC TGAACGGTTC
851 AGACGGCATT TCGGCAACGG AATCAATAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 1232; ORF 295>:

m295.pep

```
1 MLGMARHDDQ QRIAAILLPR RQOFFRLVFT PINARAAAHG NRPASDAFFK
51 LPRQRFHLFR RYDVVFGLAA HLHGCRAQFR QPRRIRLCLR QTPRQRSGGR
101 TDQAADFQIT VQRFRRQPRI RQKQRHTRAP AFPHQVGPDP GFHQNAEHRA
151 VFAQKLPYPR FFVIRKIAAL RIGKQNLGRF PERRGHLRHQ QRRIGKTPPQ
201 LAYQGLGGTR FSDRNGVYPN RAGNGIRIRL AETLVPMRPI CRGTSGAFVQ
251 ITPYPYRRKQ PQYIIKPLEH LSISCKTNAV XTQTAERQR NQIS*
```

m295/g295 93.9% identity in 294 aa overlap

	10	20	30	40	50	60
m295.pep	MLGMARHDDQORIAAILLPRRQOFFRLVFTPINARAAAHGNRPASDAFFKLPQRQFHLFR					
g295	MLGMARHDDQGGIAAILLPRRQOFFRLVFAPINARAAAHGNRPASDAFFKLPQRQFHVFR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m295.pep	RYDVVFGLAAHLHGCRAQFRQPRRIRLCLRQTPRQRSGGRTDQAADFQITVQRFRRQPRI					
g295	RHQVVFGLAAHLHGCRAQFRQPRRIRLRLRQTARQSRGCGTDQAADFQITVQRFRRQPRI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m295.pep	RQKQRHTRAPAFPHQVGPDPGFHQNAEHRVFAQKLPYPRFFVIRKIAALRIGKQNLGRF					
g295	RQKQRHTRSPAFHLQIGPDFGFHQNAEHRVFAQKLPYPRFFVIRKIAALRIGKQNLGRF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m295.pep	PPRRGHLRHQRRIGKTPPQLAYQGLGGTRFSDRNGVYPN RAGNGIRIRLAETLVPMRPI					
g295	PSRRGHLRHQRRIGKTPPQLAYQGLGGTRFSDRNGVYPN RAGNGIRMRLAETLVPMRPV					
	190	200	210	220	230	240
	250	260	270	280	290	
m295.pep	CRGTSGAFVQITPYPYRRKQPQYIIKPLEHLSISCKTNAVXTVQTAERQRNQISX					
g295	CRGTSGAFVQITPYPYRRKQPQYIIKPLEHLSISCKTNAVXTVQTAERQRNQIS					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1233>:

```
a295.seq
1  ATGCTCGGGA TGGCGCGGCA CGACGACCAG CAGGGCATCG CCGCGATATT
51  GTTGCCACGC CGCCAGCAGT TTTTCCGCCT CGTCTTCACC CCGATAAACG
101 CGCGTGCTGC CGCACACGGC AACCTGCCGG TCTCCGATGC GTTTTCAAAA
151 CTGCCCCGCC AGCGTTTTCA TCTGTTCCGA CGGCATCAGG TCGTATTTGG
201 TATTGCCGCA CACCTGCACG GATGCCGCGC CCAATTTCGC CAACCGCGCC
251 GCATCCGCCT CCGTCTGTGC CAGACAGCCC GTACAGGAAG CGGCGGCAGG
301 ACGGATCAGG CTGCGGACTT TCAGATAACC GTTAGCGAT TTTTCCGACA
351 GCCGCGCATT CGCCAAAAAC AGCGGCACAC CCGTGCGCCG GCATTCCTTC
401 ATCAGATTGG GCCAGATTTC GGTTCATC AAAATGCCGA ACATCGGGCG
451 GTGTTGCGGC AAAAAGTACC GTACCCACGT TTTTGTGCA TACGGAAGAT
501 AGCGGCATTG TGCATCAGGA AACAGAACTT GCGCGGTTTC CCGTCCCGTC
551 GGGGTCATCT GCGTCATCAG CAGCGGCGCA TCGGGAAAAAC GCTGCCGCAA
601 CTCGCGTATC AAAGGTTGGG CGGCACGCGT TTCCCGGACC GAAACGGCGT
651 GTATCCAAAC CGCGCCGGTA ACGGGATTCT GATACGGCTT GCCGAAACGC
701 TCGCCCCGAT GCGCCCGATA TGCAGGGGCA CTTCGGAGC GTTTGTCCAA
751 ATAACGCCGT ATCCATATCG GCGCAAGCAG CCACAATACA TCATAAAGCC
801 ATTGGAACAT CTTTCTATTT CCTGCAAAAC AAATGCCGTC CGAACGGTTC
851 GGACGGCATT TCGGCAACGG AATCAAATAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 1234; ORF 295.a>:

```
a295.pep
1  MLGMARHDDQ QGIAAILLPR RQOFFRLVFT PINARAAAHG NLPVSDAFFK
51  LPRQRHFLFR RHQVVFGLIA HLHGCRAQFR QPRRIRLRLC QTARQSSGGR
101 TDQAADFQIT V*RRFRQPRI RQKQRHTRAP AFLHQIGPDF GFHQNAEHRA
151 VFAQKLPYPR FFVIRKIAAL CIRKQNLRGF PSRRGHLRHQ QRRIGKTLPO
201 LAYQRLGGTR FPDNRGVYPN RAGNGIRIRL AETLAPMRPI CRGTSGAFVQ
251 ITPYPYRRKQ PQYIIKPLEH LSISCKTNAV RTVRTAFRQR NQIS*
```

m295/a295 93.2% identity in 294 aa overlap

m295.pep	10	20	30	40	50	60
a295	10	20	30	40	50	60
m295.pep	70	80	90	100	110	120
a295	70	80	90	100	110	120
m295.pep	130	140	150	160	170	180
a295	130	140	150	160	170	180
m295.pep	190	200	210	220	230	240
a295	190	200	210	220	230	240
m295.pep	250	260	270	280	290	
a295	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1235>:

```
g297.seq
1  ATGGCTGTCT TCCCACTTTC GGCAAAACAT CGGAAATACG CGCTGCGCGC
```

```

51 GCTTGCCGTT TCGATTATTC TGGTGtcgGC GGCATACATT Gcttcgacag
101 aggggaccga ggcgctcaga ccgcAGCGCG TggaacaaAA ACTGCCGCCG
151 CTGTCTtGGg ggcgcaacgg CGTtcagacg gcaTATTGGG TGCAGGAGGC
201 GGTGCagccg ggggactcgC TGGCGGACGT GCTGGCGCGT TCGGGTATGG
251 CGCGGGacga gattgCCcga ATcacGGAAA aataTggcgG CGAAGCCGAT
301 TTGCGgcatt tGCGTGCCGA CCAGTCGGTT CATGTTTTGG TCGGCGGCGA
351 CGGCAGTGCG CGCGAAGTGC AGTTTTttaC CGACGAAGAC GGCAGGCGCA
401 aTctGGTcGC TTTGGAAAAA AAAGGCGGCA TATGGCGGCG GTCGGCTTCT
451 GATGCGGATA TGAAGGTTTT GCCGACACTG CGTTCGGTCG TGGTCAAAAC
501 GTCGGCGCGC GGTTCGCTGG CGCGGGCGGA AGTGCCCGTC GAAATCCGCG
551 AATCCTTAAG CGGGATTTTT GCCGGCCGCT TCAGCCTTGA CGGTTTGAAG
601 GAAGGCGATG CCGTGCGCCT GCTTTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG CGCGGCGATA TTTTGGCGGC GGAAGTTGTC AAGGCGGCGA
701 CAACCCATCA GCGCTTCTAT TACCGTTCGG ACAAGGAAGG CGGAGGGGGC
751 GGCATATTAT ACATGAAGA CGGCAGGGTG TTGCAGGAAA AAGGCGGCTT
801 CAACATCgaG CCGCTGGTCT ATACGCGCAT TTCTTCGCCG TTCGGCTACC
851 GTATGCACCC CATCCTGCAC ACATGGCGGC TGCACACGGG CATCGATTAT
901 GCCGCACCGC AGGGAACGCC GGTCAAGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGCG GATACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GAAACGCTG TACGCGCACT TGAGCGCGTT TTCGCAGGCA
1051 CAAGGCAATG TGC GCGGCGG CGAGGTCATC GGTTTTGTG GTTTCGACAGG
1101 GCGTTCGACC GGGCCGCACC TGCATTACGA GGC GCGCATC AACGGGCAGC
1151 CCGTCAATCC TGTTCGGTC GCATTGCCGA CACCCGAATT GACGAGGCG
1201 GACAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1236; ORF 297.ng>:

g297.pep

```

1 MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTEGTERVR PQRVEQKLPP
51 LSWGNGVQT AYWVQEAQVP GDSLADVLAR SGMARDEIAR ITEKYGGEAD
101 LRHLRADQSV HVLVGGDGSA REVQFFTDED GERNLVALEK KGGIWRRSAS
151 LADMKVLPPL RSVVVKTSAR GSLARAEPV EIRESLSGIF AGRFSLDGLK
201 EGDVRLLYD SLYFHGQOVA AGDILAAEVV KGGTTHQAFY YRSDKEGGGG
251 GNYDEDEGRV LQEKGGFNIE PLVYTRISSP FGIRMHPILH TWRLHTGIDY
301 AAPQGTFPVA SADGVITFKG RKGGYGNAMV IRHANGVETL YAHLSAFSQA
351 QGNVRGGEVI GFVGSTGRST GPHLHYEAR NGQPNPVSFV ALPTFELTQA
401 DKAAPFAQKQ KADALLARLR GIPVTVSQSD *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1237>:

m297.seq

```

1 ATGGCTGTCT TCCCACCTTC GGCAAAACAT CGGAAATACG CGCTGCGTGC
51 GCTTGCCGTT TCGATTATTT TGGTGTCGGC GGCATACATT GCTTCGACAG
101 AGAGGACGGA GCGCGTCAGA CCGCAGCGCG TGGAAACAAA TCTGCCGCCG
151 CTGTCTTGGG GCGGCGAGCG CGTTCAGACG GCATATTGGG TGCAGGAGGC
201 GGTGCAGCCG GCGGACTCGC TGGCGGACGT GCTGGCGCGT TCGGGTATGG
251 CGCGGGACGA GATTGCCCGA ATCAGGAAA AATATGGCGG CGAAGCCGAT
301 TTGCGGCATT TGCCTGCCGA CCAGTCGGTT CATGTTTTGG TCGGCGGCGA
351 CGGCGGCGCG CGCGAAGTGC AGTTTTTTAC CGACGAAGAC GGCAGGCGCA
401 ATCTGGTcGC TTTGGAAAAA AAAGGCGGCA TATGGCGGCG GTCGGCTTCT
451 GAGGCGGATA TGAAGGTTTT GCCGACGCTG CGTTCGGTCG TGGTCAAAAC
501 GTCGGCGCGC GGTTCGCTGG CGCGGGCGGA AGTGCCCGTC GAAATCCGCG
551 AATCCTTAAG CGGGATTTTT GCCGGCCGCT TCAGCCTTGA CGGTTTGAAG
601 GAAGGCGATG CCGTGCGCCT GATGTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG GCGGCGGATA TTTTGGCGGC TGAAGTCGTT AAGGCGGCGA
701 CAAGGCATCA GCGCTTCTAT TACCGTTCGG ACAAGGAAGG CGGAGGGGGC
751 GGCATATTAT ATGATGAAGA CGGCAAGGTG TTGCAGGAAA AAGGCGGCTT
801 CAACATCGAG CCGCTGGTCT ATACGCGCAT TTCTTCGCCG TTCGGCTACC
851 GTATGCACCC CATCCTGCAC ACATGGCGGC TGCACACGGG CATCGATTAT
901 GCCGCACCGC AGGGAACGCC GGTCAAGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGCG GATACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GAAACGCTG TACGCGCACT TGAGCGCGTT TTCGCAGGCG
1051 GAAGGCAATG TGC GCGGCGG CGAGGTCATC GGTTTTGTG GTTTCGACCGG
1101 GCGTTCGACC GGGCCGCACC TGCATTACGA GGC GCGCATC AACGGGCAGC
1151 CCGTCAATCC TGTTCGGTC GCATTGCCGA CACCCGAATT GACGAGGCG
1201 GACAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1238; ORF 297>:

m297.pep

```

1 MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTERTERV PQRVEQNLPP
51 LSWGSGVQT AYWVQEAQVP GDSLADVLAR SGMARDEIAR ITEKYGGEAD
101 LRHLRADQSV HVLVGGDGGA REVQFFTDED GERNLVALEK KGGIWRRSAS
151 EADMKVLPPL RSVVVKTSAR GSLARAEPV EIRESLSGIF AGRFSLDGLK

```

687

201 EGDVRLMYD SLYFHGQOVA AGDILAAEVV KGGTRHQAFY YRSDKEGGGG
 251 GNYDEDEGKV LQEKGGFNIE PLVYTRISSP FGyRMHPILH TWRLHTGIDY
 301 AAPQGTTPVRA SADGVITFKG RGGYGNAV M IRHANGVETL YAHLSAFSQA
 351 EGNVRGGEVI GFVGSTGRST GPHLHYEARI NGQPVNPVSV ALPTPELTQA
 401 DKAFAAQKQ KADALLARLR GIPVTVSQSD *

m297/g297 97.9% identity in 430 aa overlap

	10	20	30	40	50	60
m297.pep	MAVFPLSAKHKYALRALAVSIILVSAAYIASTERTERVRPQORVEQNLPLPSWGGSGVQT					
g297	MAVFPLSAKHKYALRALAVSIILVSAAYIASTEGTERVRPQORVEQKLPPLSWGGNGVQT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m297.pep	AYWVQEAVQPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGDGGGA					
g297	AYWVQEAVQPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGDGSA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m297.pep	REVQFFTDDEGERNLVALEKKGGIWRSSASEADMKVLP TLRSVVVKTSARGSLARAEVVPV					
g297	REVQFFTDDEGERNLVALEKKGGIWRSSASDADMKVLP TLRSVVVKTSARGSLARAEVVPV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m297.pep	EIRESLSGIFAGRFSLDGLKEGDAVRLMYDSLYFHGQOVAAGDILAAEVVKGGTRHQAFY					
g297	EIRESLSGIFAGRFSLDGLKEGDAVRLLYDSLYFHGQOVAAGDILAAEVVKGGTTHQAFY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m297.pep	YRSDKEGGGGGNYDEDEGKVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY					
g297	YRSDKEGGGGGNYDEDEGKVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY					
	250	260	270	280	290	300
	310	320	330	340	350	360
m297.pep	AAPQGTTPVRASADGVITFKGRKGGYGNAV MIRHANGVETLYAHLSAFSQAEGNVRGGEVI					
g297	AAPQGTTPVRASADGVITFKGRKGGYGNAV MIRHANGVETLYAHLSAFSQAQGNVRGGEVI					
	310	320	330	340	350	360
	370	380	390	400	410	420
m297.pep	GFVGSTGRSTGPHLHYEARINGQPVNPVSV ALPTPELTQADKAFAAQKQKADALLARLR					
g297	GFVGSTGRSTGPHLHYEARINGQPVNPVSV ALPTPELTQADKAFAAQKQKADALLARLR					
	370	380	390	400	410	420
	430					
m297.pep	GIPVTVSQSDX					
g297	GIPVTVSQSDX					
	430					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1239>:

a297.seq

1	ATGGCTGTCT	TCCCACTTTC	GGCAAAACAT	CGGAAATACG	CGCTGCGCGC
51	GCTTGCCGTT	TCGATTATTT	TGGTGTCGGC	GGCATAACATT	GCTTCGACAG
101	AGAGGACGGA	GCGCGTCAGA	CCGACGCGCG	TGGAACAAAA	ACTGCCGCCG
151	CTGTCTTGGG	GCGGCAGCGG	TGTTACAGACG	GCATATTGGG	TGCAGGAGGC
201	GGTGCAGCCA	GGCGACTCGC	TGGCGGACGT	GCTGGCGCGT	TCGGGTATGG
251	CGCGGGACGA	AATTGCCCGA	ATAACGGAAA	AATATGGCGG	CGAAGCCGAT
301	TTGCGGCATT	TGCGTGCCGA	CCAGTCGGTT	CATGTTTTGG	TCGGCGGCGA
351	CGCGGCGCG	CGCGAAGTGC	AGTTTTTTAC	CGACGAAGAC	GGCGAGCGCA
401	ATCTGGTCGC	TTTGGAAAAA	AAAGGCGGCA	TATGGCGGCG	GTCGGCTTCT
451	GAGGCGGATA	TGAAGTTTTT	GCCGACGCTG	CGTTCGGTCG	TGGTCAAAAC
501	GTCGCGCGCG	GGTTCGCTGG	CGCGGGCGGA	AGTGCCCGTC	GAAATTCGCG

```
551 AATCCTTAAG CGGGATTTTC GCCGGCCGCT TCAGCCTTGA TGGTTTGAAG
601 GAAGGCGATG CCGTGCGCCT GATTTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG GCGGGCGATA TTCTGGCGGC GGAAGTCGTT AAGGGCGGCA
701 CAAGGCATCA GCGGTTCTAT TACCGTTCGG ACAAGGAAGG AGGAGGGGCG
751 GGCAATTATT ACGATGAAGA CGGCAGGGTG TTGCAGGAAA AAGGCGGCTT
801 CAACATCGAG CCACTGGTCT ATACGCGCAT TTCTTCGCCG TTCGGCTACC
851 GTATGCACCC CATCTGCAC ACTTGGCGGC TGCACACGGG CATCGATTAT
901 CCCGCACCGC AGGGAACGCC GGTCAGGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGTG GCTACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAAACGCTG TATGCGCACT TGAGCGCGTT TTCTCAGGCA
1051 GAAGGCAATG TCGCGGCGG CGAGGTCATC GGTTTTGTG GTTCGACCGG
1101 GCGTTCGACG GGGCCGCACT TGCATTACGA GCGCGGCATC AATGGGCAGC
1151 CCGTCAATCC TGTTTCGGTC GCATTGCCGA CACCCGAATT GACGCAGGCG
1201 GACAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA
```

This corresponds to the amino acid sequence <SEQ ID 1240; ORF 297.a>:

```
a297.pep
1 MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTERTERV RPORVEQKLPP
51 LSWGGSGVQT AYWVQEAQVP GDSLADVLAR SGMARDEIAR ITEKYGGEAD
101 LRHLRADQSV HVLVGGDGGG REVQFFTTDED GERNLVALEK KGGIWRRSAS
151 EADMKVLP TLRSVVVKT SARGLSARAEVPV EIRESLSGIF AGRFSLDGLK
201 EGDVRLIYD SLYFHGQQVA AGDILAAEVV KGGTRHQAFY YRSDKEGGGG
251 GNYDEDEGRV LQEKGGFNIE PLVYTRISSP FGYRMHPILH TWRLHTGIDY
301 AAPQGTPVRA SADGVITFKG RKGGYGNVAM IRHANGVETL YAHLSAFSQA
351 EGNVRGGEVI GFVGTGRST GPHLHYEAR NGQPVNPVSV ALPTPELTQA
401 DKAFAAQKQ KADALLARLR GIPVTVSQSD *
```

m297/a297 99.3% identity in 430 aa overlap

```
10 20 30 40 50 60
m297.pep MAVFPLSAKHKRYALRALAVSIILVSAAYIASTERTERV RPORVEQNLPPLSWGGSGVQT
|||||
a297 MAVFPLSAKHKRYALRALAVSIILVSAAYIASTERTERV RPORVEQKLPPPLSWGGSGVQT
10 20 30 40 50 60

70 80 90 100 110 120
m297.pep AYWVQEAQVP GDSLADVLAR SGMARDEIAR ITEKYGGEAD LRHLRADQSV HVLVGGDGGG
|||||
a297 AYWVQEAQVP GDSLADVLAR SGMARDEIAR ITEKYGGEAD LRHLRADQSV HVLVGGDGGG
70 80 90 100 110 120

130 140 150 160 170 180
m297.pep REVQFFTTDEDGERNLVALEKKGGIWRRSASEADMKVLP TLRSVVVKT SARGSLARAEVPV
|||||
a297 REVQFFTTDEDGERNLVALEKKGGIWRRSASEADMKVLP TLRSVVVKT SARGSLARAEVPV
130 140 150 160 170 180

190 200 210 220 230 240
m297.pep EIRESLSGIFAGRFSLDGLKEGDAVRLMYDSLYFHGQQVAAGDILAAEVVKGGRHQAFY
|||||
a297 EIRESLSGIFAGRFSLDGLKEGDAVRLIYDSLYFHGQQVAAGDILAAEVVKGGRHQAFY
190 200 210 220 230 240

250 260 270 280 290 300
m297.pep YRSDKEGGGGGNYDEDEGKVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY
|||||
a297 YRSDKEGGGGGNYDEDEGRVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY
250 260 270 280 290 300

310 320 330 340 350 360
m297.pep AAPQGT PVRASADGVITFKGRKGGYGNVAMIRHANGVETLYAHLSAFSQAEGNVRGGEVI
|||||
a297 AAPQGT PVRASADGVITFKGRKGGYGNVAMIRHANGVETLYAHLSAFSQAEGNVRGGEVI
310 320 330 340 350 360
```

689

	370	380	390	400	410	420
m297.pep	GFVVGSTGRSTGPHLHYEARINGQPVNPVSVALPTPELTQADKAAFAAQKQKADALLARLR					
a297	GFVVGSTGRSTGPHLHYEARINGQPVNPVSVALPTPELTQADKAAFAAQKQKADALLARLR					
	370	380	390	400	410	420
	430					
m297.pep	GIPVTVSQSDX					
a297	GIPVTVSQSDX					
	430					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1241>:

g298.seq

```

1  ATGAAAAACT TTCTTTCCCT TTTGCGCTCC ATACTGATGT CTGCCCTGAT
51  TGCCGTGTGG TTCAGCCAAA ACCCCATCAA CGCCTACTGG CAGCAGACCT
101 ACCACCGCAA CAGCCCGCTC GAACCGCTTG CCGCCTACGG ATGGTGGCGG
151 AGCGGAGCGG CGTTGCAAGA AAACGCCTAC GCCCTTTCAG ACGGCATCAA
201 AACCTTCCTG TCCGGCGAAA cgcgcgcac ggCTCAAGAC GGCGGTTCTG
251 CAGATATGCC GCCTGAAGCC GCCGCATCCG AAGCCGCCCC GCCGCGCGGC
301 GGAACAGAAT GGAACAAGG CACCGAAGCC GCCGCCGTCC GCAGCGGCGA
351 CAAAGTCTTT TTCGCCGAG ATTGCTGAT GCAGGGCGTT GCGCCTTTCG
401 TGCAAAAAGC CCTGAAACAG CAATACGGCA TCGAATCCGC CAACCTCAGC
451 AAACAAAGCA CGGGGCTTTC CTATCCCTCA TTCTTCGACT GGCCGAAAAC
501 GATTGAAGAA ACCTGAAAAA AACATCCCGA AATCAGCGTA CTCGCCGTCT
551 TCCTCGGCCC GAACGACCCG TGGGATTTC CCGTCGGCAA ACGCTACCTC
601 AAATTCGCTT CCGACGAATG GCGCAAGAA TACCTGAAAC GCGTCGACCG
651 CATCCTTGAA GCCGCACACA CGCACC CGT CCAAGTCGTC TGGCTCGGCA
701 TCCCTTACAT GAAAAAAGTC AAGCTCGACG GTCAGATGCG CTACCTCGAC
751 AAATGCTTT CGGAACACTT GAAAGGCAAA ATCATCTCTA TTCCCACCGC
801 GCAAAACACT AGCGGCGGGA AAGGCCGCTA CACCGATTCC GTCAACGTCA
851 ACGGCAAACC CGTCCGCTAC CGCAGTAAGG ACGGCATACA CTTTACCGCC
901 GAAGGACAAA AACTGCTGGC GGAAAAATA ATGGAAAAAA TCGTTTTTGA
951 ACCGAGTACG CAACCATCAA GTACACAGCC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1242; ORF 298.ng>:

g298.pep

```

1  MKNFLSLFAS ILMSALIAVW FSQNPINAYW QQTYHRNSPL EPLAAYGWWR
51  SGAALQENAY ALSDGIKTFL SGETPPTAQD GGSADMPPEA AASEAAPPA
101 GTEWKQGTET AAVRSGDKVF FAGDSLMOGV APFVQKSLKQ QYGIESANLS
151 KQSTGLSYPS FFDWPKTIEE TLKKHPEISV LAVFLGPNDP WDFPVGKRYL
201 KFASDEWAQE YLKRVDRILE AAHTRVQVW WLGIPLYMKV KLDGQMRYLD
251 KLLSEHLKKG IILIPTAOTL SGGKGRYTDV VNVNGKPVRY RSKDGIHFTA
301 EGQKLLAEKI MEKIVFEPST QPSSTQP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1243>:

m298.seq

```

1  ATGAAAAACT TTCTTTCCCT TTTCTCCTCC ATACTGATGT CTGCCCTGAT
51  TGCCGTGTGG TTCAGCCAAA ACCCCATCAA CGCCTACTGG CAGCAGACCT
101 ACCACCGCAA CAGCCCGCTC GAACCGCTTG CCGCCTACGG ATGGTGGCGG
151 AGCGGTGCGG CGTTGCAAGA AAACGCCTAC GCCCTTTCAG ACGGCATCAA
201 AGCCTTCCTG TCCGGCGAAA CGCCGCGGAC GGCTCAAGAC GGCGGTTCTG
251 CAGATATGCC GTCTGAAGCC GCCGCATCCG AAGCCGTCCC TCAAACCGGT
301 GAAACAGAAT GGAACAAGA CACCGAAGCC GCCGCCGTCC GCAGCGGCGA
351 CAAAGTCTTT TTTGTGCGCG ACTCGCTGAT GCAGGGCGTT GCGCCCTTCG
401 TGCAAAAAGC CCTGAAACAG CAATACGGCA TCGAATCCGT CAACCTCAGC
451 AAACAAAGCA CGGGCTGTC CTACCCCTCA TTCTTCGACT GGCCGAAAAC
501 GATTGAAGAA ACCCTGCAA AACATCCCGA AATCAGCGTA CTCGCCGTCT
551 TCCTCGGACC GAACGACCCG TGGGATTTC CCGTCGGCAA ACTCTATCTC
601 AAATTCGCTT CCGACGAATG GCGCAAGAA TACCTGAAAC GTGTCGACCG
651 CATCCTTGAA GCCGCACACA CGCACC CGT CCAAGTCGTC TGGCTCGGCA
701 TCCCTTACAT GAAAAAAGCC AAGCTCGACG GACAGATGCG CTACCTAGAC
751 AAATGCTTT CGGAACATTT GAAAGGCAAA ATCATCTCTA TTCCCACCA
801 GCACACCTG AGCGGCGGGA AAGACCCTA CACCGACTCC GTCAACGTCA
851 ACGGCAAACC CGTCCGCTAC CGCAGCAAGG ACGGCATACA CTTTACCGCC
901 GAAGGACAAA AACTGCTGGC GGCAAAAATA ATGGAAAAAA TCGTTTTTGA
951 ACCAAGTACG CAACCATCAA GTACACAGCC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1244; ORF 298>:

m298.pep

```

1  MKNFLSLFSS ILSALIAVW FSONPINAYW QQTYHRNSPL EPLAAYGWWR
51  SGAALQENAY ALSDGIKAFI SGETPPTAQD GGSADMPSEA AASEAVPQTG
101 ETEWKQDTEA AAVRSGDKVF FVGDSLMOGV APFVQKSLKQ QYGIESVNLS
151 KQSTGLSYPS FFDWPKTIEE TLQKHPEISV LAVFLGPNPD WDFPVGKLYL
201 KFASDEWAQE YLKRVDRIE AAHTRVQVW WLGI PYMKKA KLDGQMRYL
251 KLLSEHLKKG IILIPHTHTL SGGKDRYTDV NVNKGKPVRY RSKDGIHFTA
301 EGQKLLAAKI MEKIVFEPST QPSSTQP*

```

m298/g298 94.8% identity in 327 aa overlap

	10	20	30	40	50	60
m298.pep	MKNFLSLFSSILMSALIAVWFSONPINAYWQQTYHRNSPLEPLAAYGWWRS					
g298	MKNFLSLFASILMSALIAVWFSONPINAYWQQTYHRNSPLEPLAAYGWWRS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m298.pep	ALSDGIKAFISGETPPTAQDGGSDMPSEAAASEAVPQTGETEWKQDTEAAAVRSGDKVF					
g298	ALSDGIKIFLSGETPPTAQDGGSDMPPEAAASEAAPAGGTEWKQGTAAAVRSGDKVF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m298.pep	FVGDSLMOGVAPFVQKSLKQYQYIESVNLSKQSTGLSYPSFFDWPKTIEETLQKHPEISV					
g298	FAGDSLMOGVAPFVQKSLKQYQYIESANLSKQSTGLSYPSFFDWPKTIEETLKKHPEISV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m298.pep	LAVFLGPNPDWDFPVGKLYLKFASDEWAQEYLKRVDRIEAAHTRVQVWVWLGIPYMKKA					
g298	LAVFLGPNPDWDFPVGKRYLKFASDEWAQEYLKRVDRIEAAHTRVQVWVWLGIPYMKKV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m298.pep	KLDGQMRYLKLLSEHLKGGKIILIPHTHTLSGGKDRYTDVNVNKGKPVRYRSKDGIHFTA					
g298	KLDGQMRYLKLLSEHLKGGKIILIPHTHTLSGGKGRYTDVNVNKGKPVRYRSKDGIHFTA					
	250	260	270	280	290	300
	310	320				
m298.pep	EGQKLLAAKIMEKIVFEPSTQPSSTQPX					
g298	EGQKLLAEKIMEKIVFEPSTQPSSTQPX					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1245>:

a298.seq

```

1  ATGAAAAACT TTCTTTCCCT TTTCCGCTCC ATACTGATGT CTGCCCTGAT
51  TGCCGTGTGG TTCAGCCAAA ACCCCATCAA CGCCTACTGG CAGCAGACCT
101 ACCACCGCAA CAGCCCGCTC GAACCGCTTG CCGCTACGG ATGGTGGCGG
151 AGCGGTGCGG CATTGCAAGA AAACGCCTAC GCCCTTTCAG ACGGCATCAA
201 AGCCTTCTTG TCCGGCGAAA CGCCGCCGAC GGCTCAAGAC GCGGTTCCGG
251 CAGATATGCC GTCTGAAGCC GCCGCACCCG AAACCGCCCC TCAAACCTGGC
301 GAAACAGAAAT GGAAACAAAA CACCGAAGCC GCCGCCGTCC GAACAGGGGA
351 CAAAGTCTTT TTCGCCGGCG ACTCGCTGAT GCAGGGCGTT GCACCTTCG
401 TGCAAAAAAG CCTGAAACAG CAATACGGCA TCGAATCCGT CAACCTCAGC
451 AAACAAAGCA CGGGGCTGTC CTACCCCTCA TTCTTCGACT GGCCGAAAAA
501 GATTGAAGAA ACCCTGAAAA AACATCCCGA AATCAGCGTG CTCGCCGTCT
551 TCCTCGGTCC GAACGACCCG TGGGATTTC CCGTTGGCAA ACGCTACCTC
601 AAATTCGCTT CCGACGAATG GGCGCAAGAA TACCTGAAAC GCGTCGACCG
651 CATCCTTGAA GCCGCACACA CGCACTACGT CCAAGTCGTC TGGCTCGGCA
701 TCCCCTACAT GAAAAAAGCC AAGCTCGACG GACAGATGCG CTACCTAGAC

```

```

751  AAAGTCTTT  CGGAATATTT  GAAAGGCAAA  ATCATCCTGA  TTCCCACCGC
801  GCACACCCCTG AGCGGCGGGA  AAGACCGCTA  CACCGACTCC  GTCAACGTCA
851  ACGGCAAACC  CGTCCGCTAC  CGCAGCAAGG  ACGGCATACA  CTTTACCGCC
901  GAAGGACAAA  AACTGCTGGC  GGCAAAAATA  ATGGAAAAAA  TCGTTTTTGA
951  ACCAAGTACG  CAACCATCAA  GTACACAGCC  ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1246; ORF 298.a>:

```

a298.pep
1  MKNFLSLFAS  ILSALIAVW  FSQNPINAYW  QQTYHRNSPL  EPLAAYGWWR
51  SGAALQENAY  ALSDGIKAF  LSGETPPTAQD  GGSADMPSEA  AAPETAPQTG
101  ETEWKQNTA  AAVRTGDKV  F FAGDSLMOGV  APFVQKSLKQ  QYGIESVNL
151  KQSTGLSYPS  FFDWPKTIE  E TLKKHPEISV  LAVFLGPNDF  WDFPVGKRYL
201  KFASDEWAE  YLKRVDRI  L AAHTHYVQV  V WLGI P YMKKA  KLDGQMR YLD
251  KLLSEYLGK  I ILIPTAHT  L SGGKDRYTDS  VNVNGKPVRY  RSKDGIHFTA
301  EGQKLLAAKI  MEKIVFEP  ST QPSSTQP*

```

m298/a298 96.3% identity in 327 aa overlap

```

m298.pep      10      20      30      40      50      60
MKNFLSLFSSILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY
|||||:|||||
a298           10      20      30      40      50      60
MKNFLSLFASILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY

m298.pep      70      80      90      100     110     120
ALSDGIKAFSLSGETPPTAQDGGSDAMPSEAAASEAVPQTGETEWKQDTEAAAVRSGDKVF
|||||:|||||
a298           70      80      90      100     110     120
ALSDGIKAFSLSGETPPTAQDGGSDAMPSEAAAPETAPQTGETEWKQNTAEEAAVRTGDKVF

m298.pep      130     140     150     160     170     180
FVGDSLMOGVAPFVQKSLKQYQYIESVNLKQSTGLSYPSFFDWPKTIEETLQKHPEISV
|:|||||
a298           130     140     150     160     170     180
FAGDSLMOGVAPFVQKSLKQYQYIESVNLKQSTGLSYPSFFDWPKTIEETLQKHPEISV

m298.pep      190     200     210     220     230     240
LAVFLGPNDFWDFPVGKLYLKFADEWAEYLKRVDRIEAAHTRVQVWVWLGIPYMKKA
|||||:|||||
a298           190     200     210     220     230     240
LAVFLGPNDFWDFPVGKRYLKFADEWAEYLKRVDRIEAAHTRVQVWVWLGIPYMKKA

m298.pep      250     260     270     280     290     300
KLDGQMR YLDKLLSEHLKGIILIPTHTLSSGGKDRYTDSVNVNGKPVRYRSKDGIFHTA
|||||:|||||
a298           250     260     270     280     290     300
KLDGQMR YLDKLLSEYLGKIIILIPTAHTLSSGGKDRYTDSVNVNGKPVRYRSKDGIFHTA

m298.pep      310     320
EGQKLLAAKIMEKIVFEPSTQPSSTQPX
|||||:|||||
a298           310     320
EGQKLLAAKIMEKIVFEPSTQPSSTQPX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1247>:

```

g299.seq
1  ATGAACCCCA  AACACTTCAT  CGCATTITTC  GCCCTGTTTG  CCGCCACGCA
51  GGCAGAAGCC  CTGCCCCTCG  CCTCCGTCAG  CCCCACACCC  GTTACCGTTT
101  CCCCCTCCGC  CCCCTACACC  GATACAAACG  GGCTGCTGAC  CGACTACGGC
151  AACGCCGCCG  CCTCGCCTTG  GATGAAAAAA  CTCCGATCCG  TCGCACAAGG
201  CAGCGGCGAG  GCCTTCGCGA  TCCTGCAAAT  CGGCGACTCG  CATACCGCCG
251  GCGACTTCTT  TACCGACGCC  CTGCGCAAA  GCCTGCAAAA  AACATGGGGC
301  GACGGCGGCA  TAGGCTGGGT  TTACCCCGCC  AACGTCAAAG  GGCAGCGCAT
351  GCGGCGCGTC  CGTCACAGCG  GCAACTGGCA  AAGCTTCACC  AGCAGGAACA
401  ATACCGGAGA  TTTCCCGCTC  GCGGCGATCC  TCGCCCAAC  CCGCAGCGGC
451  GCGGCGATGA  CCCTGACCGC  GTCTGACGGC  AAAACCGGCA  AACAGCGCGT

```

501	TTCCTGTTT	GCCAAACCGC	TGCTCGCCGA	ACAAACCCGT	ACCGTCAACG
551	GCAACACCGT	CTCCGCCAAC	GGCGGCGCGT	GCAGGTACT	GGATACGGGC
601	GCGGCATCGC	CCCTGGCCAT	ACAGACCGAA	ATGCCGTGGG	ACATCGGCTT
651	CATCAACATC	GAAAATCCCG	CCGGCGGCAT	TACCGTTTCC	CGCATGGGTA
701	TCAACGCGCG	ACAATTAGCC	CAGTGGTCGA	AATGGCGCTC	CGACCCGTAT
751	AACGACCTTG	CCCAAAACGG	GCCCGATTGG	GTTATCCTTT	CCTACGGCAC
801	CAACGAAGCC	TCCAACAACA	ACATCGACAT	TGCCGATACC	GAAACAAAAT
851	GGCTGGATAC	CGTCCGCCAA	ATCCGCGACA	GCCTGCCCGC	CGCCGGCATC
901	CTCATCATCG	GCGCGCCCGA	ATCCCTGAAA	AACACGCTCG	CGGTATCGGG
951	CACGCGCCCC	TCTCTCTGA	CGCAAGTCCA	ACAGATGCAG	CGGCGCGTGC
1001	CCCGTCAGGG	GCAGACGATG	TTTTGGTCTT	GGCAAAACGC	AATGGGCGGC
1051	ATATGTCAGCA	TGAAAAAAGT	GCTCAACCGA	GGATGGGCGG	CCAAAGACGG
1101	CGTACACTTC	TCCGCCCAAG	GCTACCCGGG	CGCGGCGGAA	ATGCTTGGCG
1151	ACAGCCTCGA	GAAACTCGTC	CGCCGCGCGC	CAATCAGGCA	ATAA

This corresponds to the amino acid sequence <SEQ ID 1248; ORF 299.ng>:

g299.pcp

1	<u>MNPKHFIASF</u>	<u>ALFAATQAEA</u>	LPVASVSPDT	VTVSPSPAPYT	DTNGLLLTDYG
51	NAAASPWMKK	LRSVAQGSSE	AFRIQLQIGDS	HTAGDFFTDA	LRKRLQKWTWG
101	DGGIGWVYP	NVKGQRMMAV	RKSGNWSQST	SRNNTGDFPL	GGILAQKTSGS
151	GMTLTASDG	KTGKQRVSLF	AKPLLAEBQL	TVNGTIVTSAN	GGGWQVLDTG
201	AALPLAIQTE	MPWDIGFINI	ENPAGGITVS	AMGINGAQLT	QWSKWRADRM
251	NDLAQTGADL	VILSYGTNEA	FNNNDIADT	EQKWLDTVRQ	IRDSLPAAGI
301	LIIGAPESLK	NLTGVCGRTP	VALLTEVQQMQ	RRVARQGGTM	FWSQWNAAMGG
351	ICSMKNWLNQ	GWAACKDVGHF	SAQGYVRAAE	MLADSLEELV	RAAAIRO*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1249>:

m299.seq

1	ATGAACCCCA	AACACCTCAT	CGCATTTTCC	GCCTATTTCG	CCGCCACGCA
51	GGCAGAAGCC	CTACCTGTGC	CCTCCGTCAG	CCTCGACACC	GTTACCGTTT
101	CCCCGTCGCC	CCCCTACACC	GATACAACGC	GGCTGCTGAC	CGCATACGGC
151	AAGCGCTCCG	CCTCGCCTTG	GATGAAAAAA	CTCAAACTCG	TGCGACAAGG
201	CAGCGGCGAG	ACCTTCCGTA	TCCTGCAAAT	CGGCGACTCG	CATACCGCCG
251	GGCACTTCTT	TACCGACAGC	CTGCGCAAA	GCCTGCAAAA	AACTTGGGGC
301	GACGGCGGCA	TAGGCTGGGT	TTACCCCGCC	AACGTCAAAG	GGCAGCGCAT
351	GGCGGCGGTC	CGGCACAACG	GTAACCTGCA	AGCCTCAC	AGCAGGAACA
401	ACACCGGAGA	CTTCCGCTC	GGCGGCATCC	TCGCCCACAC	CGGCAGCGGC
451	GGCAGATGTA	CCCTGACCGC	ATCGGACGGC	ATAGCAAGCA	AGCAGCAACG
501	TTCCCTGTTT	GCCAAACCCC	TGCTTGCCGA	ACAAACCCCTG	ACCGTCAACG
551	GCAACACCGT	TCCGCCAAC	CGCGGCGGCT	GGCAGGTACT	GGATACGGGC
601	GCGGCACTGC	CCCTGACCAT	ACACACCGAA	ATGCCGTGGG	ACATCGGCTT
651	CATCAACATC	GAAAACTCCG	CGCGCGGCAT	TACCGTTTCC	GGCATGGGTA
701	TCAACGGCGC	ACAATTAACC	CAGTGGTTCG	AATGGCGTGC	CGACCGGTAG
751	AACGACCTCG	CCCAACCGG	CGCGGATTTG	GTTATCTCTT	CTACCGGCAC
801	CAACGAAGCT	TTCAACAACA	ACATCGACAT	TGCCGACACC	GAACAAAAAT
851	GGCTGGATAC	CGTCCGCCAA	ATCCCGCACA	GCCTGCCTCG	CGCCGGCATC
901	CTCATCATCG	GCGCACCCGA	ATCCCTGAAA	AACACGCTCG	CGGTATGCGC
951	CACACGCCCC	TCCCGCTTGA	CCGAAGTCCA	ACAGATGCAG	CGCGCGGTGC
1001	CCCGTCAGGG	GCAGACGATG	TTCTGGTCTT	GGCAAAACGC	CATGGGCGGC
1051	ATATGCAGCA	TGAAAAACTG	GCTCAACCGG	GGATGGGCGC	CCAAAGACGG
1101	CGTACACTTC	TCCGCGCAAG	GCTACCCGGA	CGCGGCGGAA	ATGCTCGCCG
1151	ACAGCCTCGA	AGAACTCGTC	CGCTCCGCTG	CAATCAGGCA	ATAA

This corresponds to the amino acid sequence <SEQ ID 1250; ORF 299>:

m299.pgp

1	<u>MNP</u> KHLIAF <u>S</u>	<u>AL</u> FAATQAE <u>A</u>	LPVASVSLDT	VTVSPSAPYT	DTNGLLTDYG
51	NASASIPWMKK	LQSVAQGSSE	TFRILQIGDS	HTAGDFFTDS	LRKRLQKWTG
101	DGGIGWVYP	NUVGQRMVA	RKHNWQSLT	SRNNTGDFPL	GGILATGSG
151	GSMTLTASD	ISAKQRVSLF	APHLLEAQT	TVNGNTVSAN	GGGWQVLDTG
201	AALPLTIHTE	MPWDIGFINI	ENPAGGITVS	AMGINGAQLT	QWSKWRADRM
251	NDLAQTGADL	VILSYGTNEA	FNNNDIADT	EQKWNLDTVRQ	IRDSLPAAGI
301	LIIGAPESLK	NTLGVCGRTP	VLRTVEVQMQ	RRVARQQTGV	FWSQWNAAMGG
351	ICSMKNWLNQ	GWAACKDVHF	SAGKYRRAAE	MLADSLEELV	RSAAIRO*

m299/g299 95.5% identity in 397 aa overlap

m299.pep MNPKHLIAFSALFAATQAEALPVASVSLDTVTVSPSAPYTDINGLLTDYGNASASPWMKK

g299	MNPKEHFIASFALFAATQAEALPVASVSPDVTVTSPSAPYTDNGLLTDYGNAAASPWMKK
	10 20 30 40 50 60
m299.pep	LQSV AQSGSETFRILQIGDSHTAGDFFTDLSLRKRLQKTWGDGGIGWVYPANVKGQRMMAAV
g299	LRSV AQSGGEAFRILQIGDSHTAGDFFTDALRKRLQKTWGDGGIGWVYPANVKGQRMMAAV
	70 80 90 100 110 120
m299.pep	RHNGNWQSLTSRNNTGDFPLGGILAHGTSGGSMTLTASDGIASKQRVSLFAKPLLAEQTL
g299	RHSGNWQSFTRSNNTGDFPLGGILAHGTSGGSMTLTASDGKTGKQRVSLFAKPLLAEQTL
	130 140 150 160 170 180
m299.pep	TVNGNTVSANGGGWQVLDTGAAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT
g299	TVNGNTVSANGGGWQVLDTGAAALPLAIQTEMPWDIGFINIENPAGGITVSAMGINGAQLT
	190 200 210 220 230 240
m299.pep	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTEQKWLDTVRQIRDSLPAAGI
g299	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTEQKWLDTVRQIRDSLPAAGI
	250 260 270 280 290 300
m299.pep	LIIGAPESLKNLTGVCGTRPVRLTEVQQMQRVARQGQTMFWSWQNAMGGICSMKNWLNQ
g299	LIIGAPESLKNLTGVCGTRPVLLTEVQQMQRVARQGQTMFWSWQNAMGGICSMKNWLNQ
	310 320 330 340 350 360
m299.pep	GWAAKDGVHFSAGYRRAEMLADSLEELVRSAAIRQX
g299	GWAAKDGVHFSAGYRRAEMLADSLEELVRAAAIRQX
	370 380 390

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1251>:

a299.seq

```

1  ATGAACCCCA AACACCTCAT CGCATTTTCC GCCCTATTCG CCGCCACGCA
51  GGCAGAAGCC CTACCTGTCG CCTCAGTCAG CCTCGACACC GTTACCGTTT
101 CCCCCTCCGC CCCCTACACC GATACAAACG GGCTGCTGAC CGACTACGGC
151 AACGCTCCG CCTCGCCTG GATGAAAAA CTCCAATCCG TCGCACAAGG
201 CAGCGGCGAG ACCTTCCGTA TCCTGCAAAT CGGCGACTCG CATACCGCCG
251 GCGACTTCTT TACCGACAGC CTGCGCAAAC GCCTACAAA AACTTGGGGC
301 GACGCGGGCA TAGGCTGGGT TTACCCCGCC AACGTCAAAG GGCAGCGCAT
351 GCGGCGGTC CGGCACAACG GTAACGGCA AAGCCTCACC AGCAGGAACA
401 ACACCGGAGA CTTCCTGCTC GCGGCGATCC TCGCCACAC CGGCAGCGGC
451 GGCAGCATGA CCCTGACCGC ATCGGACGGC ATAGCAAGCA AGCAGCGCGT
501 TTCCCTGTTT GCCAAACCCC TGCTTGCCGA ACAAACCTG ACCGTCAACG
551 GCAACACCGT CTCGCGCAAC GCGGCGGGCT GGCAGGTACT GGATACGGGC
601 GCGGCACTGC CCCTGACCAT ACACACCGAA ATGCCGTGGG ACATCGGCTT
651 CATCAACATC GAAATCCCG CCGCGGCGAT TACCGTTTCC GCGATGGGCA
701 TCAACGGCGC ACAATTAACC CAGTGGTCGA AATGGCGTGC CGACCGTATG
751 AACGACCTTG CCCAAACCGG CGCCGATCTA GTCATCCTTG CCTACGGTAC
801 CAACGAAGCC TTCGGCGACA ACATCGACAT TGCCGATACC GAACAGAAAT
851 GGCTGGATAC CGTCCGCCAA ATCCGCGACA GCCTACCTGC CGCGGCATC
901 CTCATCATCG GCGCGCCCGA ATCCCTGAAA AACACGCTCG GCGTATGCGG
951 CACACGCCCC GTCCGCTGA CCGAAGTCCA ACAGATGCAG CGGCGCATCG
1001 CCCGTCAGGG GCAGACGATG TTCTGGTCTT GGCAAAACGC GATGGGCGGC
1051 GTTTCAGCA TGAAAACTG GCTCAACCAC GGATGGGCGG CCAAAGACGG
1101 CGTACACTTT TCCGCCAAAG GCTACCAACG GTCGGCGGAA ATGCTCGCCG
1151 ACAGCCTCGA AGAAGCTCGT CGCTCCGCTG CAATCAGGCA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 1252; ORF 299.a>:

```
a299.pep
  1  MNPKHLIAFS ALFAATQAEA LPVASVSLDT VTVSPSAPYT DTNGLLTDYG
 51  NASASPWMKK LQSV AQSGE TFRILQIGDS HTAGDFFTD LKRLQKTWG
101  DGGIGWVPA NVKGQMAAV RHNGNWQSLT SRNNTGDFPL GGILAHTGSG
151  GSMTLTASDG IASKQVSLF AKPLLAEQTL TVNGNTVSAN GGGWQVLDTG
201  AALPLTIHTE MPWDIGFINI ENPAGGITVS AMGINGAQLT QWSKWRADRM
251  NDLAQTGADL VILAYGTNEA FGDNIDIADT EQKWLDTVRQ IRDSLPAAGI
301  LIIGAPESLK NTLGVCGRP VRLTEVQQMQ RRIARQGQTM FWSWQNAMGG
351  VCSMKNLNH GWAAKDGVHF SAKGYQSAE MLADSLEELV RSAAIRQ*
```

m299/a299 98.0% identity in 397 aa overlap

	10	20	30	40	50	60
m299.pep	MNPKHLIAFSALFAATQAEALPVASVSLDTVT	TVSPSAPYTD	TNGLLTDYGN	NASASPWMKK		
a299	MNPKHLIAFSALFAATQAEALPVASVSLDTVT	TVSPSAPYTD	TNGLLTDYGN	NASASPWMKK		
	70	80	90	100	110	120
m299.pep	LQSV AQSGE TFRILQIGDSHTAGDFFTD	SLRKRLQKTWG	GDGGIGWVYPANVKGQMAAV			
a299	LQSV AQSGE TFRILQIGDSHTAGDFFTD	SLRKRLQKTWG	GDGGIGWVYPANVKGQMAAV			
	130	140	150	160	170	180
m299.pep	RHNGNWQSLTSRNNTGDFPLGGILAHTGSGGSMTLTASDGIASKQVSLFAKPLLAEQTL					
a299	RHNGNWQSLTSRNNTGDFPLGGILAHTGSGGSMTLTASDGIASKQVSLFAKPLLAEQTL					
	190	200	210	220	230	240
m299.pep	TVNGNTVSANGGGWQVLDTGAAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT					
a299	TVNGNTVSANGGGWQVLDTGAAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT					
	250	260	270	280	290	300
m299.pep	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTEQKWLDTVRQIRDSLPAAGI					
a299	QWSKWRADRMNDLAQTGADLVILAYGTNEAFGDNIDIADTEQKWLDTVRQIRDSLPAAGI					
	310	320	330	340	350	360
m299.pep	LIIGAPESLKNTLGVCGRPVRLETVQQMQRRVARQGQTMFWSWQNAMGGICSMKNWLNQ					
a299	LIIGAPESLKNTLGVCGRPVRLETVQQMQRRRIARQGQTMFWSWQNAMGGVCSMKNLNH					
	370	380	390			
m299.pep	GWAAKDGVHFSAGYRRAEMLADSLEELVRSAAIRQX					
a299	GWAAKDGVHFSAGYQRSAEMLADSLEELVRSAAIRQX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1253>:

```
g302.seq
  1  ATGCACTCAA TATATTTTTT TAAGGAGAAG CAGATGAGTC AAACCGACGC
 51  GCGTCGTAGC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101  TGCCGCACCC GGTTACGCTT TTTATTATTT TCATTGTGTT ATTGCTGATT
151  GCCTCTGCCG TCGGTGCGTA TTTCGGACTA TCCGTCCCCG ATCCGCGTCC
201  TGTGTTGGGCG AAAGGACGTG CCGATGACGG TTGATTACAC GTTGTCAGCC
251  TGCTCGATGC CGACGGTTTG ATCAAAATCC TGACGCATAC CGTTAAAAAT
301  TTCACCGGTT TCGCGCCGTT GGAACGGTG TTGGTTTCTT TATTGGGCGT
```

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351  GGGGATTGCG  GAAAAATCGG  GCTTGATTTC  CGCATTAATG  CGCTTATTGC
401  TCACAAAATC  CCCACGCAAA  CTCACTACTT  TTATGGTTGT  TTTTACAGGG
451  ATTTTATCCA  ATACGGCTTC  TGAATTGGGC  TATGTCGTCC  TAATCCCTTT
501  GTCCGCCGTC  ATCTTTTATT  CGCTCGGCCG  CCATCCGCTT  GCCGGTTTGG
551  CTGCGGCTTT  CGCCGGCGTT  TCGGGCGGTT  ATTCGGCCAA  TCTGTTCTTA
601  GGCACAATCG  ATCCGCTCTT  GGCAGGCATC  ACCCAACAGG  CGGCGCAAAT
651  CATCCATCCC  GACTACGTCG  TAGGCCCTGA  AGCCAACCTG  TTTTTTATGG
701  CAGCCAGTAC  GTTTGTGATT  GCTTTGATTG  GTTATTTTGT  TACTGAAAAA
751  ATCGTCGAAC  CGCAATTGGG  CCCTTATCAA  TCAGATTTGT  CACAAGAAGA
801  AAAAGACATT  CGGCATTCCA  ATGAAATCAC  GCCTTTGGAA  TATAAAGGAT
851  TAATTTGGGC  AGGCGTGGTG  TTTGTTGCCT  TATCCGCCCT  ATTGGCTTGG
901  AGCATCGTCC  CTGCCGACGG  TATTTTTCGT  CATCTGAAA  CAGGATTGGT
951  TGCCGGTTCG  CCGTTTTTAA  AATCGATTGT  TGTTTTTATT  TTCTGTTGT
1001  TTGCGCTGCC  GGGCATTGTT  TATGGCCGGA  TAACCCGAAG  TTTGCGCGGC
1051  GAACGGGAAG  TCGTTAATGC  GATGGCCGAA  TCGATGAGTA  CTTTGGGACT
1101  TTATTTGGTC  ATCATCTTTT  TTGCCGCACA  GTTGTGCGCA  TTTTAAATT
1151  GGACGAATAT  TGGGCAATAT  ATTGCCGTTA  AAGGGGCGGT  GTTCTTAAAA
1201  GAAGTCGGCT  TGGGCGGCAG  TGTGTTGTTT  ATCGGTTTTA  TTTAATTGT
1251  TGCTTTTATC  AATCTGATGA  TAGGCTCCGC  CTCCGCGCAA  TGGGCGGTAA
1301  CTGCGCCGAT  TTTCTGCCCT  ATGCTGATGT  TGGCCGGCTA  CGCGCCCCAA
1351  GTCATTCAAG  CCGCTTACCG  CATCGGTGAT  TCCGTTACCA  ATATTATTAC
1401  GCCGATGATG  AGTTATTTTC  GGCTGATTAT  GGCGACGGTA  ATCAAATACA
1451  AAAAAGATGC  GGGCGTAGGC  ACGCTGATT  CTATGATGTT  GCCGTATTCC
1501  GCTTTCTTCT  TAATTGCATG  GATCGCCTTA  TTCTGCATT  GGGTATTGT
1551  TTTGGGTCTG  CCCGTCGGTC  CCGGCACACC  CACATTCTAT  CCGGTGCCCT
1601  AA

```

This corresponds to the amino acid sequence <SEQ ID 1254; ORF 302.ng>:

g302.pep

```

1  MHSIYFFKEK  QMSQTDARRS  GRFLRTVEWL  GNMLPHPVTL  FIIFIVLLLI
51  ASAVGAYFGL  SVPDPRPVGA  KGRADDGLIH  VVSLLDADGL  IKILTHTVKN
101  FTGFAPLGTV  LVSLLGVGIA  EKSGGLISALM  RLLLTGKSPRK  LTFPMVVFTEG
151  ILSNTASELG  YVVLIPLSAV  IFHSLGRHPL  AGLAAAFAGV  SGGYSANLFL
201  GTIDPLLAGI  TQQAQIIHP  DYVVGPEANW  FFMAASTFVI  ALIGYFVTEK
251  IVEPQLGPYQ  SDLSQEEKDI  RHSNEITPLE  YKGLIWAGVV  FVALSALLAW
301  SIVPADGILR  HPETGLVAGS  PFLKSIVVFI  FLLFALPGIV  YGRITRSLRG
351  EREVVNAMAE  SMSTLGLYLV  IIFFAAQFVA  FFNWTNIGQY  IAVKGAVFLK
401  EVGLGGSVLF  IGFI LICA FI  NLMIGSASAQ  WAVTAPIFVP  MLMLAGYAPQ
451  VIQAAAYRIGD  SVTNIITPMM  SYFGLIMATV  IKYKKDAGVG  TLISMMLPYS
501  AFFLIAWIAL  FCIWVFLGL  PVGPGTPTFY  PVP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1255>:

m302.seq

```

1  ATGCACTCAA  TATATTTTTT  TAAGGAGAAG  CAGATGAGTC  AAACCGATAC
51  GCAACGGGAC  GGACGATTTT  TACGCACAGT  CGAATGGCTG  GGCAATATGT
101  TGCCGCATCC  GGTTACGCTT  TTTATTATTT  TCATTGTGTT  ATTGCTGATT
151  GCCTCTGCCG  TCGGTGCGTA  TTTCCGACTA  TCCGTCCCCG  ATCCGCGCCCC
201  TGTTGGTGCG  AAAGGACGTG  CCGATGACGG  TTTGATTTAC  ATTGTCAGCC
251  TGCTCAATGC  CGACGGTTTT  ATCAAAATCC  TGACGCATAC  CGTTAAAAAT
301  TTCACCGGTT  TCGCGCCGTT  GGAACGGTG  TTGGTTTCTT  TATTGGGCGT
351  GGGGATTGCG  GAAAAATCGG  GCTTGATTTC  CGCATTAATG  CGCTTATTGC
401  TCACAAAATC  GCCACGCAAA  CTCACTACTT  TTATGGTTGT  TTTTACAGGG
451  ATTTTATCTA  ATACCGCTTC  TGAATTGGGC  TATGTCGTCC  TAATCCCTTT
501  GTCCGCCATC  ATCTTTCATT  CCCTCGGCCG  CCATCCGCTT  GCCGGTCTGG
551  CTGCGGCTTT  CGCCGGCGTT  TCGGGCGGTT  ATTCGGCCAA  TCTGTTCTTA
601  AGCACAATCG  ATCCGCTCTT  GGCATGCATC  ACCCATCAGG  CGGCGGTCGT
651  AGGCCCTGAA  GCCAACTGGT  TTTTATGGT  AGCCAGTACG  TTTGTGATTG
701  CTTTGATTGG  TTATTTTGT  ACTGAAAAAA  TCGTCGAACC  GCAATTGGGC
751  CCTTATCAAT  CAGATTTGTC  ACAAGAAGAA  AAAGACATTC  GGCATTCCAA
801  TGAAATCACG  CCTTTGGAAT  ATAAAGGATT  AATTTGGGCT  GGCGTGGTGT
851  TTGTTGCCTT  ATCCGCCCTA  TTGGCTTGGA  GCATCGTCCC  TGCCGACGGT
901  ATTTTTCGTC  ATCTGAAAC  AGGATTGGTT  TCCGTTTCGC  CGTTTTTAAA
951  ATCGATTGTT  GTTTTATTT  TCTTGTGTT  TGCATGyCG  GGCmTTGTTT
1001  ATGGmCGGGT  AACCCGAAGT  TTGCGCGGCG  AACAGGAAGT  CGTTAATGCG

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```

1051 ATGCCCGAAT CGATGAGTAC TCTGGsGCTT TmTTTGswCA kcATCTTTTT
1101 TGCCGCACAG TTTGTGCGCAT TTTTAAATTG GACGAATATT GGGCAATATA
1151 TTGCCGTAA AGGGGCGACG TTCTTAAAAG AAGTCGGCTT GGGCGGCAGC
1201 GTGTTGTTTA TCGGTTTAT TTTAATTGT GCTTTTATCA ATCTGATGAT
1251 AGGCTCCGCC TCCGCGCAAT GGGCGGTAAC TGCGCCGATT TTCGTCCCTA
1301 TGCTGATGTT GGCCGGCTAC GCGCCCGAAG TCATTCAAGC CGCTTACCGC
1351 ATCGGTGATT CCGTTACCAA TATTATTACG CCGATGATGA GTTATTTCGG
1401 GCTGATTATG GCGACGGTGA TCAAATACAA AAAAGATGCG GGCCTGGGTA
1451 CGCTGATTTT TATGATGTTG CCGTATTCCG CTTTCTTCTT GATTGCGTGG
1501 ATTGCCTTAT TCTGCATTTG GGTATTTGTT TTGGGCCTGC CCGTCGGTCC
1551 CGGCGCGCCC ACATTCTATC CCGCACCTTA A

```

This corresponds to the amino acid sequence <SEQ ID 1256; ORF 302>:

m302.pep

```

1  MHSIYFFKEK QMSQTDQORD GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
51  ASAVGAYFGL SVPDPRPVGA KGRADDGLIY IVSLLNADGF IKILTHTVKN
101 FTGFAPLGTV LVSLLGVGIA EKSLISALM RLLLTSPRK LTTFMVVFTG
151 ILSNTASELG YVVLIPLSAI IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 STIDPLLACI THQAAVVGPE ANWFFMVAST FVIALIGYFV TEKIVEPOLG
251 PYQSDLSQEE KDIRHSNEIT PLEYKGLIWA GVVVFALSAL LAWSIVPADG
301 ILRHPETGLV SGSPFLKSIV VFIFLLFALX GXVYGRVTRS LRGEQEVVNA
351 MAESMSTLXL XLXXIFFAAQ FVAFFNWTNI GQYIAVKGAT FLKEVGLGGS
401 VLFIFILIC AFINLMIGSA SAQWAVTAPI FVPMLMLAGY APEVIQAAAYR
451 IGDVSTNIIT PMMSYFGLIM ATVIKYKKA GVGTLISMML PYSAFFLIAW
501 IALFCIWVFEV LGLPVGPGAP TFYPAP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 302 shows 94.0% identity over a 533 aa overlap with a predicted ORF (ORF 302.ng) from *N. gonorrhoeae*:

m302/g302

m302.pep	10	20	30	40	50	60
	MHSIYFFKEKQMSQTDQORDGRFLRTVEWLGNMLPHPVTLFIIFIVLLLIASAVGAYFGL					
g302	MHSIYFFKEKQMSQTDARRSGRFLRTVEWLGNMLPHPVTLFIIFIVLLLIASAVGAYFGL					
	10	20	30	40	50	60
m302.pep	70	80	90	100	110	120
	SVPDPRPVGAKGRADDGLIYIVSLLNADGFIKILTHTVKNFTGFAPLGTVLVSLLGVGIA					
g302	SVPDPRPVGAKGRADDGLIHVVSLLDADGLIKILTHTVKNFTGFAPLGTVLVSLLGVGIA					
	70	80	90	100	110	120
m302.pep	130	140	150	160	170	180
	EKSLISALMRLLLTSPRKLTTFMVVFTGILSNTASELGYVVLIPLSAIIFHSLGRHPL					
g302	EKSLISALMRLLLTSPRKLTTFMVVFTGILSNTASELGYVVLIPLSAIIFHSLGRHPL					
	130	140	150	160	170	180
m302.pep	190	200	210	220	230	
	AGLAAAFAGVSGGYSANLFLSTIDPLLACITHQAA-----VVGPEANWFFMVASTFVI					
g302	AGLAAAFAGVSGGYSANLFLGTIDPLLAGITQQAQIIHPDYVVGPEANWFFMAASTFVI					
	190	200	210	220	230	240
m302.pep	240	250	260	270	280	290
	ALIGYFVTEKIVEPOLGPYQSDLSQEEKDIRHSNEITPLEYKGLIWAGVVVFALSALLAW					
g302	ALIGYFVTEKIVEPOLGPYQSDLSQEEKDIRHSNEITPLEYKGLIWAGVVVFALSALLAW					
	250	260	270	280	290	300
	300	310	320	330	340	350

```

m302.pep  SIVPADGILRHPETGLVSGSPFLKSIVVFIFLLFALXGXVYGRVTRSLRGEQEVVNAMAE
          |||||:|||||:|||||:|||||:|||||
g302      SIVPADGILRHPETGLVAGSPFLKSIVVFIFLLFALPGIVYGRITRSLRGEREVVNAMAE
          310      320      330      340      350      360

          360      370      380      390      400      410
m302.pep  SMSTLXLXLXXIFFAAQFVAFFNWTNIGQYIAVKGATFLKEVGLGGSVLFIGFILICAFI
          |||||:|||||:|||||:|||||:|||||
g302      SMSTLGLYLVIIFFAAQFVAFFNWTNIGQYIAVKGAVFLKEVGLGGSVLFIGFILICAFI
          370      380      390      400      410      420

          420      430      440      450      460      470
m302.pep  NLMIGSASAQWAVTAPIFVPMMLLAGYAPEVIQAAYRIGDSVTNIITPMMSYFGLIMATV
          |||||:|||||:|||||:|||||:|||||
g302      NLMIGSASAQWAVTAPIFVPMMLLAGYAPQVIQAAYRIGDSVTNIITPMMSYFGLIMATV
          430      440      450      460      470      480

          480      490      500      510      520
m302.pep  IKYKKDAGVGTLISMMLPYSAFFLIAWIALFCIWVFLGLPVGPGAPTFYPAPX
          |||||:|||||:|||||:|||||:|||||
g302      IKYKKDAGVGTLISMMLPYSAFFLIAWIALFCIWVFLGLPVGPGTPTFYPVPX
          490      500      510      520      530

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1257>:

```

a302.seq
1   ATGCACTCAA TATATTTTTT TAAGGAGAAG CAGATGAGTC AAACCGATAC
51  GCAACGGGAC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101 TGCCGCACCC GGTACGCTT TTTATTATTT TCATTGTGTT ATTGCTGATT
151 GCCTCTGCCG CCGGTGCGTA TTTCGACTA TCCGTCCCGG ATCCGCGCCC
201 TGTGTGGTGC AAAGGACGTG CCGATGACGG TTTGATTACG GTTGTCAGCC
251 TGCTCGATGC TGACGGTTTG ATCAAAATCC TGACGCATAC CGTTAAAAAT
301 TTCACCGGTT TCGCGCCGTT GGGAACGGTG TTGGTTTCTT TATTGGCGGT
351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTATG CGCTTATTGC
401 TCACAAAATC TCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCTA ATACCGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 GTCCGCCATC ATCTTTCATT CCCTCGGCGG CCATCCGCTT GCCGGTCTGG
551 CTGCGGCTTT CGCCGGCGTT TCGGGCGGTT ATTTCGGCAA TCTGTTCTTA
601 GGCACAATCG ATCCGCTCTT GGCAGGCATC ACCCAACAGG CGGCGCAAT
651 CATCCATCCC GACTACGTCG TAGGCCCTGA AGCCAACTGG TTTTATATGG
701 TAGCCAGTAC GTTTGTGATT GCTTTGATTG GTTATTTTGT TACTGAAAAA
751 ATCGTCGAAC CGCAATTGGG CCCTTATCAA TCAGATTGTG CACAAGAAGA
801 AAAAGACATT CGACATTCCA ATGAAATCAC GCCTTTGGAA TATAAAGGAT
851 TAATTTGGGC TGGCGTGGTG TTTGTTGCCT TATCCGCCCT ATTGGCTTGG
901 AGCATCGTCC CTGCCGACGG TATTTTGCGT CATCCTGAAA CAGGATTGGT
951 TTCCGGTTCG CCGTTTTTAA AATCAATTGT TGTTTTTATT TTCTTGTTGT
1001 TTGCACTGCC GGGCATTGTT TATGGCCGGG TAACCCGAAG TTTGCGCGGC
1051 GAACAGGAAG TCGTTAATGC GATGGCCGAA TCGATGAGTA CTCTGGGGCT
1101 TTATTTGGTC ATCATCTTTT TTGCCGCACA GTTTGTCGCA TTTTAAATT
1151 GGACGAATAT TGGGCAATAT ATTGCCGTTA AAGGGCGGAC GTTCTTAAAA
1201 GAAGTCGGCT TGGGCGGCAG CGTGTTGTTT ATCGGTTTTA TTTTAATTG
1251 TGCTTTTATC AATCTGATGA TAGGCTCCGC CTCCGCGCAA TGGGCGGTAA
1301 CTGCGCCGAT TTTCTGCCCT ATGCTGATGT TGGCCGGCTA CGCGCCGAA
1351 GTCATTCAAG CCGCTTACCG CATCGGTGAT TCCGTTACCA ATATTATTAC
1401 GCCGATGATG AGTTATTTTC GGCTGATTAT GGCGACGGTG ATCAAATACA
1451 AAAAAGATGC GGGCGTGGGT ACGCTGATTT CTATGATGTT GCCGTATTCC
1501 GCTTTCTTCT TGATTGCGTG GATTGCCTTA TTCTGCATTT GGGTATTGTG
1551 TTTGGGCCCTG CCCGTCGGTC CCGGCGCGCC CACATTCTAT CCCGCACCTT
1601 AA

```

This corresponds to the amino acid sequence <SEQ ID 1258; ORF 302.a>:

```

a302.pep
1   MHSIYFFKEK QMSQTDTQRD GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
51  ASAAGAYFGL SVPDPRPVGA KGRADDGLIH VVSLLDADGL IKILTHTVKN
101 FTGFAPLGTV LVSLLGVGIA EKSGLISALM RLLLTKSPRK LTTFMVVFTG

```

```

151 ILSNTASELG YVVLIPLSAI IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 GTIDPLLAGI TQAAQIIHP DYVVGPEANW FFMVASTFVI ALIGYFVTEK
251 IVEPQLGPYQ SDLSQEEKDI RHSNEITPLE YKGLIWAGVV FVALSALLAW
301 SIVPADGILR HPETGLVSGS PFLKSIVVFI FLLFALPGIV YGRVTRSLRG
351 EQEVVNAMAE SMSTLGLYLV IIFFAAQFVA FFNWTNIGQY IAVKGATFLK
401 EVGLGGSVLF IGFILICAFI NLMIGSASAQ WAVTAPIFVP MLMLAGYAPE
451 VIQAAYRIGD SVTNIITPMM SYFGLIMATV IKYKKGAVG TLISMMLPYS
501 AFFLIAWIAL FCIWVFLGL PVGPGAPTFY PAP*

```

m302/a302 96.1% identity in 533 aa overlap

```

      10      20      30      40      50      60
m302.pep MHSIYFFKEKQMSQTDQTDGRFLRTVEWLGNMPLPHPVTLFIIIFIVLLLIASAVGAYFGL
          |||||
a302      MHSIYFFKEKQMSQTDQTDGRFLRTVEWLGNMPLPHPVTLFIIIFIVLLLIASAAGAYFGL
      10      20      30      40      50      60

      70      80      90     100     110     120
m302.pep SVPDPRPVGAKGRADDGLIYVSLNADGFIKILHTVKNFTGFAPLGTVLVSLLGVGIA
          |||||
a302      SVPDPRPVGAKGRADDGLIHVVSLLDADGLIKILHTVKNFTGFAPLGTVLVSLLGVGIA
      70      80      90     100     110     120

      130     140     150     160     170     180
m302.pep EKSGLISALMRLLLTKSPRKLTTFMVFTGILSNTASELGYVVLIPLSAIIFHSLGRHPL
          |||||
a302      EKSGLISALMRLLLTKSPRKLTTFMVFTGILSNTASELGYVVLIPLSAIIFHSLGRHPL
      130     140     150     160     170     180

      190     200     210     220     230
m302.pep AGLAAAFAGVSGGYSANLFLSTIDPLLAGITQAAQIIHPDYVVGPEANWFFMVASTFVI
          |||||
a302      AGLAAAFAGVSGGYSANLFLGTIDPLLAGITQAAQIIHPDYVVGPEANWFFMVASTFVI
      190     200     210     220     230     240

      240     250     260     270     280     290
m302.pep ALIGYFVTEKIVEPQLGPYQSDLSQEEKDIRHSNEITPLEYKGLIWAGVVFVALSALLAW
          |||||
a302      ALIGYFVTEKIVEPQLGPYQSDLSQEEKDIRHSNEITPLEYKGLIWAGVVFVALSALLAW
      250     260     270     280     290     300

      300     310     320     330     340     350
m302.pep SIVPADGILRHPETGLVSGSPFLKSIVVFIFLLFALXGXVYGRVTRSLRGEQEVVNAMAE
          |||||
a302      SIVPADGILRHPETGLVSGSPFLKSIVVFIFLLFALPGIVYGRVTRSLRGEQEVVNAMAE
      310     320     330     340     350     360

      360     370     380     390     400     410
m302.pep SMSTLXLXLXXIIFFAAQFVAFFNWTNIGQYIAVKGATFLKEVGLGGSVLFIFIGFILICAFI
          |||||
a302      SMSTLGLYLVIIFFAAQFVAFFNWTNIGQYIAVKGATFLKEVGLGGSVLFIFIGFILICAFI
      370     380     390     400     410     420

      420     430     440     450     460     470
m302.pep NLMIGSASAQWAVTAPIFVPMMLLAGYAPEVIQAAYRIGDSVTNIITPMMSYFGLIMATV
          |||||
a302      NLMIGSASAQWAVTAPIFVPMMLLAGYAPEVIQAAYRIGDSVTNIITPMMSYFGLIMATV
      430     440     450     460     470     480

      480     490     500     510     520
m302.pep IKYKKGAVGTLISMMLPYSAFFLIAWIALFCIWVFLGLPVGPGAPTFYPAPX
          |||||
a302      IKYKKGAVGTLISMMLPYSAFFLIAWIALFCIWVFLGLPVGPGAPTFYPAPX
      490     500     510     520     530

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1259>:

g305.seq

```

1  ATGGATTTTT  TGATTGTCCT  GAAAGCCCTG  ATGATGGGCT  TGGTAGAAGG
51  TTTTACCGAA  TTTTACCGA  TTTCCAGCAC  CGGACATTG  ATTGTGTTG
101 GCAATCTGAT  TGGTTTTTAC  AGCAATCACA  AGGTTTTTGA  AATTGCCATC
151 CAGCTCGGTG  CGGTTTTTGG  GGTAGTGTTT  GAATACCGGC  AGCGTTTCAG
201 CAATGTGTTG  CATGGCGTGG  GAAAAGACCG  GAAAGCCAAC  CGTTTCGTCC
251 TCAATCTTGC  CATTGCTTTT  ATACCTGCCG  CCGTGATGGG  GCTGTTGTTC
301 GACAAACAAA  TCAAAGAGTA  TCTGTTTAAC  CCCTTGAGTG  TTGCAGTCAT
351 GCTGGTTTTG  GCGGTTTTTT  TTATTTTGTG  GGTGGAGAAA  CGCCAAAGCC
401 GAGCAGAGCC  TAAAATTGCC  GATGTTGATG  CATTGCGTCC  GATTGATGCG
451 TTGATGATCG  GTGTTGCCCA  AGTGTGTTGA  CTGGTTCCGG  GTACGTCCCG
501 TTCGGGCAGT  ACGGTTATGG  GCGGGATGCT  TTGGGGAATC  GAGCGGAAAA
551 CGGCAACGGA  GTTTTCATTT  TTCTTGCGCG  TTCCGATGAT  GGTGTCAGCA
601 ACGGCTTATG  ATGTCCTGAA  ACATTACCGA  TTTTTCACCC  TGCATGATGT
651 CGGTTTGATT  TTGATAGGCT  TTATTGCCGC  TTTTGTGTTCC  GGTGTTGGTAG
701 CGGTTAAAGC  ACTGCTGAAG  TTTGTTTCCA  AGAAAACTA  TATCCCGTTT
751 GCCTATTACC  GCATTGTTTT  CGGCATTGTC  ATCATAATAT  TGTGGTTGTC
801 GGGCTGGATA  AGTTGGGAAT  GA

```

This corresponds to the amino acid sequence <SEQ ID 1260; ORF 305.ng>:

g305.pep

```

1  MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIGFH SNHKVFEIAI
51  QLGAVLAVVF EYRQRFNSVL HGVGKDRKAN RFVLNLAI AF IPAAVMGLLF
101 DKQIKEYLFN PLSVAVMLVL GGFFILWVEK RQSRAPKIA DVDALRPIDA
151 LMIGVAQVFA LVPGTSRSGS TVMGMLWGI ERKTATEFSF FLAVPMMVAA
201 TAYDVLKHYR FFTLHDVGLI LIGFIAAFVS GLVAVKALLK FVSKKNYIPF
251 AYYRIVFGIV IILWLSGWI SWE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1261>:

m305.seq (partial)

```

1  AtGGATTTTC  TGATTGTCCT  GAAAGCCCTG  ATGATGGGCT  TGGTAGAAGG
51  TTTTACCGAA  TTTTACCGA  TTTCCAGCAC  CGGACATTG  ATTGTGTTG
101 GCAATCTGAT  TGGTTTTTAC  AGCAATCACA  AGGTTTTTGA  AATTGCCATC
151 CAGCTCGGTG  CAGTTTTTGG  GGTAGTGTTT  GAATACCGGC  AACGTTTCAG
201 CAATGTGTTG  CACGGCTTGG  GAAAAGACCG  GAAAGCCAAC  CGCTTCGTCC
251 TTAATCTTGC  CATTGCTTTT  ATACCTGCCG  CCGTGATGGG  GCTGTTGTTC
301 GGCawACAAA  TCAAAGAGyA  TCTGTTTAAC  CCCTTGAGTG  TTGCAGTCAT
351 GCTGGTtTG  GrCGGTTTTT  yTATTTTGTG  GGTGGAGAAA  CGCCAAAGCC
401 GAGCAGAGCC  TAAAATTGCC  GATGTTGATG  CATTGCGTCC  GATTGATGCC
451 TTGATGATCG  GCGTTGCCCA  AGTGTGTTGA  CTGGTTCCGG  GTACGTCCCG
501 TTCGGGCAGT  ACGATTATGG  GCGGGATGCT  TTGGGGCATC  GAACGGAAAA
551 CTGCGACAGA  ATTCTCGTTT  TTCTTGCTG  TGCCGATGAT  GGTGCGCGCA
601 ACGGCTTATG  ATGTCCTGAA  ACATTACCGA  TTTTTCACCC  TGCATGATGT
651 CGGTTTGATT  CTGATAGGCT  TTATTGCTGC  CTTTGTGTTCA  GGCTTGGTAG
701 CGGTAAAAGC  GTTGCTGAGG  TTTGTTTCGG  GTAC...

```

This corresponds to the amino acid sequence <SEQ ID 1262; ORF 305>:

m305.pep (partial)

```

1  MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIGFH SNHKVFEIAI
51  QLGAVLAVVF EYRQRFNSVL HGLGKDRKAN RFVLNLAI AF IPAAVMGLLF
101 GXQIKEXLFN PLSVAVMLVL XGFXILWVEK RQSRAPKIA DVDALRPIDA
151 LMIGVAQVFA LVPGTSRSGS TIMGMLWGI ERKTATEFSF FLAVPMMVAA
201 TAYDVLKHYR FFTLHDVGLI LIGFIAAFVS GLVAVKALLR FVSG...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 305 shows 96.7% identity over a 243 aa overlap with a predicted ORF (ORF 305.ng) from *N. gonorrhoeae*:

g305/m305

	10	20	30	40	50	60
g305.pep	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHKVFEIAIQLGAVLAVVF					
m305	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHKVFEIAIQLGAVLAVVF					
	10	20	30	40	50	60

700

	70	80	90	100	110	120
g305.pep	EYRQRFNSVLHGVGKDRKANRFVLNLAIAFIPAAVMGLLFDKQIKEYLFNPLSVAVMLVL					
m305	EYRQRFNSVLHGLGKDRKANRFVLNLAIAFIPAAVMGLLFGXQIKEYLFNPLSVAVMLVL					
	70	80	90	100	110	120
	130	140	150	160	170	180
g305.pep	GGFFILWVEKRSRAEPKIADVDALRPIDALMIGVAQVFALVPGTSRSGSTVMGMLWGI					
m305	XGFXILWVEKRSRAEPKIADVDALRPIDALMIGVAQVFALVPGTSRSGSTIMGMLWGI					
	130	140	150	160	170	180
	190	200	210	220	230	240
g305.pep	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFIAAFVSGLVAVKALLK					
m305	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFIAAFVSGLVAVKALLR					
	190	200	210	220	230	240
	250	260	270			
g305.pep	FVSKKNYIPFAYYRIVFGIVIIILWLSGWISWEX					
m305	FVSG					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1263>:

```

a305.seq
1   ATGGATTTTC TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG
51  TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTTCG
101 GCAATCTGAT TGATTTTCAC AGCAATCACA AGGTTTTTGA AATTACCATC
151 CAGCTCGGTG CGGTTTGGC GGTAGTGTTT GAATACCGGC AGCGTTTCAG
201 CAATGTGTTG CATGGCGTGG GAAAAGACCG GAAAGCCAAC CGTTTCGTCC
251 TTAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTGTTTC
301 GGCAAACAAA TCAAAGAGTA TCTGTTTAAC CCCTTGAGTG TTGCAGTCAT
351 GCTGGTTTTG GCGGTTTTTT TTATTTTGTG GGTGGAGAAA CGCCAAAGCC
401 GAGCAGAGCC TAAAATTGTC GATGTTGATG CATTGCGTCC GATTGATCCG
451 TTGATGATCG GCGTTGCCCA AGTGTTTGCA CTGGTTCCAG GTACGTCCCG
501 TTCGGGCAGT ACGATTATGG GCGGGATGCT TTGGGGAATC GAGCGGAAAA
551 CGGCAACGGA GTTTTCATTT TTCTTGCCCG TTCCGATGAT GGTTGCAGCA
601 ACGGCTTATG ATGTCCTGAA GCATTACCGG TTTTTCACCC TGCATGATGT
651 CGGTTTGATT TTGATTGGCT TTGTTGCTGC CTTTGTTCCTA GGCTTGGTGG
701 CCGTCAAAGC GTTGCTGAGG TTTGTTTCCA AGAAAAATTA TATTCCTTTT
751 GCCTATTACC GCATTGTTTT TGGTATTGCC ATCATTATAT TGTGGCTGTC
801 AGGCTGGATA AGTTGGGAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 1264; ORF 305.a>:

```

a305.pep
1   MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIDFH SNHKVFEITI
51  QLGAVLAVVF EYRQRFNSVL HGVGKDRKAN RFVLNLAIAE IPAAVMGLLF
101 GKQIKEYLFN PLSVAVMLVL GGFFILWVEK RQSRAPKIV DVDALRPIDA
151 LMIGVAQVFA LVPGTSRSGS TIMGMLWGI ERKTATEFSF FLAVPMMVAA
201 TAYDVLKHYR FFTLHDVGLI LIGFVAAFVS GLVAVKALLR FVSKKNYIPF
251 AYYRIVFGIA IILWLSGWI SWE*

```

m305/a305 96.3% identity in 243 aa overlap

	10	20	30	40	50	60
m305.pep	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHKVFEIAIQLGAVLAVVF					
a305	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIDFHSNHKVFEITIQLGAVLAVVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m305.pep	EYRQRFNSVLHGLGKDRKANRFVLNLAIAFIPAAVMGLLFGXQIKEYLFNPLSVAVMLVL					
a305	EYRQRFNSVLHGVGKDRKANRFVLNLAIAFIPAAVMGLLFGKQIKEYLFNPLSVAVMLVL					

701

	70	80	90	100	110	120
	130	140	150	160	170	180
m305.pep	XGFXILWVEKRSRAEPK	ADVDALRPIDALMIGVAQVF	ALVPGTSRSGSTIMG	MLWGI		
a305	GGFFILWVEKRSRAEPK	IVDVALRPIDALMIGVAQVF	ALVPGTSRSGSTIMG	MLWGI		
	130	140	150	160	170	180
	190	200	210	220	230	240
m305.pep	ERKTATEFSFFLAVPMMVA	AATAYDVLKHYRFFTLHDV	GLILIGFIAAFVSG	LVAVKALLR		
a305	ERKTATEFSFFLAVPMMVA	AATAYDVLKHYRFFTLHDV	GLILIGFVAAFVSG	LVAVKALLR		
	190	200	210	220	230	240
m305.pep	FVSG					
a305	FVSKKNYIPFAYYRIVFG	IAIIILWLSGWISWEX				
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1265>:

```

g306.seq
1  ATGTTTATGA  ACAAATTTTC  CCAATCCGGA  AAAGGTCTGT  CCGGTTTCTT
51  CTTCCGTTTG  ATACTGGCAA  CGGTCATTAT  TGCCGGTATT  TTGCTTTATC
101 TGAACCAGGG  CGGTCAAAAT  GCGTTCAAAA  TCCCGGCTCC  GTCGAAGCAG
151 CCTGCAGAAA  CGGAAATCCT  GAAACTGAAA  AACCAGCCTA  AGGAAGACAT
201 CCAACCTGAA  CCGGCCGATC  AAAACGCCTT  GTCCGAACCG  GATGTTGCGA
251 AAGAGGCAGA  GCAGTCGGAT  GCGGAAAAAG  CTGCCGACAA  GCAGCCCGTT
301 GCCGACAAAG  CCGACGAGGT  TGAAGAAAAG  GCGGGCGAGC  CGGAACGGGA
351 AGAGCCGGAC  GGACAGGCAG  TGCGCAAGAA  AGCACTGACT  GAAGAGCGTG
401 AACAAACCGT  CAGGGAAAAA  GCGCAGAAGA  AAGATGCCGA  AACGGTTAAA
451 AAAAAAGCGG  TAAAACCGTC  TAAAGAAACA  GAGAAAAAAG  CTTCAAAAGA
501 AGAGAAAAAG  GCGGCGAAAG  AAAAAAGTTG  ACCCAAACCG  ACCCCGGAAC
551 AAATCCTCAA  CAGCCGCAGT  ATCGAAAAAG  CGCGTAGTGC  CGCTGCCAAA
601 GAAGTGCAGA  AAATGAAAAA  CTTTGGGCAA  GGCGGAAGCC  AACGCATTAT
651 CTGCAAATGG  GCGCGTATGC  CGAACCCCGG  AGCGCGGAAG  GGCAGCGTGC
701 CAAACTGGCA  ATCTTGGGCA  TATCTTCCGA  AGTGGTCGGC  TATCAGGCGG
751 GACATAAAAC  GCTTTACCGC  GTGCAAAGCG  GCAATATGTC  CGCCGATGCG
801 GTGA

```

This corresponds to the amino acid sequence <SEQ ID 1266; ORF 306.ng>:

```

g306.pep
1  MFMNKFSQSG  KGLSGFFFGL  ILATVIIAGI  LLYLNQGGQN  AFKIPAPSKQ
51  PAETEILKLK  NQPKEDIQPE  PADQNALSEP  DVAKEAEQSD  AEKAADKQPV
101 ADKADEVEEK  AGEPEREEDP  GQAVRKKALT  EEREQTVREK  AQKKDAETVK
151 KKAVKPSKET  EKKASKEEKK  AAKEKVAPKP  TPEQILNSRS  IEKARSAAAK
201 EVQKMKNFGQ  GGSQRIICKW  ARMPNPGARK  GSVPNWQSWA  YLPKWSAIRR
251 DIKRFTACKA  AICPPMR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1267>:

```

m306.seq (partial)
1  ..GGTTTGTCT  TCGGTTTGAT  ACTGGCGACG  GTCATTATTG  CCGGTATTTT
51  GTTTTATCTG  AACCAGAGCG  GTCAAAATGC  GTTCAAAATC  CCGGCTTCGT
101 CGAAGCAGCC  TGCAGAAACG  GAAATCCTGA  AACCAGmAwAA  CCAGCyTAAG
151 GAAGACATCC  AACCTGAwCC  GGCCGATCAA  AACGCCTTGT  CCGAACCGGA
201 TGCTGCGACA  GAGGCAGAGC  AGTCGGATGC  GGAAAAwGCT  GCCGACAAGC
251 AGCCCGTTGC  CGATAAAGCC  GACGAGGTTG  AAGAAAAGGC  GGGCGAGCCG
301 GAACGGGAAG  AGCCGGACGG  ACAGGCAGTG  CGTAAGAAAG  CGCTGACGGA
351 AGAGCGTGAA  CAAACCGTCA  GGGAAAAAGC  GCAGAAGAAA  GATGCCGAAA
401 CGGTTAAAAw  ACAAGCGGTA  AAACCGTCTA  AAGAAACAGA  GAAAAAGCT
451 TCAAAAGAAG  AGAAAAAGGC  GGCGAAGGAA  AAAGTTGCAC  CCAAACCAAC
501 CCCGGAACAA  ATCCTCAACA  GCGGCAGCAT  CGAAAAAGCG  CGCAGTGCCG
551 CCGCCAAAGA  AGTGCAGAAA  ATGAAAACGC  CGACAAGGCG  GAAGCAACGC

```

601 ATTATCTGCA AATGGGCGCG TATGCCGACC GTCAGAGCGC GGAAGGGCAG
 651 CGTGCCAAAC TGGCAATCTT GGCATATCT TCCAAGGTGG TCGGTTATCA
 701 GCGGGGACAT AAAACGCTTT ACCGGGTGCA AAGCGGCAAT ATGTCTGCCG
 751 ATGCGGTGA

This corresponds to the amino acid sequence <SEQ ID 1268; ORF 306>:

m306.pep (partial)
 1 ..GLFFGLILAT VIIAGILFYL NQSGQNAFKI PASSKQPAET EILKPNQXK
 51 EDIQXPADQ NALSEPDAAT EAEQSDAEXA ADKQPVADKA DEVEEKAGEP
 101 EREEPDQAV RKKALTEERE QTVREKAQKK DAETVKXQAV KPSKETEKKA
 151 SKEEKAAKE KVAPKPTPEQ ILNSGSIEKA RSAAAKEVQK MKTPTRRKQR
 201 IICKWARMPT VRARKGSPVN WQSWAYLPRW SVIRRDIKRF TGCKAAICLP
 251 MR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 306 shows 88.9% identity over a 253 aa overlap with a predicted ORF (ORF 306.ng) from *N. gonorrhoeae*:

m306/g306

m306.pep	10	20	30	40
	GLFFGLILATVIIAGILFYL NQSGQNAFKI PASSKQPAETEILKPX			
g306	MFMNKFSQSGKLSGFFGLILATVIIAGILLYLNQGGQNAFKI PAPSQPAETEILKLK			
	10	20	30	40
	50	60	70	80
m306.pep	NQXKEDIQXPADQNALSEPDAATEAEQSDAEXAADKQPVADKADEVEEKAGEPEREEDP			
g306	NQPKEDIQPEPADQNALSEPDVAKEAEQSDAEXAADKQPVADKADEVEEKAGEPEREEDP			
	70	80	90	100
	110	120	130	140
m306.pep	GQAVRKKALTEEREQTVREKAQKKDAETVKXQAVKPSKETEKKASKEEKAAKEKVAPKP			
g306	GQAVRKKALTEEREQTVREKAQKKDAETVKKKAVKPSKETEKKASKEEKAAKEKVAPKP			
	130	140	150	160
	170	180	190	200
m306.pep	TPEQILNSGSIEKARSAAAKEVQKMKTPTRR-KQRIICKWARMPTVRARKGSPVNWQSWA			
g306	TPEQILNSRSIEKARSAAAKEVQKMNFGGGSQRIICKWARMNPNGARKGSPVNWQSWA			
	190	200	210	220
	230	240	250	
m306.pep	YLPRWSVIRRDIKRFTGCKAAICLPMRX			
g306	YLPKWSAIRRDIKRFTACKAAICPPMRX			
	250	260		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1269>:

a306.seq
 1 ATGTTTATGA ACAAATTTTC CCAATCCGGA AAAGGTCTGT CCGGTTTTTT
 51 CTTCGGTTTG ATACTGGCGA CGGTCATTAT TGCCGGTATT TTGTTTTATC
 101 TGAACCAGAG CGGTCAAAAT GCGTTCAAAA TCCCGGTTC GTCGAAGCAG
 151 CCTGCAGAAA CGGAAATCCT GAAACCGAAA AACCAGCCTA AGGAAGACAT
 201 CCAACCTGAA CCGGCCGATC AAAACGCCTT GTCCGAACCG GATGCTGCGA
 251 AAGAGGCAGA GCAGTCGGAT GCGGAAAAAG CTGCCGACAA GCAGCCCGTT
 301 GCCGACAAAG CCGACGAGGT TGAGGAAAAAG GCGGACGAGC CGGAGCGGGA
 351 AAAGTCGGAC GGACAGGCAG TGCGCAAGAA AGCACTGACG GAAGAGCGTG
 401 AACAAACCGT CGGGGAAAAA GCGCAGAAGA AAGATGCCGA AACGGTTAAA
 451 AAACAAGCGG TAAAACCATC TAAAGAAACA GAGAAAAAAG CTTCAAAGA
 501 AGAGAAAAAG GCGGAGAAGG AAAAAGTTGC ACCCAAACCG ACCCCGGAAC
 551 AAATCCTCAA CAGCGGCAGC ATCGAAAAAG CGCGCAGTGC CGCTGCCAAA

```

601 GAAGTGCAGA AAATGAAAAC GCCGACAAGG CGGAAGCAAC GCATTATCTG
651 CAAATGGGCG CGTATGCCGA CCGCCGGAGC GCGGAAGGGC AGCGTGCCAA
701 ACTGGCAATC TTGGGCATAT CTTCCAAGGT GGTCCGGTAT CAGGCGGGAC
751 ATAAAACGCT TTACCGGGTG CAAAGCGGCA ATATGTCTGC CGATGCGGGT
801 A

```

This corresponds to the amino acid sequence <SEQ ID 1270; ORF 306.a>:

```

a306.pep
1 MFMNKFSQSG KGLSGFFFGL ILATVIIAGI LFYLNQSGQN AFKIPVPSKQ
51 PAETEILKPK NQPKEDIQPE PADQNALSEP DAAKEAEQSD AEKAADKQPV
101 ADKADEVEEK ADEPEREKSD GQAVRKKALT EEREQTVGEK AQKKDAETVK
151 KQAVKPSKET EKKASKEEK AEKEKVAPKP TPEQILNSGS IEKARSAAAK
201 EVQKMKTPTR RKQRIICKWA RMPTAGARKG SVPNWQSWAY LPRWSVIRRD
251 IKRFTGCKAA ICLPMR*

```

m306/a306 93.7% identity in 252 aa overlap

```

m306.pep          10      20      30      40
                    GLFFGLILATVIIAGILFYLNQSGQNAFKIPASSKQPAETEILKPK
                    |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a306              MFMNKFSQSGKGLSGFFFGLILATVIIAGILFYLNQSGQNAFKIPVPSKQPAETEILKPK
                    10      20      30      40      50      60

m306.pep          50      60      70      80      90      100
                    NQXKEDIQXPADQNALSEPDAAATEAEQSDAEAXADKQPVADKADEVEEKAGEPEREEDP
                    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||:|
a306              NQPKEDIQPEPADQNALSEPDAAKEAEQSDAEKAADKQPVADKADEVEEKADEPEREKSD
                    70      80      90      100     110     120

m306.pep          110     120     130     140     150     160
                    GQAVRKKALTEEREQTVREKAQKKDAETVKKQAVKPSKETEKKASKEEKKAKEKVAPKP
                    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a306              GQAVRKKALTEEREQTVGEKAQKKDAETVKKQAVKPSKETEKKASKEEKKAKEKVAPKP
                    130     140     150     160     170     180

m306.pep          170     180     190     200     210     220
                    TPEQILNSGSIEKARSAAAKEVQKMKTPTRRKQRIICKWARMPTVRARKGSVPNWQSWAY
                    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a306              TPEQILNSGSIEKARSAAAKEVQKMKTPTRRKQRIICKWARMPTAGARKGSVPNWQSWAY
                    190     200     210     220     230     240

m306.pep          230     240     250
                    LPRWSVIRRDIKRFTGCKAAICLPMRX
                    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a306              LPRWSVIRRDIKRFTGCKAAICLPMRX
                    250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1271>:

```

g307.seq
1 atgaaaacct tcttcaaaac ctttcgacc gcgtcactcg cgctcatcct
51 cgagcctgc ggcggtcaaa aagacagcgc gcccgagcc tctgccgccg
101 ccccttctgc cgataacggc gcggcgaaaa aagaaatcgt cttcggcacg
151 accgtgggcg acttcggcga tatggtcaaa gaacaaatcc aagccgagct
201 ggagaaaaaa ggctacaccg tcaaattggt cgaatttacc gactatgtgc
251 gccgaatct ggcatggcg gagggcgagt tggacatcaa cgtcttccaa
301 cacaaacct atcttgacga tttcaaaaaa gaacacaacc tggacatcac
351 cgaagccttc caagtgccga ccgcgccttt gggactgtat ccgggcaaac
401 tgaaatcgct ggaagaagtc aaagacggca gcaccgtatc cgcgcccaac
451 gaccgcgtcca acttcgcacg cgccttggtg atgctgaacg aactggggtg
501 gatcaaaact aaagacggca tcaatccgct gaccgcatcc aaagccgaca
551 tcgcgaaaaa cctgaaaaac atcaaaatcg tcgagcttga agccgcacaa
601 ctgccgcgca gccgcgccga cgtggatttt gccgtcgtca acggcaacta
651 cgccataagc agcggcatga agctgaccga agccctgttc caagagccga

```

```

701 gctttgccta tgtcaactgg tctgccgtca aaaccgccga caaagacagc
751 caatggctta aagacgtaac cgaggcctat aactccgacg cgttcaaagc
801 ctacgcgcac aaacgcttcg agggctacaa ataccctgcc gcatggaatg
851 aaggcgcagc caaataa

```

This corresponds to the amino acid sequence <SEQ ID 1272; ORF 307.ng>:

```

g307.pep
  1 MKTFFKTLST ASLALILAAC GGQKDSAPAA SAAAPSDNG AAKKEIVFGT
 51 TVGDFGDMVK EQIQAELEKK GYTVKLVEFT DYVRPNLALA EGELDINVFQ
101 HKPYLDDFKK EHNLDITEAF QVPTAPLGLY PGKLSLEEY KDGSTVSAPN
151 DPSNFARALV MLNELGWIKL KGINPLTAS KADIAENLKN IKIVELEAAQ
201 LPRSRADVDF AVVNGNYAIS SGMKLTEALF QEPSFAYVNW SAVKTADKDS
251 QWLKDVTEAY NSDAFKAYAH KRFEQYKYP A WNEGA AK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1273>:

```

m307.seq (partial)
  1 ..CAATGGCTTA AAGACGTAAC CGAGGCCTAT AACTCCGACG CGTTCAAAGC
 51 CTACGCGCAC AAACGCTTCG AGGGCTACAA ATCCCCTGCC GCATGGAATG
101 AAGGCGCAGC CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1274; ORF 307>:

```

m307.pep (partial)
  1 ..QWLKDVTEAY NSDAFKAYAH KRFEQYKSPA A WNEGA AK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 307 shows 97.4% identity over a 38 aa overlap with a predicted ORF (ORF 307.ng) from *N. gonorrhoeae*:

```

m307/g307

m307.pep                                10      20      30
                                QWLKDVTEAYNSDAFKAYAHKRFEQYKSPA
g307      SGMKLTEALFQEPSFAYVNWSAVKTDKDSQWLKDVTEAYNSDAFKAYAHKRFEQYKSPA
                                230      240      250      260      270      280

m307.pep      39
      A WNEGA AKX
g307      A WNEGA AKX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1275>:

```

a307.seq
  1 ATGAAAACCT TCTTCAAAAC CCTTTCCGCC GCCGCACTCG CGCTCATCCT
 51 CGCCGCCGTC GCGGTCAAA AAGATAGCGC GCCCGCCGCA TCCGCTTCTG
101 CCGCCGCCGA CAACGGCGCG GCGAAAAAAG NAATCGTCTT CCGCACGACC
151 GTCGGCGACT TCGGCGATAT GGTCAAAGAA CAAATCCAAC CCGAGCTGGA
201 GAAAAAAGGC TACACCGTCA AACTGGTCTG GTTTACCGAC TATGTGCGCC
251 CGAATCTGGC ATTGGCTGAG GGCGAGTNGG ACATCAACGT CTTCCAACAC
301 AAACCTATC TTGACGACTT CAAAAAAGAA CACAATCTGG ACATCACCGA
351 AGTCTTCCAA GTGCCGACCG CGCCTTTGGG ACTGTACCCG GGCAAGCTGA
401 AATCGCTGGA AGAAGTCAA GACGGCAGCA CCGTATCCGC GCCCAACGAC
451 CCGTCCAAC TCGCCCGCGT CTTGGTGATG CTCGACGAAC TGGGTTGGAT
501 CAACTCAA GANGGCATCA ATCCGCTGAC CGCATCCAAA GCGGACATTG
551 CCGAAAACCT GAAAAACATC AAAATCGTCT AGCTTGAAGC CGCGCAACTG
601 CCGCGTAGCC GCGCCGACGT GGATTTTGNC GTCGTCAACG GCAANTACGC
651 CATAAGCAGC GGCATGAAGC TGACCGAAGC CCTGTTCCAA GAACCGAGCT
701 TTGCCTATGT CAACTGGTCT GCGTCAAAA CCGCCGACAA AGACAGCCAA
751 TGGCTTAAAG ACGTAACCGA GGCCTATAAC TCCGACGCGT TCAAAGCCTA
801 CGCGCACAAA CGCTTCGAGG GCTACAAATC CCCTGCCGCA TGAATGAAG
851 GCGCAGCCAA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 1276; ORF 307.a>:

```

a307.pep
  1 MKTFFKTLA AALALILAAC GGQKDSAPAA SASAAADNGA AKKXIVFGTT

```

705

```

51  VGDFGDMVKE  QIQPELEKKG  YTVKLVEFTD  YVRPNLALAE  GEXDINVFOH
101 KPYLDDFKKE  HNLDITEVFQ  VPTAPLGLYP  GKLSLEEVK  DGSTVSAPND
151 PSNFARVLVM  LDELGWIKLK  XGINPLTASK  ADIAENLKNI  KIVELEAAQL
201 PRSRADVDFX  VVNGXYAISS  GMKLTEALFQ  EPSFAYVNWS  AVKTADKDSQ
251 WLKDVTEAYN  SDAFKAYAHK  RFEQYKSPAA  WNEGAAK*

```

m307/a307 100.0% identity in 38 aa overlap

```

                                10      20      30
m307.pep                                QWLKDVTEAYNSDAFKAYAHKRFEQYKSPA
                                |||||
a307      SGMKLTEALFQEPSFAYVNWSAVKTADKDSQWLKDVTEAYNSDAFKAYAHKRFEQYKSPA
          220      230      240      250      260      270

          39
m307.pep      AWNEGAAXX
          |||||
a307      AWNEGAAXX
          280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1277>:

```

g308.seq
1  ATGTAAATC  GGGTATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGTGTTTA  TCGGATTTCT  GTTTTTTCAC  TATAATAGCC  GGTTTGCCGT
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGCG  GGGCGAGCGG  TTTCCAATAC  GGCGTGAAGG  CTTTGGAAC
201 TTTGCGCGCG  CAAGATGTCG  AAACGCACCT  TGTGGTATCG  AAAGGCGCGG
251 AGATGGCGCG  CGCTTCGGAA  ACGGATTATA  CGAAAGACGA  AGTATATGCC
301 TTGGCTGATT  TCGTCCATCC  GATCGGCAAT  ATCGGGGCGT  GCATTGCCAG
351 CCGTACGTTT  AAAACGGACG  GGATGCTGGT  CGCACCTCTG  TCGATGCCGA
401 CGCTTGCCCT  TGTCGCGCAC  GGCTTCGGCG  ACAACCTCTT  GACGCGTGCG
451 GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAAGCGG  GTAACGGAAA
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTTCTTG  CGATGTACCG  CAAGCCGCGA
601 ACGGCGGACG  ACATAGTGGC  GCACAGTATC  GCACACACGC  TGTCGCTGTT
651 CGGAATCGAT  ACGCCGGATT  TGGCGGAATG  GCAGGGAATG  GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1278; ORF 308.ng>:

```

g308.pep
1  MLNRVYRIL  GVADNLYPCL  SDFCFFTIIA  GLPLQAVLWE  RRMVRRLLII
51  GISGASGFQY  GVKALELLRA  QDVETHLVVS  KGAEMARASE  TDYTKDEVYA
101 LADFVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVAH  GFGDNLTLRA
151 ADVVLKERRR  LVLVRETPL  NLAHLDNMKR  VTEMGGVVFP  PVPAMYRKPO
201 TADDIVAHSI  AHTLSLFGID  TPDLAEWQGM  AD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1279>:

```

m308.seq (partial)
1  ATGTAAATC  GGGTATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGCGTTTA  TCGGATTTCT  GTTTTTTCAC  TATAATAGCC  GGTTTGCCGT
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGCG  GGGCGAGCGG  TTTCCAATAC  GGCGTGAAGG  CTTTGGAAC
201 TTTGCGCGCG  CAAGATGTCG  AAACGCACCT  TGTGGTATCG  AAAGGTGCGG
251 AGATGGCGCG  CGCTTCGGAA  ACGGCTTATG  CGAGAGACGA  GGTATATGCC
301 TTGGCGGACT  TCGTGCATCC  GATCGGCAAT  ATCGGGGCGT  GCATTGCCAG
351 CCGTACGTTT  AAAACGGATG  GGATGCTGGT  CGCCCCCTGT  TCGATGCCGA
401 CGCTTGCCCT  TGTCGCGCAC  GGCTTCGGCG  ACAATCTGcT  GACGCGTGCG
451 GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAAGCGG  GWAACGGAAA
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTTCTTG  CGATGTACCG  CAAACCGCAG
601 ACGGCGGACG  ACATAGTGGC  GCACAGTGTG  GCACACGcT  TGTCGCTGTT
651 CGGAATCGAT  ACGCCGGATT  CGGCGGAATG  GCAGGGAATG  gcG...

```

This corresponds to the amino acid sequence <SEQ ID 1280; ORF 308>:

m308.pep (partial)

```

1  MLNRVFYRIL  GVADNLYPRL  SDFCFFTTIIA  GLPLQAVLWE  RRMVRRLLII
51  GISGASGFQY  GVKALELLRA  QDVETHLVVS  KGAEMARASE  TAYARDEVYA
101 LADFVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVAH  GFGDNLTRA
151 ADVVLKERRR  LVLVRETPL  NLAHLNMXR  XTEMGGVVFP  PVPAMYRKPO
201 TADDIVAHSV  AHASLFGID  TPDSAEOQGM  A..

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 308 shows 96.5% identity over a 231 aa overlap with a predicted ORF (ORF 308.ng) from *N. gonorrhoeae*:

m308/g308

m308.pep	10	20	30	40	50	60
	MLNRVFYRILGVADNLYPRLSDFCFFTTIIAGLPLQAVLWERRMMVRRLLIIIGISGASGFQY					
g308	MLNRVFYRILGVADNLYPCLSDFCFFTTIIAGLPLQAVLWERRMMVRRLLIIIGISGASGFQY					
	10	20	30	40	50	60
m308.pep	70	80	90	100	110	120
	GVKALELLRAQDVETHLVVSKGAEMARASETAYARDEVYALADFVHPIGNIGACIASGTF					
g308	GVKALELLRAQDVETHLVVSKGAEMARASETDYTKDEVYALADFVHPIGNIGACIASGTF					
	70	80	90	100	110	120
m308.pep	130	140	150	160	170	180
	KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLNMXR					
g308	KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLNMXR					
	130	140	150	160	170	180
m308.pep	190	200	210	220	230	
	XTEMGGVVFPVPAMYRKPOADDIVAHVAHLSLFGIDTPDSAEOQGM					
g308	VTEMGGVVFPVPAMYRKPOADDIVAHSLAHTLSLFGIDTPDLAEOQGMADX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1281>:

a308.seq

```

1  ATGTAAATC  GGATATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGTATTTA  TCGGATTTCT  GTTTTTTCAC  TATAATAGCC  GGTTTGCCGT
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGTG  GGGCGAGCGG  TTTCCAATAC  GCGGTGAAGG  CTTTGGANCT
201 TTTACGCGCG  CAAGATATCG  AAACGCACCT  TGTGGTATCG  AAAGGTGCGG
251 AGATGGCGCG  CGCTTCGGAA  ACGGNTTATG  CGAGAGACGA  NGTATATGCC
301 TTGGCGGACT  TNGTGCATCC  GATCGGCAAT  ATCGGGGCGT  GCATTGCCAG
351 CGGTACGTTT  AAAACGGACG  GGATGCTGGT  CGCCCCCTGT  TCGATGCGGA
401 CGCTTGCCCT  GGTCGTGCAC  GGCTTCGGCG  ACAACCTCTT  GACGCGTGCG
451 GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAANCGG  GTAACGGAAA
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTTCTTG  CGATGTACCG  CAAACCGCAG
601 ACGGCGGACG  ACATAGTGGC  GCACAGTGTT  GCACACGCTT  TGTCGCTGTT
651 CGGAATCGAT  ACGCCGATT  CGGCGGAATG  GCAGGGAATG  GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1282; ORF 308.a>:

a308.pep

```

1  MLNRIFYRIL  GVADNLYPYL  SDFCFFTTIIA  GLPLQAVLWE  RRMVRRLLII
51  GISGASGFQY  GVKALXLLRA  QDIETHLVVS  KGAEMARASE  TXYARDXVYA
101 LADXVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVVH  GFGDNLTRA
151 ADVVLKERRR  LVLVRETPL  NLAHLNMXR  VTEMGGVVFP  PVPAMYRKPO
201 TADDIVAHSV  AHASLFGID  TPDSAEOQGM  AD*

```

m308/a308 95.7% identity in 231 aa overlap

	10	20	30	40	50	60
m308.pep	MLNRV	FYRIL	GVADNLYPRL	SDFCFFTII	IAGLPLQAVLWERRMMVRLII	IGISGASGFQY
a308	MLNRIF	YRILG	VADNLYPYLS	DFCFFTII	IAGLPLQAVLWERRMMVRLII	IGISGASGFQY
	10	20	30	40	50	60
	70	80	90	100	110	120
m308.pep	GVKALELLRAQDVETHLVVSKGAEMARASE	TAYARDEVYALAD	DFVHPIGNIGACIASGTF			
a308	GVKALXLLRAQDIETHLVVSKGAEMARASE	TXYARDXVYALAD	XVHPIGNIGACIASGTF			
	70	80	90	100	110	120
	130	140	150	160	170	180
m308.pep	KTDGMLVAPCSMR	TLASVAHGF	DNLLTRAADV	LKERRRLVLMVRET	PLNLAHL	DNMNR
a308	KTDGMLVAPCSMR	TLASVVHGF	DNLLTRAADV	LKERRRLVLMVRET	PLNLAHL	DNMNR
	130	140	150	160	170	180
	190	200	210	220	230	
m308.pep	XTEMG	GVVFPVP	PAMYRKPQT	ADDDIVAH	SVAHSLFGID	TPDSA
a308	VTEMG	GVVFPVP	PAMYRKPQT	ADDDIVAH	SVAHSLFGID	TPDSA
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1283>:

g308-1.seq

```

1  ATGTTAAATC GGGTATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA
51  TCCGTGTTTA TCGGATTTCT GTTTTTTCAC TATAATAGCC GGTTCGCCGT
101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTCCAATAC GGCCTGAAGG CTTTGGAAC
201 TTTGCGCGCG CAAGATGTCG AAACGCACCT TGTGGTATCG AAAGCGCGCG
251 AGATGGCGCG CGCTTCGGAA ACGGATTATA CGAAAGACGA AGTATATGCC
301 TTGGCTGATT TCGTCCATCC GATCGGCAAT ATCGGGGCGT GCATTGCCAG
351 CCGTACGTTT AAAACGGACG GGATGCTGGT CGCACCTGT TCGATGCGGA
401 CGCTTGCCCT TGTCGCGCAC GGCTTCGGCG ACAACCTCTT GACGCGTGCG
451 GCGGATGTGG TTTGAAGGA AAGCGGCGCG CTGGTGCTGA TGGTGCGCGA
501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GTAACGGAAA
551 TGGGCGGCGT GGTGTTTCCC CCTGTTCCGT CGATGTACCG CAAGCCGCAG
601 ACGGCGGACG ACATAGTGGC GCACAGTATC GCACACACGC TGTCGCTGTT
651 CGGAATCGAT ACGCCGGATT TGGCGGAATG GCAGGGAATG GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1284; ORF 308-1.ng>:

g308-1.pep

```

1  MLNRVFYRIL GVADNLYPCL SDFCFFTIIA GLPLQAVLWE RRMVVRLLII
51  GISGASGFQY GVKALELLRA QDVETHLVVS KGAEMARASE TDYTKDEVYA
101 LADFVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVAH GFGDNLLTRA
151 ADVVLKERRR LVLVRETPL NLAHLDNMNR VTEMGVVFP PVPAMYRKPQ
201 TADDDIVAHSI AHTLSLFGID TPDLAEWQGM AD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1285>:

m308-1.seq

```

1  ATGTTAAATC GGGTATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA
51  TCCGCGTTTA TCGGATTTCT GTTTTTTCAC TATAATAGCC GGTTCGCCGT
101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTCCAATAC GGCCTGAAGG CTTTGGAAC
201 TTTGCGCGCG CAAGATGTCG AAACGCACCT TGTGGTATCG AAAGGTGCGG
251 AGATGGCGCG CGCTTCGGAA ACGGCTTATG CGAGAGACGA GGTATATGCC
301 TTGGCGGACT TCGTGCATCC GATCGGCAAT ATCGGGGCGT GCATTGCCAG
351 CCGTACGTTT AAAACGGATG GGATGCTGGT CGCCCCCTGT TCGATGCGGA
401 CGCTTGCCCT TGTCGCGCAC GGCTTCGGCG ACAATCTGCT GACGCGTGCG
451 GCGGATGTGG TTTGAAGGA AAGCGGCGCG CTGGTGCTGA TGGTGCGCGA
501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GTAACGGAAA
551 TGGGCGGCGT GGTGTTTCCC CCTGTTCCGT CGATGTACCG CAAACCGCAG
601 ACGGCGGACG ACATAGTGGC GCACAGTGTG GCACACGCTT TGTCGCTGTT
651 CGGAATCGAT ACGCCGGATT CGGCGGAATG GCAGGGAATG GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1286; ORF 308-1>:

m308-1.pep

```

1  MLNRVFYRIL GVADNLYPRL SDFCFFTIIA GLPLQAVLWE RRMVVRLLII

```

51 GISGASGFQY GVKALELLRA QDVETHLVVS KGAEMARASE TAYARDEVYA
101 LADVFHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVAH GFGDNLTRA
151 ADVVLKERRR LVLVRETPL NLAHLDNMKR VTEMGGVVFP PVPAMYRKPO
201 TADDIVAHSV AHALSFGID TPDSAEOQGM AD*

m308-1/g308-1 97.0% identity in 232 aa overlap

	10	20	30	40	50	60
m308-1.pep	MLNRV	FYRILGVADNLYPRLSDFCF	FTIIAGLPLQAVLWERRMMV	RRLLIIGISGASGFQY		
g308-1	MLNRV	FYRILGVADNLYPRLSDFCF	FTIIAGLPLQAVLWERRMMV	RRLLIIGISGASGFQY		
	10	20	30	40	50	60
	70	80	90	100	110	120
m308-1.pep	GVKALELLRAQDVETHLVVSKGAEMARASE	TAYARDEVYALADVFHPIGNIGACIASGTF				
g308-1	GVKALELLRAQDVETHLVVSKGAEMARASE	TDYTKDEVYALADVFHPIGNIGACIASGTF				
	70	80	90	100	110	120
	130	140	150	160	170	180
m308-1.pep	KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR					
g308-1	KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR					
	130	140	150	160	170	180
	190	200	210	220	230	
m308-1.pep	VTEMGGVVFPVPAMYRKPO	TADDIVAHSAHLSFGIDTPDSAEOQMAD	X			
g308-1	VTEMGGVVFPVPAMYRKPO	TADDIVAHSAHLSFGIDTPDLAEOQMAD	X			
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1287>:

a308-1.seq

1 ATGTTAAATC GGATATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA
51 TCCGTATTTA TCGGATTTCT GTTTTTCAC TATAATAGCC GGTGTTGCCG
101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
151 GGCATCAGTG GGGCGAGCGG TTTCCAATAC GGCCTGAAGG CTTGGANCT
201 TTTACGCGCG CAAGATATCG AAACGCACCT TGTGGTATCG AAAGGTGCGG
251 AGATGGCGCG CGCTTCGGAA ACGGNTTATG CGAGAGACGA NGTATATGCC
301 TTGGCGGACT TNGTGCATCC GATCGGCAAT ATCGGGGCGT GCATTGCCAG
351 CCGTACGTTT AAAACGGACG GGATGCTGTT CGCCCCCTGT TCGATGCGGA
401 CGCTTGCCCT GGTCTGCAC GGCTTCGGCG ACAACCTCTT GACGCGTGCG
451 GCGGATGTGG TTTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGCGCGA
501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAANCGG GTAACGGAAA
551 TGCGCGCGCT GGTGTTTCCC CCGTTCCTG CGATGTACCG CAAACCGCAG
601 ACGGCGGACG ACATAGTGGC GCACAGTGT GCACACGCTT TGTCGCTGTT
651 CGGAATCGAT ACGCCGGATT CGGCGGAATG GCAGGGAATG GCGGATTAA

This corresponds to the amino acid sequence <SEQ ID 1288; ORF 308-1.a>:

a308-1.pep

1 MLNRIFYRIL GVADNLYPYL SDFCFFTIIA GLPLQAVLWE RRMVRRLLI
51 GISGASGFQY GVKALXLLRA QDIETHLVVS KGAEMARASE TXYARDXVYA
101 LADXVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVH GFGDNLTRA
151 ADVVLKERRR LVLVRETPL NLAHLDNMKR VTEMGGVVFP PVPAMYRKPO
201 TADDIVAHSV AHALSFGID TPDSAEOQGM AD*

a308-1/m308-1 96.1% identity in 232 aa overlap

	10	20	30	40	50	60
a308-1	MLNRIFYRILGVADNLYPYLSDFCF	FTIIAGLPLQAVLWERRMMV	RRLLIIGISGASGFQY			
m308-1	MLNRV	FYRILGVADNLYPRLSDFCF	FTIIAGLPLQAVLWERRMMV	RRLLIIGISGASGFQY		
	10	20	30	40	50	60
	70	80	90	100	110	120
a308-1	GVKALXLLRAQDIETHLVVSKGAEMARASE	TXYARDXVYALADXVHPIGNIGACIASGTF				
m308-1	GVKALELLRAQDVETHLVVSKGAEMARASE	TAYARDEVYALADVFHPIGNIGACIASGTF				
	70	80	90	100	110	120
	130	140	150	160	170	180
a308-1	KTDGMLVAPCSMRTLASVHGF	GDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR				


```

m308-1      KTDGMLVAPCSMRTLASVAHGFGDNL LTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR
              130      140      150      160      170      180

              190      200      210      220      230
a308-1      VTEMGGVVFPVPVAMYRK PQ TADDIVAH SVAHALSLFGIDTPDSA EWQGMADX
              |||||
m308-1      VTEMGGVVFPVPVAMYRK PQ TADDIVAH SVAHALSLFGIDTPDSA EWQGMADX
              190      200      210      220      230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1289>:

g311.seq

```

1   atgttcagtt tcggtcgggc gtttgaccgc ccgcagtatg agttgggttc
51  gctgtcgccct gttgcggcac ttgctgtccg gcgcgctttg ggggtgtttgg
101 gtttggaac gcaaatcaag tggccaaacg atttggtcgt cggacgcgac
151 aaattggcgc gcatctctgat tgaaacagtc agggcgggcg gtaaaacggt
201 tgccgtggtc ggtatcggca tcaatttcgt gctgcccaag gaagtggaaa
251 acgccgcttc cgtgcagtcg ctgtttcaga cggcatcgcg gcggggcaat
301 gccgatgccg ccgtattgct ggaaacattg cttgcggaac tgggcgcggt
351 gttggaacaa tatgcggaag aagggttcgc gccattttta aatgagtatg
401 aaacggccaa ccgcgaccac ggcaaggcgg tattgctgtt gcgcgacggc
451 gaaaccgtgt gcgaaggcac ggttaaaggc gtggacggac gaggcgcttc
501 gcacttgga acggcagaag gcgaacagac ggtcgtcagc ggcgaaatca
551 gcctgcggcc cgacaacagg tcggtttccg tgccgaagcg gccggattcg
601 gaacgttttt tctgtgttga aggcgggaac agccggctca agtgggcgtg
651 ggtggaaaac ggcacgttcg caaccgtggg cagcgcgccg taccgcgatt
701 tgtcgccttt gggcgcgga gggcgggaaa aggcggatgg aaatgtccgc
751 atcgtcggtt gcgcgctgtg cggagaatcc aaaaaggcac aagtgaagga
801 acagctcgcc cgaaaaatcg agtggctgcc gtcttcgcga caggctttgg
851 gcatacgcaa ccaactaccg caccgcgaag aacacggttc cgaccgttgg
901 ttcaacgcct tgggcagccg ccgcttcagc cgcaacgcct gcgtcgtcgt
951 cagttgcggc acggcggtta cggttgacgc gctcaccgat gacggacatt
1001 atctcggcgg aaccatcatg cccggttccc acctgatgaa agaatcgcctc
1051 gccgtccgaa ccgccaacct caaccgcccc gccggcaaac gttacccttt
1101 cccgaccaca acgggcaacg ccgtcgcaag cggcatgatg gacgcggttt
1151 gcggctcgat aatgatgatg caccgcccgt tgaaagaaaa aaacggcgcg
1201 ggcaagcctg tcgatgtcat cattaccggc ggcggcgcgcg cgaaagtccg
1251 cgaagccctg ccgcctgcat ttttggcgga aaataccgtg cgcgtggcgg
1301 acaacctcgt catccacggg ctgctgaacc tgattgccgc cgaaggcggg
1351 gaatcggaac acgcttaa

```

This corresponds to the amino acid sequence <SEQ ID 1290; ORF 311.ng>:

g311.pep

```

1   MFSFGWAFDR PQYELGSLSP VAALACRRAL GCLGLETQIK WPNDLVVGRD
51  KLGGILIE TV RAGGKTVAVV GIGINFLPK EVENAASVQS LFQTASRRGN
101 ADAAVLLE TL LAELGAVLEQ YAEFGFAPFL NEYETANRDH GKAVLLLRDG
151 ETVCEGTVKG VDGRGVHLLE TAEGEQTVVS GEISLRPDNR SVSVPKRPDS
201 ERFLLLLE GN SRLKWAVVEN GTFATVGSAP YRDLSP LGAE WAEKADGNVR
251 IVGCAVCGES KKAQVKEQLA RKIEWLPSSA QALGIRNH YR HPEEHGSDRW
301 FNAIGSR RFS RNACVVVSCG TAVTVDALTD DGHYLG GTIM PGFHLMKESL
351 AVRTANLN RP AGKRYPFPTT TGNVAVSGMM DAVCGS IMMM HGRLKEKNGA
401 GKPVDVIITG GGAAKVAEAL PPAFLAENTV RVADNLVIHG LLNLIAAEGG
451 ESEHA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1291>:

m311.seq (partial)

```

1   ATGTTTCAGTT TTGGCTGGGT GTTTGACCGG CCGCAGTATG AGTTGGGTTC
51  GCTGTCGCCT GTTGCGGCAG TGGCGTGTG CGCGCCTTG TCGCGTTTAG
101 GTTTGGATGT GCATATTAA GGGCCCAATG ATTTGGTTGT CCGACGCGAC
151 AAATTGGCGC GCATTCTGAT TGAAACG GTC AGGACGGGCG GCAAAACGGT
201 TGCCGTGGTC GGTATCGGCA TCAATTTTGT CCTGCCCAAn GAAGTAGAAA
251 ATGCCGCTTC CGTGCAATCG CTGTTTCAGA CGGCATCGCG GCGGGGCAAT
301 GCCGATGCCG CCGTGCTGCT nnnnnnnnnn nnnnnnnnnn nnnnGGAAT
351 CAGCCTGCGG TCCGACnACA GGCCGGTTTC CTGnCGAAG CGCGGGGATT

```

```

401 CGGAACGTTT TCTGCTGTTG GACGGCGGCA ACAGCCGGCT CAAGTGGgCG
451 TGGGTGGA AAAACGGCACGTT CGCAACCGTC GGTAGCGCGC CGTACCgCGA
501 TTTGTGCGCCT TTGGGCGCGG AGTGGGCGGA AAAGGCGGAT GGAAATGTCC
551 GCATCGTCGG TTGCGCTGTG TGCGGAGAAT TCAAAAAGGC ACAAGTGCAG
601 GAACAGCTCG CCCGAAAAAT CGAGTGGCTG CCGTCTTCCG CACAGGCTTT
651 GTTTGGCATA CGCAACCACT ACCGCCACCC CGAAGAACAC GGTTCCGACC
701 GCTGGTTCAA CGCCTTGGGC AGCCGCGGCT TCAGCCGCAA CGCyTGCCTC
751 GTCGTCA GTT GCGGCACGGC GGTAACGGT GACGCGCTCA CCGATGACGG
801 ACATTATCTC GGrgGAACCA TCATGCCCCG TTTCCACCTG ATGAAAGAAT
851 CGCTCGCCGT CCGAACCGCC AACCTCAACC GGCACGCCGG TAAGCGTTAT
901 CCTTTCCCGA CCACAACGGG CAATGCCGTC GCCAGCGGCA TGATGGATGC
951 GGTTTGGCGC TCGGTTATGA TGATGCACGG GCGTTTGAAA GAAAAAACCG
1001 GGGCGGGCAA GCCTGTCGAT GTCATCATT CCGGCGGCGG CGCGGCAAAA
1051 GTTGCCGAAG CCCTGCCGCC TGCATTTTGT GCGGAAAATA CCGTGCGCGT
1101 GGCGGACAAC CTCGTCAATT ACGGGTTGTT GAACATGATT GCCGCCGAAG
1151 GCAGGAATA TGAACAT...

```

This corresponds to the amino acid sequence <SEQ ID 1292; ORF 311>:

```

m311.pep (partial)
1 MFSFGWVFD R PQYELGSLSP VAAVACRRAL SRLGLDVQIK WPNDLVVGRD
51 KLGGIL IETV RTGGKT VAVV GIGINFVLPX EVENAASVQS LFQTASRRGN
101 ADAAVLLXXX XXXXXEISLR SDXRPVSXK RRDSE RFLLL DGGNSRLKWA
151 WVENGTFATV GSAPYRDLSP LGAEWA EKAD GNVRI VCAV CGEFKKAQVQ
201 EQLARKIEWL PSSAQALFGI RNHYRHPEEH GSDRWFNALG SRRFSRNACV
251 VVSCGTAVTV DALTD DGHYL GGTIMPGFHL MKESLAVRTA NLNRHAGKRY
301 PFPTTTGNAV ASGMMDAVCG SVMMMHGR LK EKTGAGK PVD VIITGGGA AK
351 VAEALPPAFL AENTVRVADN LVIYGLLNMI AEGREYEH...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 311 shows 78.5% identity over a 455 aa overlap with a predicted ORF (ORF 311.ng) from *N. gonorrhoeae*:

```

m311/g311
      10      20      30      40      50      60
m311.pep MFSFGWVFD RPQYELGSLSPVA AVACRRALSRLGLDVQIKWPNDLVVGRD KLGGIL IETV
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g311      MFSFGWAFDRPQYELGSLSPVAALACRRALGCLGLETQIKWPNDLVVGRD KLGGIL IETV
          10      20      30      40      50      60

      70      80      90      100     110
m311.pep RTGGKT VAVVGIGINFVLPXEVENAASVQSLFQTASRRGNADA AVLLXXX-----
          |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g311      RAGGKT VAVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA AVLLLETL LAELGAVLEQ
          70      80      90      100     110     120

m311.pep -----XXXXXXXX
g311      YAEEGFAPFLNEYETANRDHGKAVLLLRDGETVCEGTVKGVDGRGVLHLETAEGEQTVVS
          130     140     150     160     170     180

      120     130     140     150     160     170
m311.pep XEISLRSDXRPVSXKRRDSE RFLLLDGGNSRLKWA WVENGTFATVGSAPYRDL SPLGAE
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g311      GEISLRPDNRSVSVKRPDSE RFLLLLEGGNSRLKWA WVENGTFATVGSAPYRDL SPLGAE
          190     200     210     220     230     240

      180     190     200     210     220     230
m311.pep WAEKADGNVRI VCAVCGEFKKAQVQEQ LARKIEWLPSSAQALFGIRNHYRHPEEHGSDR
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g311      WAEKADGNVRI VCAVCGESKKAQVKEQLARKIEWLPSSAQAL-GIRNHYRHPEEHGSDR
          250     260     270     280     290

```

711

	240	250	260	270	280	290
m311.pep	WFNALGSRRFSRNACVVVSCGTAVTVDALTDGGHYLGGTIMPGFHLMKESLAVRTANLNR					
g311	WFNALGSRRFSRNACVVVSCGTAVTVDALTDGGHYLGGTIMPGFHLMKESLAVRTANLNR					
	300	310	320	330	340	350
m311.pep	HAGKRYPFPTTTGNAVASGMMDAVCGSVMMHGRLEKKTGAGKPVVDVIITGGGAAKVAEA					
g311	PAGKRYPFPTTTGNAVASGMMDAVCGSIMMHGRLEKKNAGKPVVDVIITGGGAAKVAEA					
	360	370	380	390	400	410
m311.pep	LPPAFLAENTVRVADNLVIYGLLNMIAAEGREYEH					
g311	LPPAFLAENTVRVADNLVIHGLLNLIAAEGGESEHAX					
	420	430	440	450		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1293>:

```

a311.seq
1   ATGTTTCAGTT TTGGCTGGGT GTTTGACCGG CCGCAGTATG AGTTGGGTTTC
51  GCTGTGCGCCT GTTGCGGCAG TGGCGTGCCG GCGCGCCTTG TCGCGTTTGG
101 GTTTGGAAAC GCAAATCAAG TGGCCAAACG ATTTGGTCGT CCGACGCGAC
151 AAATTGGGCG GCATTCTGAT TGAAACGGTC AGGACGGGCG GCAAACGGT
201 TGCCGTGGTC GGTATCGGCA TCAATTTCGT GCTGCCCAAG GAAAGTGGAAA
251 ACGCCGCTTC CGTGCAATCG CTGTTTCAGA CGGCATCGCG GCGGGGAAAT
301 GCCGATGCCG CCGTGTGTCT GGAAACGCTG TTGGCGGAAC TTGATGCGGT
351 GTTGTTGCAA TATGCGCGGG ACGGATTTCG GCCTTTTGTG GCGGAATATC
401 AGGCTGCCAA CCGCGACCAC GGCAAGGCGG TATTGCTGTT GCGCGACGGC
451 GAAACCGTGT TCGAAGGCAC GGTAAAGGC GTGGACGGAC AAGGCGTTCT
501 GCACTTGGA ACGGCAGAGG GCAAACAGAC GGTCTCAGC GCGGAAATCA
551 GCCTGCGGTC CGACGACAGG CCGGTTTCCG TGCCGAAGCG GCGGGATTTCG
601 GAACGTTTTT TGCTGTTGGA CGGCGGCAAC AGCCGGCTCA AGTGGGCGTG
651 GGTGGAAAC GGCACGTTCT CAACCGTCGG TAGCGCGCCG TACCGCGATT
701 TGTCGCCTTT GGGCGCGGAG TGGCGGAAA AGGTGGATGG AAATGTCCGC
751 ATCGTCGGTT GCGCCGTGTG CGGAGAATTC AAAAAGGCAC AAGTGCAGGA
801 ACAGCTCGCC CGAAAAATCG AGTGGCTGCC GTCTTCCGCA CAGGCTTTGG
851 GCATACGCAA CCACTACCGC CACCCCGAAG AACACGGTTC CGACCGCTGG
901 TTCAACGCC TGGGCAGCCG CCGCTTCAGC CGCAACGCCT GCGTCGTCGT
951 CAGTTGCGGC ACGGCGGTAA CGGTTGACGC GCTCACCGAT GACGGACATT
1001 ATCTCGGGG AACCATCATG CCCGGTTTCC ACCTGATGAA AGAATCGCTC
1051 GCCGTCCGAA CCGCCAACCT CAACCGGCAC GCCGTAAGC GTTATCCTTT
1101 CCCGACCACA ACGGGCAATG CCGTCGCCAG CGGCATGATG GATGCGGTTT
1151 CCGGCTCGGT TATGATGATG CACGGGCGTT TGAAAGAAAA AACCAGGGCG
1201 GGCAAGCCTG TCGATGTCAT CATTACCGGC GCGGCGCGCG CAAAAGTTGC
1251 CGAAGCCCTG CCGCTGCAT TTTTGGCGGA AAATACCGTG CGCGTGGCGG
1301 ACAACCTCGT CATTACGGG CTGCTGAACC TGATTCCCGC CGAAGGCGGG
1351 GAATCGGAAC ATACTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1294; ORF 311.a>:

```

a311.pep
1   MFSFGWVFD R PQYELGSLSP VAAVACRRAL SRLGLKTQIK WPNDLVVGRD
51  KLGGILIE TV RTGGKTVAVV GIGINFLPK EVENAASVQS LFQTASRRGN
101 ADAAVLLE TL LAELDAVLLQ YARDGFAPFV AEYQANRDH GKAVLLLRDG
151 ETVFEGTV KG VDGQGVHLH LE TAEGKQTVVS GEISLRSDDR PVSVPKRRDS
201 ERFLLLD GGN SRLKWAVVEN GTFATVGSAP YRDLSPLGAE WAEKVDGNVR
251 IVGCAVCE GF KKAQVQEQLA RKIEWLPSSA QALGIRNHYR HPPEHGS DRW
301 FNALGSRR FS RNACVVVSCG TAVTVDALTD DGHYLG GTIM PGFHLMKESL
351 AVRTANLN RH AGKRYPFPTT TGNASVSGMM DAVCGSVMM HGRLEKKTGA
401 GKPVDVI ITG GGAAKVAEAL PPAFLAENTV RVADNLVIH G LLNLIAAEGG
451 ESEHT*

```

m311/a311 81.3% identity in 455 aa overlap

712

```

      10      20      30      40      50      60
m311.pep  MFSFGWVFDRPQYELGSLSPVAACRRALSRLGLDVQIKWPNDLVVGRDKLGGILIVT
a311      MFSFGWVFDRPQYELGSLSPVAACRRALSRLGLKTQIKWPNDLVVGRDKLGGILIVT
      10      20      30      40      50      60

      70      80      90     100     110
m311.pep  RTGGKTVAVVGIGINFLPXEVENAASVQSLFQTASRRGNADAALLXXXXXXXX-----
a311      RTGGKTVAVVGIGINFLPXEVENAASVQSLFQTASRRGNADAALLLETLAELDAVLLQ
      70      80      90     100     110     120

m311.pep  -----
a311      YARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGVGQGVLLHLETAEGKQTVVS
      130     140     150     160     170     180

      120     130     140     150     160     170
m311.pep  -EISLRSDXRPVSVXKRRDSEFLLLDGGSRLKWAWVNGTGFATVGSAPYRDLSPLGAE
a311      GEISLRSDDRPVSVPKRRDSEFLLLDGGSRLKWAWVNGTGFATVGSAPYRDLSPLGAE
      190     200     210     220     230     240

      180     190     200     210     220     230
m311.pep  WAEKADGNVRIVGCAVCGEFKKAQVQEQ LARKIEWLPSSAQALFGIRNHYRHPEEHGSDR
a311      WAEKVDGNVRIVGCAVCGEFKKAQVQEQ LARKIEWLPSSAQAL-GIRNHYRHPEEHGSDR
      250     260     270     280     290

      240     250     260     270     280     290
m311.pep  WFNALGSRRFSRNACVVVSCGTAVTVDAITDDGHYLGGTIMPGFHLMKESLAVRTANLNR
a311      WFNALGSRRFSRNACVVVSCGTAVTVDAITDDGHYLGGTIMPGFHLMKESLAVRTANLNR
      300     310     320     330     340     350

      300     310     320     330     340     350
m311.pep  HAGKRYPFPTTGNASGMMDAVCGSVMMHGRLEKKTGAGKPDVVIITGGGAAKVAEA
a311      HAGKRYPFPTTGNASGMMDAVCGSVMMHGRLEKKTGAGKPDVVIITGGGAAKVAEA
      360     370     380     390     400     410

      360     370     380     389
m311.pep  LPPAFLAENTVRVADNLVIYGLLNMI AEGREYEH
a311      LPPAFLAENTVRVADNLVIHGLLNLI AEGGESEHTX
      420     430     440     450

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1295>:

g311-1.seq

```

1  ATGACGGTTT TGAAGCCTTC GCATTGGCGG GTGTTGGCGG AGCTTGCCGA
51  CGGTTTGCCG CAACACGTAT CGCAATTGGC GCGTGAGGCG GACATGAAGC
101 CGCAGCAGCT CAACGGTTT TGGCAGCAGA TGCCGCGCGA TATACGCGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CCTTGGCGGT
201 TTTCGATGCC GAAGGTTTGC GCGATCTGGG GGAAGGTCG GGTTCAGCAG
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GCGGCACAAA ACCATATGCG TGACCCACCT
351 GCAAAGTAAG GGCAGGGGCG GGCAGGGGCG GAAGTGGTCG CACCGTTTGG
401 GCGAGTGCCT GATGTTCACT TTCGGCTGGG CGTTTGACCG GCCGCACTAT
451 GAGTTGGGTT CGCTGTCGCC GTTTCGCGCA CTGCGTGCC GCGCGGCTTT
501 GGGGTGTTTG GGTTCGAAA CGCAATCAA GTGGCCAAAC GATTTGGTCG
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACAGT CAGGGCGGGC
601 GGTAAACGCG TTGCCGTGGT CCGTATCGGC ATCAATTCG TGCTGCCCCA
651 GGAAGTGGAA AACCCGCTT CCGTGCAGTC GCTGTTTCAG ACGGCATCGC
701 GCGCGGGCAA TGCCGATGCC GCCGTATTG TGGAAACATT GCTTGCGGAA
751 CTGGGCGCGG TGTGGAACA ATATGCGGAA GAAGGGTTCG CGCCATTTT

```

```

801 AAATGAGTAT GAAACGGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TGCGCGACGG CGAAACCGTG TCGGAAGGCA CGGTTAAAGG CGTGGACGGA
901 CGAGGCGTTC TGCACTTGGA AACGGCAGaa ggCGAACAGa cggtcGtcag
951 cggcGaaaTC AGccTGCgGc CCGacaacag gtcggtttcc GTgccgaagc
1001 gGccggaTc GgaacgttTT tTGCTgttgg aagcggggaa cagccggctc
1051 aAGTGGgcgt gGGTggAAAA Cggcacgttc gcaaccgtgg gcAGCGCgCC
1101 gtaCCGCGAT TTGTCGCCCT TGGGCGCGGA GTGGGCGGAA AAGGCGGATG
1151 GAAATGTCCG CATCGTCGGT TGCGCCGTGT GCGGAGAAAT CAAAAAGGCA
1201 CAAGTGAAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
1301 CCGACCGTTG GTTCAACGCC TTGGGCAGCC GCCGCTTcAG CCGCAACGCC
1351 TGCGTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACCgA
1401 TGACGGACAT TATCTCGGCG GAACATCAT GCCCGGCTT CACCTGATGA
1451 AAGAATCGCT CGCCGTCGGA ACCGCCAACC TCAACCGCCC CGCCGGCAAA
1501 CGTTACCTTT TCCCgACCAC AACGGGCAAC GCCGTCGCAA GCGGCATGAT
1551 GGACGCGGTT TGCGGCTCGA TAATGATGAT GCACGGCCGT TTGAAAGAAA
1601 AAAACGCGCG GGGCAAGCCT GTCGATGTCA TCATTACCGG CGGCGGCGCG
1651 GCGAAAGTCG CCGAAGCCCT GCCGCCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATCCACGG GCTGCTGAAC CTGATTGCCG
1751 CCGAAGCGCG GGAATCGGAA CACGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1296; ORF 311-1.ng>:

g311-1.pep

```

1  MTVLKPSHWR VLAELADGLP QHVSQALAREA DMKPQQLNGF WQOMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRDLGERS GFQALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECLMFS FGWAFDRPOY
151 ELGSLSPVAA LACRRALGCL GLETQIKWPN DLVVGRDKLG GILIETVRAG
201 GKTVAUVVIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLLE
251 LGAVLEQYAE EGFAPFLNEY ETANRDHGKA VLLLRDGETV CEGTVKGVVDG
301 RGVHLHLETA GEQTVVSGEI SLRPDNRVS VPKRPDSERF LLEGGNSRL
351 KQAWVENGTF ATVGSAFYRD LSPLGAEWAE KADGNVRIVG CAVCGESKKA
401 QVKEQLARKI EWLPSAQAL GIRNHYRHE EHGSDRWfNA LGSRRFSRNA
451 CVVVSCGTAV TVDALTDGh YLGGTIMPGF HLMKESLA VR TANLNRPA GK
501 RYPFPTTTGN AVASGMMDAV CGSIMMHGR LKEKNGAGKP VDVIIITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIHGLLN LIAAEGGESE HA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1297>:

m311-1.seq

```

1  ATGACGGTTT TGAAGCTTTC GCACTGGCGG GTGTTGGCGG AGCTTGCCGA
51  CGGTTTGCCG CAACACGTCT CGCAACTGGC GCGTATGGCG GATATGAAGC
101 CGCAGCAGCT CAACGGTTTT TGGCAGCAGA TGCCGCGCGA CATACGCGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CATTGGCGGT
201 TTTCGATGCC GAAGGTTTGC GCGAGCTGGG GGAAAGGTcG GGTTTTCAGA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GGCGCACAAA ACCATATGCG TGACCCACCT
351 GCAAAGTAAG GGCAGGGGGC GGCAGGGGCG GAAGTGGTCG CACCGTTTGG
401 GCGAGTGTCT GATGTCAGT TTTGGCTGGG TGTGTTGACC GCCGCAGTAT
451 GAGTTGGGTT CGCTGTCGCC TGTTGCGGCA GTGGCGTGTC GGCGCGCCTT
501 GTCGCGTTTA GGTGTTGATG TGCAGATTAA GTGGCCCAAT GATTGTTGTTG
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACGGT CAGGACGGGC
601 CGCAAAACGG TTGCCGTGGT CGGTATCGGC ATCAATTTTG TCCTGCCCAA
651 GGAAGTAGAA AATGCCGCTT CCGTGCAATC GCTGTTTCAG ACGGCATCGC
701 GCGGGGGCAA TGCCGATGCC GCCGTGCTGC TGGAAACGCT GTTGGTGGAA
751 CTGGACGCGG TGTTGTTGCA ATATGCGCGG GACGGATTG CGCCTTTTGT
801 GGCGGAATAT CAGGCTGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TGCGCGACGG CGAAACCGTG TTCGAAGGCA CGGTTAAAGG CGTGGACGGA
901 CAAGGCGTTT TGCACCTGGA AACGGCAGAG GGCAACAGA CGGTCGTCAG
951 CGGCGAAATC AGCCTGCGGT CCGACGACAG GCCGGTTTCC GTGCCGAAGC
1001 GGCGGGATTG GGAACGTTTT CTGCTGTTGG ACGGCGGCAA CAGCCGGCTC
1051 AAGTGGGCGT GGGTGAAAAA CGGCACGTTT GCAACCGTCG GTAGCGCGCC
1101 GTACCGCGAT TTGTGCGCTT TGGGCGCGGA GTGGGCGGAA AAGGCGGATG
1151 GAAATGTCCG CATCGTCGGT TGCGCTGTGT GCGGAGAAAT CAAAAAGGCA
1201 CAAGTGCAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
1301 CCGACCGCTG GTTCAACGCC TTGGGCAGCC GCCGCTTcAG CCGCAACGCC
1351 TGCGTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACCgA
1401 TGACGGACAT TATCTCGGGG GAACATCAT GCCCGGTTT CACCTGATGA
1451 AAGAATCGCT AGCCGTCGGA ACCGCCAACC TCAACCGGCA CGCCGGTAAG
1501 CGTTATCCTT TCCCgACCAC AACGGGCAAT GCCGTCGCCA GCGGCATGAT
1551 GGATGCGGTT TGCGGCTCGG TTATGATGAT GCACGGGCGT TTGAAAGAAA
1601 AAACCGGGCG GGGCAAGCCT GTCGATGTCA TCATTACCGG CGGCGGCGCG
1651 GCAAAAGTTG CCGAAGCCCT GCCGCCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATTTACGG GTTGTGAAC ATGATTGCCG

```

1751 CCGAAGGCAG GGAATATGAA CATATTAA

This corresponds to the amino acid sequence <SEQ ID 1298; ORF 311-1>:

m311-1.pep

```
1  MTLVKLSHWR VLAELADGLP QHVSQALARM DMKPQQLNGF WQMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRELTERS GFOTALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECLMFS FGWVDFRPQY
151 ELGSLSPVAA VACRRALSRL GLDVQIKWPN DLVVGRDKLG GILLETVRTG
201 GKTAVVVGIG INFVLPKEVE NAASVQSLFO TASRRGNADA AVLLETLLVE
251 LDAVLLQYAR DGFAPFVAEY QANRDHGKA VLLLRDGETV FEGTVKGVGDG
301 QGVLHLETAE GKQTVVSGEI SLRSDDRPVS VPKRRDSERF LLLDGGNSRL
351 KWAVVENGTF ATVGSAPYRD LSPLGAEWAE KADGNVRIVG CAVCGEFKKA
401 QVQEQALARKI EWLPSAQAL GIRNHYRHPE EHGSDRFNA LGSRRFSRNA
451 CVVVSCTAV TVDALDDGH YLGGTIMPGF HLMKESLAVR TANLNRHAGK
501 RYFPPTTTGN AVASGMMDAV CGSVMHMRGR LKEKTGAGKP VDVIIITGGA
551 AKVAEALPPA FLAENTVRVA DNLVIYGLLN MIAAEGREYE HI*
```

m311-1/g311-1 93.9% identity in 591 aa overlap

m311-1.pep	10	20	30	40	50	60
	MTLVKLSHWRVLAELADGLPQHVSQALARMADMKPQQLNGFWQMPAHIRGLLRQHDGYWR					
g311-1	MTLVKPSHWRVLAELADGLPQHVSQALAREADMKPQQLNGFWQMPAHIRGLLRQHDGYWR					
	10	20	30	40	50	60
m311-1.pep	70	80	90	100	110	120
	LVRPLAVFDAEGLRELTERS GFOTALKHECASSNDEILELARIAPDKAHKTICVTHLQSK					
g311-1	LVRPLAVFDAEGLRDLGERSGFOTALKHECASSNDEILELARIAPDKAHKTICVTHLQSK					
	70	80	90	100	110	120
m311-1.pep	130	140	150	160	170	180
	GRGRQGRKWSHRLGECLMFSFGWVDFRPQYELGSLSPVAAVACRRALSRLGLDVQIKWPN					
g311-1	GRGRQGRKWSHRLGECLMFSFGWAFDRPQYELGSLSPVAAALACRRALGCLGLETQIKWPN					
	130	140	150	160	170	180
m311-1.pep	190	200	210	220	230	240
	DLVVGRDKLGGILLETVRTGGKTVAVVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA					
g311-1	DLVVGRDKLGGILLETVRAGGKTVAVVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA					
	190	200	210	220	230	240
m311-1.pep	250	260	270	280	290	300
	AVLLETLLVELDAVLLQYARDGFAPFVAEYQANRDHGKAVLLLRDGETVFEGTVKGVGDG					
g311-1	AVLLETLLAELGAVLEQYAEFGFAPFLNEYETANRDHGKAVLLLRDGETVCEGTVKGVGDG					
	250	260	270	280	290	300
m311-1.pep	310	320	330	340	350	360
	QGVLHLETAEGKQTVVSGEISLRSDDRPVSVPKRRDSERFLLLDGGNSRLKWAVVENGTF					
g311-1	RGVLHLETAEGEQTVVSGEISLRPDNRSVSVPKRPDSERFLLLEGGNSRLKWAVVENGTF					
	310	320	330	340	350	360
m311-1.pep	370	380	390	400	410	420
	ATVGSAPYRDLSPGLAEWAEEKADGNVRIVGCAVCGEFKKAQVQEQALARKIEWLPSSAQAL					
g311-1	ATVGSAPYRDLSPGLAEWAEEKADGNVRIVGCAVCGESKKAQVKEQLARKIEWLPSSAQAL					
	370	380	390	400	410	420
m311-1.pep	430	440	450	460	470	480
	GIRNHYRHPEEHGSDRFNALGSRFRSRNACVVVSCGTAVTVDALDDGHYLGGTIMPGF					
g311-1	GIRNHYRHPEEHGSDRFNALGSRFRSRNACVVVSCGTAVTVDALDDGHYLGGTIMPGF					
	430	440	450	460	470	480
m311-1.pep	490	500	510	520	530	540
	HLMKESLAVRTANLNRHAGKRYFPPTTTGNASGMMDAVCGSVMHMRGRLEKKTGAGKP					
g311-1	HLMKESLAVRTANLNRHAGKRYFPPTTTGNASGMMDAVCGSVMHMRGRLEKKTGAGKP					
	490	500	510	520	530	540
	550	560	570	580	590	

m311-1.pep VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIYGLLNMIAAEGREYEHIX
|||||:|||||
g311-1 VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIHGLLNLIAAEGGESEHAX
550 560 570 580 590

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1299>:

a311-1.seq

```
1 ATGACGGTTT TGAAGCCTTC GCACTGGCGG GTGTTGGCGG AGCTTGCCGA
51 CGGTTTGCCG CAACACGTCT CGCAACTGGC GCGTATGGCG GATATGAAGC
101 CGCAGCAGCT CAACGGTTTT TGGCAGCAGA TGCCGGCGCA CATACGCGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CATTGGCGGT
201 TTTCGATGCC GAAGGTTTGC GCGAGCTGGG GGAAAGGTCG GGTTTTCAGA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GGCGCACAAA ACCATATGTG TGACCCACCT
351 GCAAAGTAAG GGCAGGGGGC GGCAGGGGCG GAAGTGGTCG CACCGTTTGG
401 GCGAGTGTCT GATGTTCACT TTTGGCTGGG TGTTTGACCG GCCGCAGTAT
451 GAGTTGGGTT CGCTGTCGCC TGTGCGGCA GTGGCGTGCC GGCGCGCCTT
501 CTCGCGTTTG GGTTTGAAAA CGCAATCAA GTGGCCAAAC GATTTGGTCG
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACGGT CAGGACGGGC
601 GGCAAACCGG TTGCGGTGGT CGGTATCGGC ATCAATTTCG TGCTGCCCAA
651 GGAAGTGGAA AACCGCGCTT CCGTGCAATC GCTGTTTCAG ACGGCATCGC
701 GGCGGGGAAA TGCCGATGCC GCCGTGTTGC TGGAAACGCT GTTGGCGGAA
751 CTTGATGCGG TGTGTTGCA ATATGCGCGG GACGGATTG CGCCTTTTGT
801 GGCGGAATAT CAGGCTGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TGCGCGCAGG CGAAACCGTG TTCGAAGGCA CGGTTAAAGG CGTGGACGGA
901 CAAGGCGTTC TGCATTGGA AACGGCAGAG GGCAAACAGA CGGTCGTCAG
951 CGCGGAAATC AGCCTGCGGT CCGACGACAG GCCGGTTTCC GTGCCGAAGC
1001 GGCGGGATTG GGAACGTTTT CTGCTGTTGG ACGGCGGCAA CAGCCGGCTC
1051 AAGTGGGCGT GGGTGGAAAA CGGCACGTTT GCAACCGTCG GTAGCGCGCC
1101 GTACCGCGAT TTGTCGCCTT TGGGCGCGGA GTGGGCGGAA AAGGTGGATG
1151 GAAATGTCCG CATCGTCGGT TGCGCGGTGT GCGGAGAATT CAAAAAGGCA
1201 CAAGTGCAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
1301 CCGACCGCTG GTTCAACGCC TTGGGCGAGC GCCGCTTCAG CCGCAACGCC
1351 TCGCTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACCGA
1401 TGACGGACAT TATCTCGGGG GAACCATCAT GCCCGGTTT CACCTGATGA
1451 AAGAATCGCT CGCCGTCCGA ACCGCCAACC TCAACCGGCA CGCCGGTAAG
1501 CGTTATCCTT TCCCGACCAC AACGGGCAAT GCCGTCGCCA GCGGCATGAT
1551 GGATGCGGTT TGCGGCTCGG TTATGATGAT GCACGGGCGT TTGAAAGAAA
1601 AAACCGGGGC GGGCAAGCCT GTCGATGTCA TCATTACCGG CGGCGGCGCG
1651 GCAAAAGTTG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACTCG TCATTACCG GCTGCTGAAC CTGATTGCCG
1751 CCGAAGGCGG GGAATCGGAA CATACTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1300; ORF 311-1.a>:

a311-1.pep

```
1 MTVLKPSHWR VLAELADGLP QHVSQARMAD DMKPOQLNGF WQOMPAHIRG
51 LLRQHDGYWR LVRPLAVFDA EGLRELTERS GFQTLKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECIMFS FGWVDRPQY
151 ELGSLSPVAA VACRRALSRL GLKTIQKWPV DLVVRGDKLG GILLETVRTG
201 GKTVAVVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLLAE
251 LDAVLLQYAR DGFAPFVAEY QAANRDHGKA VLLLRDGETV FEGTVKGVDS
301 QGVHLHLEAE GKQTVVSGEI SLRSDDRPVS VPKRRDSERF LLLDGGNSRL
351 KWAUVENGTF ATVGSAPYRD LSPLGAEWAE KVDGNVRIVG CAVCGEFKKA
401 QVQEQLARKI EWLPSAQAL GIRNHYRHEP EHGSDRWANA LGSRRFSRNA
451 CVVVSCTGAV TVDALTDDGH YLGGTIMPGF HLMKESLAVR TANLNRHAGK
501 RYPFPTTTGN AVASGMMDAV CGSVMMHGR LKEKTGAGKP VDVIITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIHGLLN LIAAEGGESE HT*
```

a311-1/m311-1 98.5% identity in 591 aa overlap

```
10 20 30 40 50 60
a311-1.pep MTVLKPSHWRVLAELADGLPQHVSQARMADMKPOQLNGFWQOMPAHIRGLLRQHDGYWR
|||||
m311-1 MTVLKLSHWRVLAELADGLPQHVSQARMADMKPOQLNGFWQOMPAHIRGLLRQHDGYWR
10 20 30 40 50 60

70 80 90 100 110 120
a311-1.pep LVRPLAVFDAEGLRELTERSFGFQTLKHECASSNDEILELARIAPDKAHKTICVTHLQSK
|||||
m311-1 LVRPLAVFDAEGLRELTERSFGFQTLKHECASSNDEILELARIAPDKAHKTICVTHLQSK
70 80 90 100 110 120
```

a311-1.pep	130	140	150	160	170	180
	GRGRQGRKWSHRLGEC	LMFSFGWV	FD	RPQYELGSLSPVAAVACRRALSRLGLKTQIKWPN		
m311-1	GRGRQGRKWSHRLGEC	LMFSFGWV	FD	RPQYELGSLSPVAAVACRRALSRLGLDVQIKWPN		
	130	140	150	160	170	180
a311-1.pep	190	200	210	220	230	240
	DLVVGRDKLGGIL	ETVRTGGKT	VAVVGIGIN	FVLPKEVENAASVQSLFQTASRRGNADA		
m311-1	DLVVGRDKLGGIL	ETVRTGGKT	VAVVGIGIN	FVLPKEVENAASVQSLFQTASRRGNADA		
	190	200	210	220	230	240
a311-1.pep	250	260	270	280	290	300
	AVLLETLLAELDAV	LQYARDGF	FAPFVAEYQA	ANRDHGKAVLLLRDGETVFEGTVKGV	VDG	
m311-1	AVLLETLLVELDAV	LQYARDGF	FAPFVAEYQA	ANRDHGKAVLLLRDGETVFEGTVKGV	VDG	
	250	260	270	280	290	300
a311-1.pep	310	320	330	340	350	360
	QGVHLHLETAEGK	QTVVSGEIS	LRSDDRPV	SVPKRRDSE	RFLLDGGNSRLKWAWV	ENGTF
m311-1	QGVHLHLETAEGK	QTVVSGEIS	LRSDDRPV	SVPKRRDSE	RFLLDGGNSRLKWAWV	ENGTF
	310	320	330	340	350	360
a311-1.pep	370	380	390	400	410	420
	ATVGSAPYRDLSP	LGAEWA	EKV	DGNVRI	VGCAVCGE	FKAQVQEQLARKIEWLPSSAQAL
m311-1	ATVGSAPYRDLSP	LGAEWA	EKADGNV	RI	VGCAVCGE	FKAQVQEQLARKIEWLPSSAQAL
	370	380	390	400	410	420
a311-1.pep	430	440	450	460	470	480
	GIRNHYPHEEHGS	DRWFNALG	SRFRSRN	ACVVVSC	GTA	VTDALTDG
m311-1	GIRNHYPHEEHGS	DRWFNALG	SRFRSRN	ACVVVSC	GTA	VTDALTDG
	430	440	450	460	470	480
a311-1.pep	490	500	510	520	530	540
	HLMKESLAVRTAN	LNHRHAG	KRYPPFT	TTGNAVAS	GMMDAV	CGSVMMHGRLEKE
m311-1	HLMKESLAVRTAN	LNHRHAG	KRYPPFT	TTGNAVAS	GMMDAV	CGSVMMHGRLEKE
	490	500	510	520	530	540
a311-1.pep	550	560	570	580	590	
	VDVITGGGA	AKVAEAL	PPAFLA	ENTVRVAD	NLVIHGLLN	LIAAEGGESEHTX
m311-1	VDVITGGGA	AKVAEAL	PPAFLA	ENTVRVAD	NLVIYGLLN	MIAAEGREYEHIX
	550	560	570	580	590	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1301>:

g312.seq

```

1  atgaGtatCc aatCcGgcga AATTTtagaa accgtCAAAA TGGTTGCCGA
51  ccggaATttt gAtgtccgCA CCATTaccat cggcaTTgaT ttgcacgact
101 gcatcagcac cgacatcgac gtgttaAACC AAAACATtta caaCAaaaTc
151 accacggctcg gcaaagactT GGTGGCAacg Gcgaaacacc tTTccgcCAA
201 ATACGGCGTG CCGATTGTGA ATCAGCGCAT TTCCGTTACG CCGAttgccc
251 AaatcGCGGC GGcgaccaAa gccgaCAGTT AtgtcAGCgt ggcgcAGact
301 tTGGACAAGG CAGCCAAAGC CATCGGCGTG TCCTTTATCG GcggCTTTTC
351 CGCGCTGGTG CAAAAAGGTA TGTCGCCTTC GGATGAGGTG TTGATCCGTT
401 CCGTTCCCGA AGCGATGAAA ACTACCGATA TCGTGTGCAG CTCCATCAAT
451 ATCGGCAGCA CGCGTGCCGG TATCAATATG GATGCGGTCA AGCTGGCAGG
501 CGAAACCATC AAACGCACGG CTGAAATCAC ACCCGAAGGT TTCGGCTGCG
551 CCAAAATCGT CGTGTCTGC AACCGGGTGG AAGACAATCC GTTTATGGCG
601 GGTGCGTTCC ACGGCTCGGG CGAAGCGGAT GCTGTGATTA ATGTCGGCGT
651 ATCCGGTCCA GCGGTGGTCA AAGCCGCGCT GGAAATTCG GACGCGGTCA
701 GCCTGACCGA GGTGCGCGAA GTCGTGAAGA AAACCGCTTT CAAAATCACC
751 CGCGTGGGCG AACTCATCGG TCGCGAAGCC TCAAAAATGC TGAATATCCC
801 GTTCGGCATT CTCGATTGTG CGCTGGCACC GACCCCGCC GTCGGCGACT
851 CCGTGGCGCG CATTCTTGAA GAAATGGGCT TGAGCGTCTG CGGTACGCAC

```



```

901 GGCACAACAG CAGCTTTGGC ATTGCTGAAC GATGCCGTGA AAAAGGGCGG
951 CATGATGGCT TCCAGCGCGG TCGGCGGTTT GAGCGGCGCG TTTATCCCCG
1001 TTTCGAAGA CGAAGGTATG ATTGCCGCCG CCGAGGCAGG CGTGTTGACG
1051 CTGGACAAAC TCGAAGCCAT GACCGCCGTC TGCTCCGTTG GTTTGGACAT
1101 GATTGCCGTT CCCGGCGACA CGCCCGCGCA CACCATTTCG GGCATCATCG
1151 CCGACGAAGC CGCCATCGGC ATGATCAACA GCAAAACCAC CGCCGTGCGC
1201 ATTATCCGG TAACGGGCAA AACCGTCGGC GACAGCGTCG AGTTCGGCGG
1251 TCTGTTGGGC TACGCGCCTG TAATGCCGGC AAAAGAAGGT TCGTGCGAAG
1301 TGTTCTGCAA CCGGGGCGGC AGGATTCCCG CACCGGTTCA ATCGATGAAA
1351 AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1302; ORF 312.ng>:

g312.pep

```

1  MSIQSGEILE TVKMVADRNF DVRTITIGID LHDCISTDID VLNQNIYNKI
51  TTVGKDLVAT AKHLSAKYGV PIVNQRISVT PIAQIAAATK ADSYVSVAQT
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSVPEAMK TTDIVCSSIN
151 IGSTRAGINM DAVKLAGETI KRTAEITPEG FGCAKIVVFC NAVEDNPFMA
201 GAFHGSGEAD AVINVGVSGP GVVKAALENS DAVSLTEVAE VVKKTAFKIT
251 RVGELIGREA SKMLNIPFGI LDLSLAPTPA VGDSVARILE EMGLSVCGTH
301 GTTAALALLN DAVKKGGMMA SSAVGGLSGA FIPVSEDEGM IAAAEAGVLT
351 LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR
401 IIPVTGKTVG DSVEFGGLLG YAPVMPAKEG SCEVFVNRGG RIPAPVQSMK
451 N*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1303>:

m312.seq

```

1  ATGAGTATCC AATCCGGCGA AATTTTAGAA ACCGTCAAAA TGGTTGCCGA
51  CCAGAATTTT GATGTCCGCA CCATTACCAT CGGCATTGAT TTGCACGACT
101 GCATCAGCAG CGATATCAAT GTGTTGAACC AAAATATTTA CAATAAAATT
151 ACCACAGTCG GCAAAGACTT GGTCACTACG GCAAAATATC TGTCTGCCAA
201 ATACGGCGTA CCGATTGTGA ATCAGCGCAT TTCCGTTACG CCGATTGCCC
251 AAATCGCGGC GGCCACCCAT GCTGATTCTT ACGTCAGCGT GGCAGAACT
301 TTGGATAAAG CTGCCAAAGC CATCGGTGTG TCTTTTATCG GCGGTTTTTC
351 CGCGTTGGTG CAAAAAGGGA TGTCGCcTTC GGATGAGGTG TTAATCCGCT
401 CCATTCCCGA AGCGATGAAG ACTACCGATA TTGTGTGCwG CTCCATCAAT
451 ATCGGCAGTA CGCGTGCCGG TATCAATATG GATGCGGTCA AGTGGCGGG
501 CGAAACCGTc AAACGCACGG CGGAAATCAC GCCCGAAGGT TTCGGCTGCG
551 CTAAAATTGT CGTGTCTGTC AACCGGTGG AAGACAACCC GTTTWTGGCG
601 GGCGCGTTTC ATGGTTCCGG CGATGCCGTT ATCAATGTCG GCGTATCCGG
651 CCCAGGTGTC GTAAAAGCCG CGTTGGAAAA TTCAGATGCA ACGACATTGA
701 CCGAAGTTGC GGAAGTAGTG AAGAAAACTG CTTTCAAAAT TACCCGCGTG
751 GGCGAACTCA TCGGCCGCGA AGCcTCAAAA ATGCTGAATA TCCCGTTTGG
801 TATTCTCGAC TTGTGCGCGA CCCCGCCCGT CGGCGACTCA GTGGCACGCA
851 TTCTTGAAGA AATGGGCTTG AGCGTCTGCG GTACGCACGG CACAACAGCA
901 GCTTTGGCAT TGCTGAACGA TGCCGTGAAA AAAGGCGGCA TGATGGCTTC
951 CAGCGCGGTC GGGGGTTTGA GTGGCGCGTT TATCCCGGTT TCCGAAGACG
1001 AAGGTATGAT yGmCgCcGCC GAAGCAGGCG TGCTGACGCT GGACAAACTC
1051 GAAGCCATGA CCGCGGTTTG TTCGGTCGGC TTGGATATGA TTGCCGTTCC
1101 CGGCGACACG CCCGCGCACA CCATTTCGG CATCATTGCC GACGAAGCCG
1151 CCATCGGCAT GATCAACAGC AAAACCACTG CCGTGCGCAT TATTCCGGTA
1201 ACCGGTAAAA CCGTCGGCGA CACGGTCGAG TTCGGCGGCT TGTGGGCTA
1251 CGCGCCTGTG ATGCCGGTCA AAGAAGGTTT GTGCGAAGTA TTCGTCAACC
1301 GAGCGGCGAG AATTCCGGCT CCGGTTCAAT CGATGAAAAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1304; ORF 312>:

m312.pep

```

1  MSIQSGEILE TVKMVADQNF DVRTITIGID LHDCISSDIN VLNQNIYNKI
51  TTVGKDLVTT AKYLSAKYGV PIVNQRISVT PIAQIAAATH ADSYVSVAQT
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSIPEAMK TTDIVCSXIN
151 IGSTRAGINM DAVKLAGETV KRTAEITPEG FGCAKIVVFC NAVEDNPFXA
201 GAFHGSGLAV INVGVSGPGV VKAALENS DA TLTTEVAEVV KKTAFKITRV
251 GELIGREASK MLNIPFGILD LSPTPPVGDS VARILEEMGL SVCGTHGTTA
301 ALALLNDAVK KGGMMASSAV GGLSGAFIPV SEDEGMIXAA EAGVLTLDKL
351 EAMTAVCSVG LDMIAVPGDT PAHTISGIIA DEAAIGMINS KTTAVRIIPV
401 TGKTVGDTVE FGGLLGYPAP MPVKEGSEV FVNRRGGRIPA PVQSMKN*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 312 shows 95.6% identity over a 451 aa overlap with a predicted ORF (ORF 312.ng) from *N. gonorrhoeae*:

m312/g312

	10	20	30	40	50	60
m312.pep	MSIQSGEILETVKMVADQNFVDTITIGIDLHDCISSDINVLNQNIYNKITTVGKDLVTT					
	: : : : :					
g312	MSIQSGEILETVKMVADRNFDVDTITIGIDLHDCISTDIDVLNQNIYNKITTVGKDLVAT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m312.pep	AKYLSAKYGVPIVNQRISVTPIAQIAAATHADSYVSVQAQTLDKAAKAIGVSFIGGFSALV					
	: : : : :					
g312	AKHLSAKYGVPIVNQRISVTPIAQIAAATKADSYVSVQAQTLDKAAKAIGVSFIGGFSALV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m312.pep	QKGMSPSDEVLIRSIPEAMKTTDIVCXNIGSTRAGINMDAVKLAGETVKRTAEITPEG					
	: : : : :					
g312	QKGMSPSDEVLIRSVPEAMKTTDIVCSSINIGSTRAGINMDAVKLAGETIKRTAEITPEG					
	130	140	150	160	170	180
	190	200	210	220	230	
m312.pep	FGCAKIVVFCNAVEDNPFKXAGAFHSGG--DAVINVGVSFGPGVVKAALENS DATTLTEVAE					
	: : : : :					
g312	FGCAKIVVFCNAVEDNPFMAGAFHSGGEADAVINVGVSFGPGVVKAALENS DAVSLTEVAE					
	190	200	210	220	230	240
	240	250	260	270	280	290
m312.pep	VVKKTAFKITRVGELIGREASKMLNIPFGILDLS--PTPPVGDSVARILEEMGLSVCGTH					
	: : : : :					
g312	VVKKTAFKITRVGELIGREASKMLNIPFGILDLSLAPTPAVGDSVARILEEMGLSVCGTH					
	250	260	270	280	290	300
	300	310	320	330	340	350
m312.pep	GTTAALALLNDAVKKGGMMASAVGGLSGAFIPVSEDEGMIXAAEAGVLTLDKLEAMTAV					
	: : : : :					
g312	GTTAALALLNDAVKKGGMMASAVGGLSGAFIPVSEDEGMIAAAEAGVLTLDKLEAMTAV					
	310	320	330	340	350	360
	360	370	380	390	400	410
m312.pep	CSVGLDMIAPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTGVDTFEFGGLLG					
	: : : : :					
g312	CSVGLDMIAPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTGVDTSVEFGGLLG					
	370	380	390	400	410	420
	420	430	440			
m312.pep	YAPVMPVKEGSCEVFVNRRGGRIPAPVQSMKNX					
	: : : : :					
g312	YAPVMPAKEGSCEVFVNRRGGRIPAPVQSMKNX					
	430	440	450			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1305>:

a312.seq

1	ATGAGTATCC	AATCCGGCGA	AATTTTAGAA	ACCGTCAAAA	TGTTGCCGA
51	CCAGAATTTC	GATGTCCGCA	CCATTACCAT	CGGCATTGAT	TTGCACGACT
101	GCATCAGCAC	CGACATCGAC	GTGTTGAACC	AAAATATTTA	CAACAAAATT
151	ACCACGGTCG	GCAAAGACTT	GGTGGCGACA	GCAAAATATC	TGTCTGCCAA
201	ATACGGCGTG	CCGATTGTGA	ATCAGCGCAT	TTCTGTCACG	CCGATTGCC
251	AAATCGCGGC	GGCCACCCAT	GCTGATTCTT	ACGTCAGCGT	GGCGCAAAC

```

301 TTGGATAAGG CTGCCAAAGC CATCGGCGTG TCTTTTATTG GCGGCTTTTC
351 CGCGCTGGTG CAAAAAGGTA TGTCGCCTTC TGACGAGGTG TTAATCCGTT
401 CCATTCCCGA AGCGATGAAG ACTACTGATA TCGTGTGCAG CTCCATCAAT
451 ATCGGCAGTA CGCGCGCCGG TATCAATATG GACGCGGTCA GACTGGCGGG
501 CGAAACCATC AAACGCACGG CTGAAATCAC ACTAGAAGGT TTCGGCTGCG
551 CAAAATCGT CGTGTCTGCG AACGCGGTGG AAGACAACCC GTTTATGGCG
601 GGCGCGTTTC ACGGCTCAGG CGAAGCGGAT GCTGTGATTA ATGTCGCGCT
651 ATCCGGCCCG GGTGTCGTAA AAGCCGCGTT GGAAAATTTCG GATGCAACGA
701 CATTGACCGA AGTTGCCGAA GTTGTGAAGA AAACCGCCTT CAAAATTACC
751 CGCGTGGGCG AACTCATCGG CCGCGAAGCC TCAAAAATGC TGAATATCCC
801 GTTTGGTATT CTCGACTTGT CGCTGGCACC GACCCCTGCC GTCGGCGACT
851 CGGTGGCGCG CATTCTTGAA GAAATGGGTT TGAGCGTCTG CGGTACGCAC
901 GGCACAACAG CAGCTTTGGC ATTGCTGAAC GATGCCGTGA AAAAGGCGCG
951 CATGATGGCT TCGAGCGCGG TTGGCGGTTT GAGTGGCGCG TTTATCCCGG
1001 TTTCCGAAGA CGAAGGTATG ATTGCCGCCG CCGAAGCAGG CGTGCTGACG
1051 TTGGATAAAC TCGAAGCGAT GACCGCCGTT TGTTCCGGTCG GCTTGGATAT
1101 GATTGCCGTT CCCGGCGACA CACCGCGCA CACCATTTC GGCATCATTG
1151 CCGACGAAGC CGCCATCGGC ATGATCAACA GCAAAACCAC TGCCGTGCGC
1201 ATTATTCCGG TAACCGGTAA AACCGTCGGC GACAGCGTCG AGTTCGGCGG
1251 CCTGTTGGGC TACGCGCTG TAATGCCGGT AAAAGAAGGC TCATGCGAAG
1301 TGTTCTGCAA CCGGGCGGCG AGGATTCCCC CACCGGTTCA ATCGATGAAA
1351 AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1306; ORF 312.a>:

```

a312.pep
  1 MSIQSGEILE TVKMVADQNF DVRTITIGID LHDCISTDID VLNQNIYNKI
 51 TTVGKDLVAT AKYLSAKYGV PIVNQRISVT PIAQIAAATH ADSYVSVAQ
101 LDKAAKAIGV SFIGGFSAIV QKGMSPSDEV LIRSIPEAMK TTDIVCSSIN
151 IGSTRAGINM DAVRLAGETI KRTAEITLEG FGCAKIVVFC NAVEDNPFMA
201 GAFHGSGEAD AVINVGVS GPVVKAALENS DATTLTEVAE VVKKTAFKIT
251 RVGELIGREA SKMLNIPFGI LDLSLAPTPA VGDSVARILE EMGLSVCGTH
301 GTTAALALLN DAVKKGGMMA SSAVGGLSGA FIPVSEDEGM IAAAEAGVLT
351 LDKLEAMTAV CSVGLDMIIV PGDTPAHTIS GIIADEAAIG MINSKTTAVR
401 IIPVTGKTGV DSVEFGGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK
451 N*

```

m312/a312 96.7% identity in 451 aa overlap

```

          10      20      30      40      50      60
m312.pep  MSIQSGEILETVKMVADQNF DVRTITIGIDLHDCISSDINVLNQNIYNKITTVGKDLVTT
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a312       MSIQSGEILETVKMVADQNF DVRTITIGIDLHDCISTDIDVLNQNIYNKITTVGKDLVAT
          10      20      30      40      50      60

          70      80      90     100     110     120
m312.pep  AKYLSAKYGVPIVNQRISVTPIAQIAAATHADSYVSVAQTLDKAAKAIGVSFIGGFSAIV
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a312       AKYLSAKYGVPIVNQRISVTPIAQIAAATHADSYVSVAQTLDKAAKAIGVSFIGGFSAIV
          70      80      90     100     110     120

          130     140     150     160     170     180
m312.pep  QKGMSPSDEVLIRSIPEAMKTTDIVCX SINIGSTRAGINMDAVKLAGETVKRTAEITPEG
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a312       QKGMSPSDEVLIRSIPEAMKTTDIVCSSINIGSTRAGINMDAVRLAGETIKRTAEITLEG
          130     140     150     160     170     180

          190     200     210     220     230
m312.pep  FGCAKIVVFCNAVEDNPF XAGAFHGS G--DAVINVGVS GPVVKAALENS DATTLTEVAE
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a312       FGCAKIVVFCNAVEDNPF MAGAFHGS GEADAVINVGVS GPVVKAALENS DATTLTEVAE
          190     200     210     220     230     240

          240     250     260     270     280     290
m312.pep  VVKKTAFKITRVGELIGREASKMLNIPFGILDLS--PTPPVGDSVARILEEMGLSVCGTH
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a312       VVKKTAFKITRVGELIGREASKMLNIPFGILDLSLAPTPAVGDSVARILEEMGLSVCGTH

```

720

	250	260	270	280	290	300
m312.pep	300	310	320	330	340	350
	GTTAALALLNDAVKKGGMMASAVGGLSGAFIPVSEDEGMIXAAEAGVLTLDKLEAMTAV					
a312	GTTAALALLNDAVKKGGMMASAVGGLSGAFIPVSEDEGMIAAAEAGVLTLDKLEAMTAV					
	310	320	330	340	350	360
m312.pep	360	370	380	390	400	410
	CSVGLDMIAPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDTVEFGGLLG					
a312	CSVGLDMIAPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDSVEFGGLLG					
	370	380	390	400	410	420
m312.pep	420	430	440			
	YAPVMPVKEGSCEVFVNRGGRIAPVQSMKNX					
a312	YAPVMPVKEGSCEVFVNRGGRIAPVQSMKNX					
	430	440	450			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1307>:

g313.seq

```

1  atggacgacc cgcgcaccta cggatcgggc aatcccggcg cgaccaatgt
51  ttacgcgagc ggcaaaaaaa aggcggccgc gctgacgctc ttgggcgatg
101 cgcgcaaaagg tttggttgcc gttttgcttg cagcgctgct tcaagaaccg
151 ctcggtttat ccgacagcgc aatcgccgcc gtcgcactcg ccgcgctggt
201 cgggcatatg tggccggtgt ttttcggatt taagggcggc aaaggcgtgg
251 caacggcatt gggcgtgctt ctggcactct ctcccgcaac tgccttggtc
301 tgcgcgttga tttggcttgt gatggcattc ggcttcaaag tatcctccct
351 tgccgcgctg gtcgccacaa ccgccgcccc ccttgccgca ctgtttttaa
401 tgccgcatac ttcttggtt ttcgcaaccc tcgcaatcgc catattggtg
451 ttgctccgcc ataagagcaa catcctcaac ctgattaaag gcaaagaaag
501 caaaatcggc gaaaaacgct ga

```

This corresponds to the amino acid sequence <SEQ ID 1308; ORF 313.ng>:

g313.pep

```

1  MDDPRTYGS G NPGATNVLR S GKKKAAALTL LGDAAKGLVA VLLARVLQEP
51  LGLSDSAIAA VALAALVGHM WPFVFGFKGG KGVATALGLV LALSPATALV
101 CALIWLVMFA GFKVSSLAAL VATTAPLAA LFFMPHTSWI FATLAIAILV
151 LLRHKSNI LN LIKGESKIG EKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1309>:

m313.seq

```

1  ATGGACGACC CGCGCACCTA CGGATCGGGC AATCCGGGGG CAACCAATGT
51  TTTACGCAGC GGCAAAAAAA AGGCGGCCGC GCTGACGCTC TTGGGCGATG
101 CCGCCAAAGG TTTAGTTGCC GTTTTGCTTG CACGCGTGCT TCAAGAACCG
151 CTCGGTTTAT CCGACAGCGC AATCGCGGCC GTCGCACTCG CCGCGCTGGT
201 CGGGCATATG TGGCCGCTGT TTTTCGGATT TAAAGGCGGC AAAGGCGTGG
251 CAACGGCATT GGGCGTGCTT CTGGCACTCT CTCCCGCAAC TGCCTTGCTC
301 TGCGCGTTGA TTTGGCTTGT TATGGCATTC GGCTTCAAGG TGTCTCCCTT
351 TGCCGCATTA ACCGCCACAA TCGCCGCACC GGTGCGCCGA TCCTTCTTTA
401 TGCCGCACGT CTCGTGGGTT TGGGCGACCG TCGCCATTGC TTTGCTGGTG
451 TTGTTCCGCC ACAAAGTAA TATCGTCAAG CTGCTCGAAG GCAGAGAAAG
501 CAAAATCGGC GGCAGCCGCT GA

```

This corresponds to the amino acid sequence <SEQ ID 1310; ORF 313>:

m313.pep

```

1  MDDPRTYGS G NPGATNVLR S GKKKAAALTL LGDAAKGLVA VLLARVLQEP
51  LGLSDSAIAA VALAALVGHM WPFVFGFKGG KGVATALGLV LALSPATALV
101 CALIWLVMFA GFKVSSLAAL TATIAAPVAA SFFMPHVS WV WATVAIALLV
151 LFRHKSNI VK LLEGRESKIG GSR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 313 shows 90.2% identity over a 173 aa overlap with a predicted ORF (ORF 313.ng) from *N. gonorrhoeae*:

m313/g313

	10	20	30	40	50	60
m313 .pep	MDDPRTYSGNPGATNVLRSGKKKAAALTL LGDAAKGLVAVLLARVLQEP LGLSDSAIAA					
g313	MDDPRTYSGNPGATNVLRSGKKKAAALTL LGDAAKGLVAVLLARVLQEP LGLSDSAIAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m313 .pep	VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPATALVCALIWLVMF GFKVSSLAAL					
g313	VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPATALVCALIWLVMF GFKVSSLAAL					
	70	80	90	100	110	120
	130	140	150	160	170	
m313 .pep	TATIAAPVAASFFMPHVS VWVATVAIALLV LFRHKSNI VKLLEGRESKIGGSRX					
g313	VATTAAPLAALFFMPHTSWIFATLAIAILV LLRHKSNI LNLIKGESKIGEKRX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1311>:

a313.seq

```

1  ATGGACGACC CGCGCACCTA CGGATCGGGC AATCCGGGGG CAACCAATGT
51  TTTACGCAGC GGCAAAAAAA AGGCGGCCGC GCTGACGCTC TTGGGCGATG
101 CCGCCAAAGG TTTGGTTGCC GTTTTGCTTG CACGCGTGCT TCAAGAACCG
151 CTCGGTTTAT CCGACAGCGC AATCGCGGCC GTCGCACTCG CCGCGCTGGT
201 CGGGCATATG TGGCCGGTGT TTTTCGGATT TAAAGCGGCG AAAGGCGTGG
251 CAACGGCATT GGGCGTGCTT CTGGCACTCT CTCCACAAC TGCCTTGGTC
301 TGCGCGTTGA TTTGGCTTGT GATGGCATTG GGCTTCAAGG TGTCTCCCT
351 TGCCGCATTA ACCGCCACAA TCGCCGCCCC CCTTGCCGCA CTGTTTTTTA
401 TGCCGCATAC TTCTTGATT TTCGCAACCC TCGCAATCGC CATATTGGTG
451 TTGCTCCGCC ATAAGAGCAA CATCCTCAAC CTGATTAAAG GCAAAGAAAG
501 CAAAATCGGC GAAAAACGCT GA

```

This corresponds to the amino acid sequence <SEQ ID 1312; ORF 313.a>:

a313.pep

```

1  MDDPRTYSGS NPGATNVLRSGKKKAAALTL LGDAAKGLVA VLLARVLQEP
51  LGLSDSAIAA VALAALVGHM WPVFFGFKGG KGVATALGV LALSPTTALV
101 CALIWLVMF GFKVSSLAAL TATIAAPLAA LFFMPHTSWI FATLAIAILV
151 LLRHKSNI LNLIKGESKIG EKR*

```

m313/a313 90.8% identity in 173 aa overlap

	10	20	30	40	50	60
m313 .pep	MDDPRTYSGNPGATNVLRSGKKKAAALTL LGDAAKGLVAVLLARVLQEP LGLSDSAIAA					
a313	MDDPRTYSGNPGATNVLRSGKKKAAALTL LGDAAKGLVAVLLARVLQEP LGLSDSAIAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m313 .pep	VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPATALVCALIWLVMF GFKVSSLAAL					
a313	VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPATALVCALIWLVMF GFKVSSLAAL					
	70	80	90	100	110	120
	130	140	150	160	170	
m313 .pep	TATIAAPVAASFFMPHVS VWVATVAIALLV LFRHKSNI VKLLEGRESKIGGSRX					
a313	TATIAAPLAALFFMPHTSWIFATLAIAILV LLRHKSNI LNLIKGESKIGEKRX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1313>:

```
g401.seq
  1  atgaaattac aacaattggc tgaagaaaaa atcggcggtc tgatttgtgtt
 51  cacgctgctt gtagtcagtg tcggtctggt gattgaagtt gtgcccttgg
101  cctttaccaa ggcggcaaca cagccggcgc cgggcgtgaa gccttacaa
151  gccctgcagg ttgccggacg cgatatttac atccgtgagg gctgttacaa
201  ctgccactct caaatgattc gtccgttccg tgcggaaacc gagcgttacg
251  gtcattactc tgttgccgga gagtcggttt acgaccatcc gttccaatgg
301  ggttccaaac gtaccggtcc tgatttggca cgtgtgggcg gccgctattc
351  cgacgaatgg caccgcatcc acctgctgaa tccccgtgat gtcgtgcctg
401  agtccaatat gccggcattc ccgtggcttg cacgcaataa agtcgatgtc
451  gatgcaaccg ttgccaacat gaaggctttg cgtaaagtag gtactcctta
501  cagtgatgag gaaattgcca aagcgctga ggctttggca aacaaatccg
551  agctggatgc ttagtcgcc tatctgcaag gattgggtct ggctttgaaa
601  aacgtaaggt aa
```

This corresponds to the amino acid sequence <SEQ ID 1314; ORF 401.ng>:

```
g401.pep
  1  MKLQQLAEEK IGV LIVFTLL VSVGLLIEV VPLAFTKAAT QPAPGVKPYN
 51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESVYDHPFQW
101  GSKRTGPDLA RVGGRYSEW HRIHLLNPRD VVPESNMPAF PWLARNKVDV
151  DATVANMKAL RKGTPYSDE EIAKAPEALA NKSELDVVA YLQGLGLALK
201  NVR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1315>:

```
m401.seq
  1  ATGAAATTAC AaCAATTGGC TGAAGAAAAA ATCGGCGTTC TGATTGTGTT
 51  CACGCTGCTT GTAGTCAGTG TCGGTCTGTT GATTGAAGTT GTGCCCTTGG
101  CCTTTACCAA GCGGCAACA CAGCCGGCGC CGGGCGTGAA GCCTTACAA
151  GCCCTGCAGG TTGCCGGACG CGATATTTAC ATCCGTGAGG GCTGTACAA
201  CTGCCACTCG CAAATGATTG GTCCGTTCCG TCGGAAACC GAGCGTTACG
251  GTCATTACTC TGTTGCCGGA GAGTCGTTT ACGACCATCC GTTCCAATGG
301  GGTTCCAAAC GTACCGGTCC TGATTGGCA CGTGTGGGCG GTCGCTATTC
351  CGACGAATGG CACCGTATCC ACCTGCTGAA TCCCCGTGAT GTCGTGCCTG
401  AGTCCAATAT GCCGGCATTG CCGTGGCTTG CACGCAATAA AGTCGATGTC
451  GATGCAACCG TTGCCAATAT GAAGGCTTTG CGTAAAGTAG GTACTCCTTA
501  CAGTGATGAG GAAATTGCGA AAGCACCTGA GGCTTTGGCA AACAAATCCG
551  AGCTGGATGC TGTAGTCGCC TATCTGCAAG GATTGGGTCT GGCTTTGAAA
601  AACGTAAGGT AA
```

This corresponds to the amino acid sequence <SEQ ID 1316; ORF 401>:

```
m401.pep
  1  MKLQQLAEEK IGV LIVFTLL VSVGLLIEV VPLAFTKAAT QPAPGVKPYN
 51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESVYDHPFQW
101  GSKRTGPDLA RVGGRYSEW HRIHLLNPRD VVPESNMPAF PWLARNKVDV
151  DATVANMKAL RKGTPYSDE EIAKAPEALA NKSELDVVA YLQGLGLALK
201  NVR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 401 shows 100.0% identity over a 203 aa overlap with a predicted ORF (ORF 401.ng) from *N. gonorrhoeae*:

```
m401/g401
      10      20      30      40      50      60
m401.pep  MKLQQLAEEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY
          |||
g401      MKLQQLAEEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY
          |||
      10      20      30      40      50      60
m401.pep  IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGRYSEW
```

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```

g401      |||||
          IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGGRYSDEW
          70      80      90      100     110     120

m401.pep      130      140      150      160      170      180
          HRIHLLNPRDVVPESNMPAF PWLARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
          |||||

g401      HRIHLLNPRDVVPESNMPAF PWLARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
          130      140      150      160      170      180

m401.pep      190      200
          NKSELDAVVAYLQGLGLALKNVRX
          |||||

g401      NKSELDAVVAYLQGLGLALKNVRX
          190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1317>:

```

a401.seq
1   ATGAAATTAC AACAAATTGGC TGAAGAAAAA ATCGGCGTTC TGATTGTGTT
51  CACGCTGCTT GTAGTCAGTG TCGGTCTGTT GATTGAAGTT GTGCCCTTGG
101 CCTTTACCAA GCGGCAACA CAGCCGCGT CGGGCGTGAA GCCTTACAAT
151 GCCCTGCAGG TTGCCGACG CGATATTTAC ATCCGTGAGG GCTGTTACAA
201 CTGCCACTCG CAAATGATTG GTCCGTTCCG TCGGGAACC GAGCGTTACG
251 GTCATTACTC TGTGCGCGA GAGTCGTTT ACGACCATCC GTTCCAATGG
301 GGTTCCAAAC GTACCGGTCC TGATTGGCA CGTGTGGCG GTCGCTATTC
351 CGACGAATGG CACCGTATCC ACCTGCTGAA TCCCGTGAT GTCGTGCCTG
401 AGTCCAATAT GCCGGCATT CCGTGCTTG CACGCAATA AGTCGATGTC
451 GATGCAACCG TTGCCAACA GAAGGCTTTG CGTAAAGTAG GTACTCCTTA
501 CAGTGATGAG GAAATTGCGA AAGCGCTGA GGCTTTGGCA AACAAATCCG
551 AGCTGGATGC TGTAGTCGCC TATCTGCAAG GATTGGGTCT GGCTTTGAAA
601 AACGTAAGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1318; ORF 401.a>:

```

a401.pep
1   MKLQQLAEK IGVLVFTLL VVSVGLLIEV VPLAFTKAAT QPASGVKPYN
51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESVYDHPFQW
101 GSKRTGPDLA RVGGGRYSDEW HRIHLLNPRD VVPESNMPAF PWLARNKVDV
151 DATVANMKAL RKVGTPYSDE EIAKAPEALA NKSELDAVVA YLQGLGLALK
201 NVR*

```

m401/a401 99.5% identity in 203 aa overlap

```

m401.pep      10      20      30      40      50      60
          MKLQQLAEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY
          |||||

a401      MKLQQLAEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPASGVKPYNALQVAGRDIY
          10      20      30      40      50      60

m401.pep      70      80      90      100     110     120
          IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGGRYSDEW
          |||||

a401      IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGGRYSDEW
          70      80      90      100     110     120

m401.pep      130      140      150      160      170      180
          HRIHLLNPRDVVPESNMPAF PWLARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
          |||||

a401      HRIHLLNPRDVVPESNMPAF PWLARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
          130      140      150      160      170      180

m401.pep      190      200
          NKSELDAVVAYLQGLGLALKNVRX
          |||||

a401      NKSELDAVVAYLQGLGLALKNVRX
          190      200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1319>:

g402.seq

```

1   ATGGATATGG TGAACACTAA Accgaatact agtgtgatta atatgctttc
51  tttccttacc ggatTATTGA GCTTGGGTat agaagtCtTg tGGGTAAGGA
101 TGtttttcgTT CGCagcAcag tccgtgcctc aggCATTTTC atttattctt
151 gcctGtttttc tgACCGgtat cgcgcgtcggc gCgTATTTTG GCAAACGGAT
201 TTGCCGCAGC CGCTTTGTTG ATATTCCctT TATCGGGCAG TgcttcttgT
251 GGGCGGGTAT TgccgaTttt ttgatTTTGG GTGCTGCGTG GTTGTGACG
301 GGTTTTTTccg gtttcGTCCA CCACGCCGGT AtttTCATTA CCCTgtctgc
351 CGtcGTCAGG GGGTTGATTT TCCCACTTGT ACACCATgtg GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTTCCAATG TTTATTTTCG CAACGTTGCC
451 GGCAGTGCAT TGGGTCCGGT CTTATCGGC TTTGTGATAC TTGATTtgtt
501 gTCCACCCAA CAGATTtacc tgctcatCTG TTTGATTCT GCTGctgtcc
551 cTTTGTTTTg tacaCTGtTC CAAAAAAGTC TCCGACTGAA TGCAGTGTcG
601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTCTAC TGCCGGATTc
651 TGTCTTTCAA AATATTGCTG GCCGTCCGGA TAGGTTGATT GAAAACAAAC
701 ACGGCATTGT TCGGTTTAC CATAGAGATG GTGATAAGGT TGTTTATGGG
751 GCGAATGTAT ACGACGGCGC ATACAATACC GATATATTCA ATAGTGTCAA
801 CGGCATCGAA CGTGCCTATC TGCTACCCTC CCTGAAGTCC GGCAACGCC
851 GCATTTTCGT CGTTGGATTG AGTACAGGTT CGTGGGCGCG CGTCTGTCT
901 GCCATTCGG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGGCATA
951 CCGTAGCCTT ATCGCGGAcg agccgcAAAT CGCACCGCTT TTGCAGGACA
1001 AACGTGTTGA AATTGTATTG GATGACGGTA GGAAATGGCT GCGTCGCCAT
1051 CCTGATGAAA AATTCGACCT GATTTTGATG AATTCGACTT GGTACTGGCG
1101 TGCCTATTCC ACTAACCTGT TGAGTGCgGA ATTTTAAAA CAGGTGCAAA
1151 GCCACCTTAC CCCGGATGGT ATTGTAATGT TTAATACCAC GCACAGCCCG
1201 CATgetTTTG CTACCGCCGT ACACAGTATT CCCTATGCAT ACCGCTACGG
1251 GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTTCctt AATAAAGAAC
1301 TGCTCaagca aCGCCTTTcc cgGTTGATTT GGCCGAAAG CGGCAGgcac
1351 gtATTTGACA GCAGCACCGT GGATGCTGCA GCACAAAGG TTgtctctCG
1401 TATGCTGATT CGGATGACGG AAcctTCGGC TGGGGCGGAA GTCATTACTG
1451 ACGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1320; ORF 402.ng>:

g402.pep

```

1   MDMVNTKPNT SVINMLSFLT GLLSLGIEVL WVRMFSFAAQ SVPOAFSFLI
51  ACFLTGIavg AYFGKRICRS RFVDIPFIGQ CFLWAGIADF LILGAawllt
101 GFSGFVHHAG IFITLSAVVR GLIFPLVHHV GTDGNKSGRQ VSNVYFANVA
151 GSALGPVLIG FVILDLLSTQ QIYLLICLIS AAVPLFCTLF QKSLRLNAVS
201 VAVSLMFGIL MFLLPDSVFQ NIAGRPRDLI ENKHGIVAVY HRDGDkvvyg
251 ANVYDGAYNT DIFNSVNGIE RAYLLPSLKS GIRRI FVVGL STGSWARVLS
301 AIPEMQSMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLRRH
351 PDEKFDLILM NSTWYWRAYS TNLLSAEFLK QVQSHLTPDG IVMFNTTHSP
401 HAFATAVHSI PYAYRYGHMV VGSATPVVFP NKELLKQRLS RLIWPESGRH
451 VFDSSTVDAa AQKVSRMLI RMTEPSAGAE VITDDNMIVE YKYGRGI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1321>:

m402.seq

```

1   ATGGATATAG TGAACACTAA ACCGAATACT AGTTTGATTT ATATGCnTTC
51  TTTCTTAGC GGCTTATTGA GCTTGGGTAT AGAAGTCTTG TGGGTGAGGA
101 TGTTTTCGTT CGCAGCACAG TCCGTGCCTC AGGCATTTTC ATTTACCCCTT
151 GCTGTTTTTC TGACCGGTAT CGCCGTCGGC GCGTATTTTG GCAAACGGAT
201 TTGCCGCAGC CGCTTTGTTG ATATTCCCTT TATCGGGCAG TGCTTCTTGT
251 GGGCGGGTAT TGCCGACTTT TTGATTTTGG GTGCTGCGTG GTTGTGACG
301 GGTTTTTTCCG GCTTCGTCCA CCACGCCGGT ATCTTCATTA CCCTGTCTGC
351 CGTCGTCAsA sGGTTGATT TCCCGCTCGT ACACCATGTG GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTTCCAATG TTTATTTTCG CAmCGTTGCC
451 GGCAGTGCAT TGGGTCCGGT CTTATCGGC TTTGTGATAC TTGATTTCTT
501 GTCCACCCAA CAGATTTACC TGCTCATCTG TwTGATTCT GCTGCTGTCC
551 CTTTGTTTTG TACACTGTTT CAAAAAAGTC TCCGACTGAA TGCAGTGTcG
601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTcyTAC TGCCGGATTc

```


m402.ppt

1	<u>MDIVNTKPN</u>	<u>SLIYMXSFLS</u>	<u>GLLSLGIEVL</u>	<u>WVRMFSFAAQ</u>	<u>SVPQAFSFTL</u>
51	<u>ACFLTGI</u>	<u>AVGAYFGKRICRS</u>	<u>RFVDIPFI</u>	<u>QCFWL</u>	<u>AGIADF LILGA</u>
101	<u>WFGSGFV</u>	<u>HAGIFITLS</u>	<u>AVVXXLIF</u>	<u>PVLHHV</u>	<u>GT</u>
151	<u>GSALGPVL</u>	<u>IGFVILDFL</u>	<u>STQ</u>	<u>QIYLLIC</u>	<u>IXISAAVPL</u>
201	<u>FCTLF</u>	<u>QKSLRL</u>	<u>NAVS</u>	<u>VAVSLM</u>	<u>FGILMFL</u>
251	<u>LPDSVFQ</u>	<u>NIADRP</u>	<u>DLI</u>	<u>ENKHG</u>	<u>IVAVY</u>
301	<u>HRDGD</u>	<u>KDVVYG</u>	<u>ANVYD</u>	<u>GAYNT</u>	<u>DVFN</u>
351	<u>SVNGIE</u>	<u>RAYLL</u>	<u>P</u>	<u>SLKS</u>	<u>GIRRI</u>
401	<u>FVVG</u>	<u>L</u>	<u>STGS</u>	<u>WARVLS</u>	<u>AIPE</u>
451	<u>MQSMIV</u>	<u>AEIN</u>	<u>PAYRSL</u>	<u>IADE</u>	<u>PQIAPL</u>
	<u>LQDK</u>	<u>RVEIVL</u>	<u>DDGR</u>	<u>KWLRRH</u>	<u>PDE</u>
	<u>KFDLIL</u>	<u>MNTTWY</u>	<u>WRAYS</u>	<u>TNLL</u>	<u>SAEFLK</u>
	<u>QVQSH</u>	<u>LTPDG</u>	<u>I</u>	<u>VMFT</u>	<u>TTHTSP</u>
	<u>401</u>	<u>HAFATA</u>	<u>VHSSI</u>	<u>PYAYR</u>	<u>YGHMV</u>
	<u>VG</u>	<u>SATPV</u>	<u>VFF</u>	<u>NKELL</u>	<u>KQRLS</u>
	<u>RLW</u>	<u>PESGRH</u>	<u>451</u>	<u>V</u>	<u>EDSSTV</u>
	<u>DA</u>	<u>AOKV</u>	<u>VS</u>	<u>RMLI</u>	<u>OMTE</u>
	<u>PSGAE</u>	<u>VIT</u>	<u>DDN</u>	<u>MIVE</u>	<u>YK</u>
	<u>YGRGI</u>	<u>*</u>			

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 402 shows 97.0% identity over a 497 aa overlap with a predicted ORF (ORF 402.ng) from *N. gonorrhoeae*:

m402/q402

BNSDOCID: <WO 8957280A2 | >

726

```

g402      |||||:|||||
          250      260      270      280      290      300
          |||||
          310      320      330      340      350      360
m402.pep  AIPMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRHPDEKFDLILM
          |||||
g402      AIPMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRHPDEKFDLILM
          310      320      330      340      350      360
          |||||
          370      380      390      400      410      420
m402.pep  NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV
          |||||
g402      NSTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV
          370      380      390      400      410      420
          |||||
          430      440      450      460      470      480
m402.pep  VGSATPVVFPNKELLKQRLSRLIWPESGRHVFDSSSTDAAAQKVVSRLMIQMTPEPSAGAE
          |||||
g402      VGSATPVVFPNKELLKQRLSRLIWPESGRHVFDSSSTDAAAQKVVSRLIRMTEPSAGAE
          430      440      450      460      470      480
          |||||
          490
m402.pep  VITDDNMIVEYKYGRGIX
          |||||
g402      VITDDNMIVEYKYGRGI
          490

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1323>:

```

a402.seq
1  ATGGATATAG TGAACACTAA ACCGAATACT AGTTTGATT ATATGCTTTT
51  TTTCTTAGC GGCTTATTGA GCTTGGGTAT AGAAGTCTTG TGGGTAAGGA
101 TGTTCCTGTT CGCAGCACAG TCCGTGCCTC AGGCATTTTC ATTTACTCTT
151 GCCTGTTTTT TGACCGGTAT CGCCGTCGGC GCGTATTTTG GCAAACGGAT
201 TTGCCGCGAG CGCTTTGTTG ATATTCCTCT TATCGGGCAG TGCTTCTTGT
251 GGGCGGGTAT TGCCGACTTT TTGATTTTGG GTGCTGCGTG GTTGTGACG
301 GGTTCCTCCG GCTTCGTCCA CCACGCCGGT ATCTTCATTA CCCTGTCTGC
351 CGTCGTCAGA GGGTTGATTT TCCCGCTCGT ACACCATGTG GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTCCAATG TTTATTCGC CAACGTTGCC
451 GGCAGTGCA TGGGTCCGGT CCTTATCGGC TTTGTGATAC TTGATTCTT
501 GTCCACCAA CAGATTTACC TGCTCATCTG TTTGATTTCT GCTGCTGTCC
551 CTTTGTTCG TACACTGTTT CAAAAAAGTC TCCGACTGAA TGCAGTCTCG
601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTCTTAC TGCCGGATTC
651 TGTCTTTCAA AATATTGCTG ACCGTCCGGA TAGGCTGATT GAAAACAAAC
701 ACGGCATTGT TGCGGTTTAC CATAGAGATG GTGATAAGGT TGTATATGGG
751 GCGAATGTAT ACGACGGCGC ATACAATACC GATGTATTCA ATAGTGTCAA
801 CGGCATCGAA CGTGCCTATC TGCTACCCTC CCTGAAGTCT GGCATACGCC
851 GCATTTTCGT CGTTGGATTG AGTACAGGTT CGTGGGCGCG CGTCTTGTCT
901 GCCATTCCGG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGGCATA
951 CCGTAGCCTT ATCGCGGACG AGCCGCAAT CGCCCCGCTT TTGCAGGACA
1001 AACGTGTTGA AATTGTATTG GATGACGGTA GGAAATGGCT GCGTCGCCAT
1051 CCTGATGAAA AATTCGACCT GATTTTGATG AATACGACTT GGTACTGGCG
1101 TGCCTATTCC ACCAACCTGT TGAGTGCGGA ATTTTAAAA CAGGTGCAAA
1151 GCCACCTTAC CCGGATGGT ATTGTAATGT TTAATACCAC GCACAGCCCG
1201 CATGCTTTTG CTACCGCCGT ACACAGTATT CCCTATGCAT ACCGCTATGG
1251 GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTTCCTT AATAAAGAAC
1301 TGCTCAAGCA ACGTCTCTCC CGGTTGATTT GGCCGAAAG CGGCAGGCAC
1351 GTATTTGACA GCAGCACCGT GGATGCTGCA GCACAAAAGG TTGTCTCTCG
1401 TATGCTGATT CAGATGACGG AACCTTCGGC TGGTGGGAA GTCATTACCG
1451 ACGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1324; ORF 402.a>:

```

a402.pep
1  MDIVNTPKNT SLIYMLSFLS GLLSLGIEVL WVRMFSFAAQ SVPQAFSFTL

```

51 ACFLTGIAVG AYFGKRICRS RFVDIPFIGQ CFLWAGIADF LILGAAWLLT
101 GFSGFVHHAG IFITLSAVVR GLIFPLVHHV GTDGNKSGRQ VSNVYFANVA
151 GSALGPVLIG FVILDFLSTQ QIYLLICLIS AAVPLFCTLF QKSLRLNAVS
201 VAVSLMFGIL MFLLPDSVFQ NIADRPDRLI ENKHGIVAVY HRDGDKVYVG
251 ANVYDGAYNT DVFNSVNGIE RAYLLPSLKS GIRRIFVVGL STGSWARVLS
301 AIPMQSMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLRRH
351 PDEKFDLILM NTTWYWRAYS TNLLSAEFLK QVQSHLTPDG IVMFNTTHSP
401 HAFATAVHSI PYAYRYGHMV VGSATPVVFP NKELLKQRLS RLIWPESGRH
451 VFDSSTVDAA AQKVVSRLMI QMTEPSAGAE VITDDNMIVE YKYGRGI*

m402/a402 99.0% identity in 497 aa overlap

	10	20	30	40	50	60
m402.pep	MDIVNTKPNTSLIYMXSFLSGLLSLGIEVLWVRMFSFAAQSVPAFSTLACFLTGIAVG					
a402	MDIVNTKPNTSLIYMLSFLSGLLSLGIEVLWVRMFSFAAQSVPAFSTLACFLTGIAVG					
	10	20	30	40	50	60
m402.pep	70	80	90	100	110	120
a402	70	80	90	100	110	120
m402.pep	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVX					
a402	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVR					
m402.pep	130	140	150	160	170	180
a402	130	140	150	160	170	180
m402.pep	XLIFPLVHHVGTGDNKSGRQVSNVYFAXVAGSALGPVLIGFVILDFLSTQQIYLLICXIS					
a402	GLIFPLVHHVGTGDNKSGRQVSNVYFANVAGSALGPVLIGFVILDFLSTQQIYLLICLIS					
m402.pep	190	200	210	220	230	240
a402	190	200	210	220	230	240
m402.pep	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY					
a402	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY					
m402.pep	250	260	270	280	290	300
a402	250	260	270	280	290	300
m402.pep	HRDGDKVYVGANVYDGAYNTDVFNSVNGIERAYLLPSLKS GIRRIFVVGLSTGSWARVLS					
a402	HRDGDKVYVGANVYDGAYNTDVFNSVNGIERAYLLPSLKS GIRRIFVVGLSTGSWARVLS					
m402.pep	310	320	330	340	350	360
a402	310	320	330	340	350	360
m402.pep	AIPMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRRHPDEKFDLILM					
a402	AIPMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRRHPDEKFDLILM					
m402.pep	370	380	390	400	410	420
a402	370	380	390	400	410	420
m402.pep	NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMNTTHSPHAFATAVHSIPYAYRYGHMV					
a402	NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMNTTHSPHAFATAVHSIPYAYRYGHMV					
m402.pep	430	440	450	460	470	480
a402	430	440	450	460	470	480
m402.pep	VGSATPVVFPNKELLKQRLSRLIWPESGRHVFDSSSTVDAAAQKVVSRLMIQMTEPSAGAE					
a402	VGSATPVVFPNKELLKQRLSRLIWPESGRHVFDSSSTVDAAAQKVVSRLMIQMTEPSAGAE					
m402.pep	490					
a402	VITDDNMIVEYKYGRGIX					
	VITDDNMIVEYKYGRGIX					
	490					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1325>:

g406.seq

```

1  ATGCGGGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGCAAACGCT
101 TCGCGTTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTTAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTTCGCGC GAATACATAA ACAGCCCTGC CGTCCGCACC
301 GATTACACCT ATCCGCGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACGGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA GGAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CCAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTGCA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTTCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAAACCT GGAATATTTT GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCCA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATCAAA CCGACGGAAG GATTGATGGT CGATTTCTCC GATATCCAAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGCGAC AACATAGACA
951 AGGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1326; ORF 406>:

g406.pep

```

1  MRARLLIPIL FSVFILSACG TLTGIPSHGG GKRFAVEQEL VAASARAAVK
51  DMDLQALHGR KVALYIATMG DQSGSGLTGG RYSIDALIRG EYINSPAVRT
101 DYTPRYETT AETTSGLTGT LTSLSTLNA PALSRQSDG SGSRSSLGLN
151 IGGMGDYRNE TLTNPRDTA FLSHLVQTVF FLRGIDVVP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSIGIK PTEGLMVDFS DIQPYGNHTG NSAPSV EADN
301 SHEGYGYSDE AVRQHRQGP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1327>:

m406.seq

```

1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGTAACGCT
101 TTGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTTAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 CACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTTCGTGGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CTCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTTCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAAACCT GGAATATTTT GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATTAAA CCGACGGAAG GATTAATGGT CGATTTCTCC GATATCCGAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GTAGTGCGAC AACATAGACA
951 AGGACAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1328; ORF 406>:

m406.pep

```

1  MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFAVEQEL VAASARAAVK

```

```

51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTPRYETT AETTSGLTG LTSLSTLNA PALSRTQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSF ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSIGIK PTEGLMVDFS DIRPYGNHTG NSAPSVEADN
301 SHEGYGYSDE VVRQHRQGP *

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 406 shows 98.8% identity over a 320 aa overlap with a predicted ORF (ORF406.a) from *N. gonorrhoeae*:

g406/m406

	10	20	30	40	50	60
g406.pep	MRARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARAANKDMDLQALHGR					
	:					
m406	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARAANKDMDLQALHGR					
	10	20	30	40	50	60
g406.pep	70	80	90	100	110	120
	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGLTG					
	:					
m406	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGLTG					
	70	80	90	100	110	120
g406.pep	130	140	150	160	170	180
	LTSLSTLNAPALSRTQSDGSGSRSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF					
	:					
m406	LTSLSTLNAPALSRTQSDGSGSKSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF					
	130	140	150	160	170	180
g406.pep	190	200	210	220	230	240
	FLRGIDVVSANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	:					
m406	FLRGIDVVSANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	190	200	210	220	230	240
g406.pep	250	260	270	280	290	300
	IKPKTNAFEAAYKENYALWMGPYKVSIGIKPTEGLMVDFSIDIQPYGNHTGNSAPSVEADN					
	:					
m406	IKPKTNAFEAAYKENYALWMGPYKVSIGIKPTEGLMVFSIDIRPYGNHTGNSAPSVEADN					
	250	260	270	280	290	300
g406.pep	310	320				
	SHEGYGYSDEAVRQHRQGPX					
	:					
m406	SHEGYGYSDEVVRQHRQGPX					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1329>:

```

a406.seq
1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGTAACGCT
101 TCGCGTCTGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTTCGTGGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG

```

```

501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTTCTCCT GCCAATGCCG ATACGGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAAACCT GGAATATTTC GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGACCGTATA AAGTAAGCAA
801 AGGAATTAAA CCGACAGAAG GATTAATGGT CGATTCTCTC GATATCCAAC
851 CATACGGCAA TCATATGGGT AACTCTGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGGCAG GACATAGACA
951 AGGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1330; ORF 406.a>:

```

a406.pep
  1  MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFVEQEL VAASARAAVK
  51  DMDLQALHGR KVALYIATMG DQSGSGLTGG RYSIDALIRG EYINSPAVRT
 101  DYTYPRYETT AETTSGLTGT LTSLSTLNA PALSRTQSDG SGSKSSLGLN
 151  IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
 201  IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
 251  AYKENYALWM GPYKVSCKGIK PTEGLMVDFS DIQPYGNHMG NSAPSVEADN
 301  SHEGYGYSDE AVRRHRQGQP *

m406/a406  98.8% identity in 320 aa overlap

      10      20      30      40      50      60
m406.pep  MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFVEQELVAASARAAVKDMDLQALHGR
          |||
a406      MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFVEQELVAASARAAVKDMDLQALHGR
      10      20      30      40      50      60

      70      80      90     100     110     120
m406.pep  KVALYIATMGDQSGSGLTGGRYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGLTGT
          |||
a406      KVALYIATMGDQSGSGLTGGRYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGLTGT
      70      80      90     100     110     120

      130     140     150     160     170     180
m406.pep  LTSLSTLNA PALSRTQSDGSGSKSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF
          |||
a406      LTSLSTLNA PALSRTQSDGSGSKSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF
      130     140     150     160     170     180

      190     200     210     220     230     240
m406.pep  FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL
          |||
a406      FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL
      190     200     210     220     230     240

      250     260     270     280     290     300
m406.pep  IKPKTNAFEAAAYKENYALWMGPYKVSCKGIKPTGLMVDFS DIRPYGNHTGNSAPSVEADN
          |||
a406      IKPKTNAFEAAAYKENYALWMGPYKVSCKGIKPTGLMVDFS DIQPYGNHMGNSAPSVEADN
      250     260     270     280     290     300

      310     320
m406.pep  SHEGYGYSDEVVRQHRQGQFX
          |||
a406      SHEGYGYSDEAVRRHRQGQFX
      310     320

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1331>:

```

g501.seq
  1  atggtcgagc ggaccttgac cgcagatacc gacatatttg ttctgcttgc,
 51  ggcaggcgga gatggcaaga tgcagcatca ctttgacggc agggttgcgt

```

```

101 tcgtcaaacg attcggacac caagccgctg tctcggtcga ggccgaggggt
151 cagctgggtc atgtcgttcg agccgatgga gaagccgctg aagtattgca
201 ggaattgttc cgccaatacc gcgttgctcg gcagctcgca catcataatc
251 aggcgcaggc cgtttttgcc gcgttccaag ccgttttctt tcaatgcctt
301 aaccactgct tcggcttcgc ccaaagtgcg gacgaacgga atcatgattt
351 cgacgttggt cagaccatt tcgtcacgaa cgcgtttcaa ggctttgcat
401 tccaaggcga aacagtcttt gaagctctcg gcaacataac gcgccgcacc
451 acggaagccc aacatcgggt tttcttcatt cggttcgtat acgctgccgc
501 cgaccaggtt ggcgtattcg ttggatttga agtcggacat acggacgatg
551 gttttacgcg gataaaccga tgcggcaagc gttgccacgc cttcggcgat
601 tttatcgacg tagaagtcga caggggatgc gtaaccggcg atcgccgga
651 taatttcgcg tttcagttcg tcgtcttggt tgtcaaattc caacaaggct
701 ttcgggtgga tgcgatttg gcggttgatg ataaattcca tacgcgcaa
751 gccgatgcct tcgctgggca gattggcgaa gctgaatgcg agttcgggat
801 tgccgacgtt catcatgact ttgacgggtg cttttggcat attgtccaag
851 gcgacatcgg taatttgtag gtccagcagg ccggcataga taaagccgggt
901 atcgccctcg gcacaggata cggtaacttc ctgaccgttt tccaagagtt
951 cggtcgcatt gccgcagccg acgacggcag gaataccagc ttcgcgcgcg
1001 atgatggcgg cgtggcaggt gcgtccgccg cggttggtca cgatggcgga
1051 agcacgtttc atcacgggtt cccaatccgg atcggtcatt tcggtaacca
1101 gtacgtcgcc ggcttcgacg gaatccattc cgggaagcatc ttaatacagg
1151 cgcaccttgc cctgaccgac tttttgaccg atggcacgac cttcgcacaa
1201 gacggttttt tcgccgttga tggcgtagcg gcgcaggttg cggctgcctt
1251 cttcttggga tttgacgggt tcggggcggg cttgcaggat gtagagtttg
1301 ccgtccaggc cgtcgcgtcc ccattcgata tccatcgggc ggccgtagtg
1351 tttttcgatg gtcagcgcgt agtgtgcaa ctcggtgatt tcttcgtcgg
1401 taatggagaa gcggttgccg tcttcttcgg ggacttcgac gttggttacc
1451 gatttgccgg cttcggcttt gtcggtgaaa atcattttga tgtgtttcga
1501 accatgggtc ttgcgcagga tggcggttt gcctgctttg agcgtgggtt
1551 tgaacacata aaattcgtcc gggttgaccg cgccttgtag gacgttttcg
1601 cccagaccgt aagaggaggt aacaaagacg acttggttgt agccgattc
1651 ggtgtcgagg gtgaacatca cacctga

```

This corresponds to the amino acid sequence <SEQ ID 1332; ORF 501.ng>:

g501.pep

```

1  MVGRTLTA DT DIFVLLAAGG DGKMQHHFDG RVAFVKRFGH QAAVSVEAEG
51  QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAQAVFA AFQAVFFQCL
101 NHCFGFAQSA DERNHDFDVG QTHFVTNAFQ GFAFQGETVF EALGNITRRT
151 TEAQHRVFFM RFVYAAADQV GVFGVFEVGH TDDGFTRINR CGKRCHAFGD
201 FIDVEVDRGC VTGDAADNFR FQFVVLVFKF QQGFRVDADL AVDDKFHTRQ
251 ADAFAGQIGE AECEFGIADV HHDGDFGCFWH IVQGDIGNLY VQAGIDKAG
301 IAFGTGYGNF LTVFQEFGR I AAADDGRNTQ FARDDGGVAG ASAAVGHGDDG
351 STFHHGFPIR IGHVGNQYVA GFDGIHLGSI FNQAHLLALTD FLTDGTTFAQ
401 DGFFAVDVA AQVAAAFFLG FDGFGAGLQD VEFVAVQAVAS PFDIHRAAVV
451 FFDGQRVVCQ LGDFFVGNGE AVAVFFGDFD VGYRFAGFGF VGENHFDVFR
501 THGLAQDGGF ACFERGF EHI KFRVRDRALY DVFAQTVRGG NKDDLVLVAGF
551 GVEGEHHT*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1333>:

m501.seq

```

1  atggtcggac sggccttgac cgcagatgcc gacatatttg ttctgcttgc
51  ggcaaggcga gatggcaagg tgcagcatca ctttgacggc aggggttgcgt
101 tcgtcaaacg attcggatac caagccgctg tcgcggtcga gaccgaggggt
151 cagttgggtc atgtcgttcg agccgatgga gaagccgctg aagtattgca
201 ggaattgttc cgccaatacc gcgttgctcg gcagctcgca catcataatc
251 aggcgcaggc cgtttttgcc gcgttccaag ccgttttctt tcagggtctt
301 gacaacggmt tcggcttcgc ccaaagtgcg gacgaacgga atcatgattt
351 caacgttggg caacccatt tcatcgcgga cgcgtttcaa ggctttgcat
401 tccaaggcga aacagtcttt gaagttgtcg gcgacataac gcgccgcacc
451 acggaagccc aacatcgggt tttcttcatt cggttcgtat acggttgcgc
501 cgaccaggtt ggcgtattcg ttggatttga agtcggacat acggacgatg
551 gttttacgcg gataaaccga tgcggccaat gtcgccacgc cttcggcgat
601 tttatcgacg tagaagtcga caggggacgc gtaaccggcg atacggcggg
651 taatttcgcg ttttaattcg tcgtcttggt tgtcaaattc caacaargct

```

```

701 ttgggggtgga taccgatttg gcggttgatg ataaattcca tacgcgccaa
751 gccgatgcct tcgctgggca ggttggcgaa gctgaatgcg agttcgggat
801 tgccgacgtt catcatgact tttacaggtg ctttaggcat attgtctaag
851 gcgacatcgg taatctgtac gtccaacaga ccggcataga taaagccggt
901 atcgccctcg gcacaggata cggttaactc ttgaccgttt ttcagcaatt
951 cggttgcatt gccgcagccg acaacggcag gaatgcccaa ttcacgcgcg
1001 atgatggcgg cgtggcaggt acggccgccg cggttggtta cgatggcaga
1051 agcacgtttc atcacgggtt cccaatcccg atcggtcatg tcggtaacga
1101 gtacgtcgcc ggcttcgacg gaatccatct cggaagcatc tttaatcagg
1151 cgcaccttgc cctgaccgac tttctgaccg atggcgcggc cttcgcataa
1201 tacggttttg tcgccgttga tggcgaaagcg gcgcagggtg cggttgccct
1251 cttcttgagg ttttacggtt tcgggacggg cttgcaggat gtagagtttg
1301 ccgtccaagc cgtcgcgtcc ccattcgata tccatcgggc ggccgtagtg
1351 tttttcgatg gtcagtgcgt aatgcgccaa ctacagtaatt tcttcgctcg
1401 taatggagaa gcggttgccg tcttcctcgg ggacatcgac gttggttacg
1451 gatttaccgg cttctgcttt gtcggtaaaa atcattttga tgtgttttga
1501 acccatggtt ttacgcagga tggcgggctt gccgytttg agcgtgggtt
1551 tgaacacatr aaattcgtcc ggggtgaccg caccttgtag gacgttttcg
1601 cccagaccgt aagaggaggt aacaaagacg acytgatcgt akccggattc
1651 ggtgtcgagg gtgaacatca cacctga

```

This corresponds to the amino acid sequence <SEQ ID 1334; ORF 501>:

```

m501.pep
1  MVGXALTADA DIFVLLAAGG DGKVQHFFDG RFAFVKRFGY QAAVAVETEG
51  QLGHVVRADG EAVEVLQELF ROYRVARQLA HHNQAQAVFA AFQAVFFQGF
101 DNGFGFAQSA DERNHDFNVG QPHFIADAFQ GFAFQGETVF EVVGDITRRT
151 TEAQHRVFFM RFVYVAADQV GVFGFVGVGH TDDGFTRINR CGQCRHAFGD
201 FIDVEVDRGR VTGDTAGNFR FXFVVLVVKF QQXFGVDTDL AVDDKFHTRO
251 ADAFAGQVGE AECEFGIADV HHDFYRCFRH IVXGDIGNLY VQQTGIDKAG
301 IAFGTGYGNF LTVFQQFGCI AAADNGRNAQ FTRDDGGVAG TAAAVGNDGR
351 STFHHGFPIR IGHVGNEYVA GFDGIHLGSI FNQAHALALD FLTDGAFAFX
401 YGFVAVDGEA AQVAVALFLG FYGFGTGLQD VEFVQAVAS PFDIHRAAVV
451 FFDGQCVMRQ LSNFFVGNGE AVAVFLGDID VGYGFTGFCE VGKNHFDVFX
501 THGFTQDGLL ARFERGFEHX KFVRVDRPLY DVFAQTVRGG NKDDLIVXGF
551 GVEGEHHT*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 501 shows 86.2% identity over a 558 aa overlap with a predicted ORF (ORF 501.ng) from *N. gonorrhoeae*:

```

m501/g501
      10      20      30      40      50      60
m501.pep  MVGXALTADADIFVLLAAGGDGKVQHFFDGRFAFVKRFGYQAAVAVETEGQLGHVVRADG
          ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g501      MVGRTLTAADTIDIFVLLAAGGDGKMQHFFDGRFAFVKRFGHQAAVSVEAEGQLGHVVRADG
          10      20      30      40      50      60

      70      80      90     100     110     120
m501.pep  EAVEVLQELFRQYRVARQLAHHNQAQAVFAAFQAVFFQGFQDNGFGFAQSADERNHDFNVG
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g501      EAVEVLQELFRQYRVARQLAHHNQAQAVFAAFQAVFFQCLNHCFFGFAQSADERNHDFDVG
          70      80      90     100     110     120

      130     140     150     160     170     180
m501.pep  QPHFIADAFQGFQAFQGETVFEVVDITRRTTEAQHRVFFMRVYVAADQVGVFGFVGVGH
          | |||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g501      QTHFVTNAFQGFQAFQGETVFEALGNITRRTTEAQHRVFFMRVYVAADQVGVFGFVGVGH
          130     140     150     160     170     180

      190     200     210     220     230     240
m501.pep  TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVVKFQQXFGVDTDL
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```


733

g501	TDDGFTRINRCGKRCHAFGDFIDVEVDRGCVTGDAADNFRFQFVVLFVKFQQGFVRVDADL
	190 200 210 220 230 240
m501.pep	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDIFYRCFRHIVXGDIIGNLYVQQTGIDKAG
g501	AVDDKFHTRQADAFAGQIGAECEFGIADVHHDIFYRCFRHIVXGDIIGNLYVQQTGIDKAG
	250 260 270 280 290 300
m501.pep	IAFGTGYGNFLTVFQQFGCIAAADNGRNAQFTRDDGGVAGTAAAVGNDGRSTFHHGFPIR
g501	IAFGTGYGNFLTVFQEFGRIAAADNGRNTQFARDDGGVAGASAAVGHGDSSTFHHGFPIR
	310 320 330 340 350 360
m501.pep	IGHVGNQYVAGFDGIHLGSI FNQAH LALTD FLTDGAAFA XYGFVAVDGEAAQVAVALFLG
g501	IGHVGNQYVAGFDGIHLGSI FNQAH LALTD FLTDGTTFAQDGF FAVDGVAAQVAAFFLG
	370 380 390 400 410 420
m501.pep	FYGFGLQDVEFAVQAVASPFDIHRAAVVFFDGGQVMRQLSNFFVGNGEAVAVFLGDID
g501	FDGFGAGLQDVEFAVQAVASPFDIHRAAVVFFDGGQVVCQLGDFVGNGEAVAVFFGDFD
	430 440 450 460 470 480
m501.pep	VGYGFTGFCFVGKNHFDVFXTHGFTQDGGGLARFERGFEXXKFVRVDRTLVDVFAQTVRGG
g501	VGYRFAGFGFVGENHFDVFRTHGLAQDGGFACFERGFEXIKFVRVDRALVDVFAQTVRGG
	490 500 510 520 530 540
m501.pep	NKDDLIVXGFGVGEHEHT
g501	NKDDLIVVAGFGVGEHEHT
	550

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1335>:

a501.seq (partial)

1	ATGGTCGGAC	GGGCCTTGAC	CGCAGATGCC	GACATATTTG	TTCTGCTTGC
51	GGCAGGCGGA	GATGGCAAGG	TGCAGCATCA	CTTTGACGGC	AGGGTTGCGT
101	TCGTCAAACG	ATTCGGATAC	CAAGCCGCTG	TCGCGGTCGA	GACCGAGGGT
151	CAGTTGGGTC	ATGTCGTTTC	AGCCGATGGA	GAAGCCGTCG	AAGTATTGCA
201	GGAATTGTTT	CGCCAATACC	GCGTTGCTCG	GCAGCTCGCA	CATCATAATC
251	AGGCGCAGGC	CGTTTTTGCC	GCGTTCCAAG	CCGTTTTCTT	TCAGGGCTTT
301	GACAACGGCT	TCGGCTTCGC	CCAAAGTGCG	GACGAACGGA	ATCATGATTT
351	CAACGTTGGT	CAACCCCAT	TCATCGCGGA	CGCGTTTCAA	GGCTTTGTCAT
401	TCCAAGGCGA	AACAGTCTTT	GAAGTTGTCG	GCGACATAAC	GCGCCGCACC
451	ACGGAAGCCC	AACATCGGGT	TTTCTTCATG	CGGTTTCGTAT	ACGTTGCCGC
501	CGACCAGGTT	GGCGTATTCG	TTGGATTTGA	AGTCGGACAT	ACGGACGATG
551	GTTTTACGCG	GATAAACC	TGCGGCCAAT	GTCGCCACGC	CTTCGGCGAT
601	TTTATCGACG	TAGAAGTCGA	CAGGGGACGC	GTAACCGGCG	ATACGGCGGG
651	TAATTTCCGC	TTTAAATTCG	TCGTCTTGTT	TGTCAAATTC	CAACAAGGCT
701	TTGGGGTGGA	TACCGATTG	GCGGTTGATG	ATAAATTCCA	TACGCGCCAA
751	GCCGATGCCT	TCGCTGGGCA	GGTTGGCGAA	GCTGAATGCG	AGTTCGGGAT
801	TGCCGACGTT	CATCATGACT	TTTACAGGTG	CTTTAGGCAT	GTTGTCCAAA
851	GCAACATCGG	TAATTTGTAC	GTCCAGCAGG	CCGGAGTAGA	TGAAGCCGGT
901	ATCGCCTTCG	GCACAGGATA	CGGTAACCTC	TTGACCGTTT	TTTACGCAAT
951	CGGTTGCATT	GCCGCAGCCG	ACAACGGCAG	GAATACCCAG	TTTCGCGCGC

```
1001 ATGATGGCGG CGTGGCAGGT ACGTCCGCCC CTGTTGGTCA CGATGGCGGA
1051 AGCGCGTTTC ATCACCAGGT CCCAATCTGG GTCGGTCATG TCGGTAACCA
1101 GTACGTCGCC GGCTTCGACG GAATCCATCT CGGAAGCATC TTTAATCAGG
1151 CGTACCTTGC CCTGACCGAC TTTCTGACCG ATGGCGCGGC CTTGCGACAA
1201 GACGGTTTTT TCGCCGTTGA TAGAAAAGCG GCGCAGGTTG CGGCTGCCTT
1251 CTTCTTGGGA TTTGACGGTT TCGGGACGGG CTTGCAGGAT GTAGAGTTTG
1301 CCGTCCAAGC CGTCGCGTCC CCATTGATG TCCATCGGGC GGCCGTAGTG
1351 TTTTTCGATG GTCAGTGCCT AATGCGCCAA CTCGGTGATT TCTTCGTCGG
1401 TAATGGAGAA GCGGTTGCGG TCTTCTTCGG GGACATCGAC GTTGTTTACC
1451 GATTTGCCGG CTTCTGCTTT GTCGGTAAAA ATCATTTTGA TGTGTTTTGA
1501 GCCCATGGTT TTGCGCAGGA TGGCAGGTTT GCCTGCTTTC AGCGTGGGTT
1551 TGAACACATA GAATTCGTCG GGATTGACTG CGCCTTGATC GACGTTTTCG
1601 CCCAGACCGT AGGATGAAGT GACAAAGACG ACTTGGTCGT AACCGGATTG
1651 GGTATCGAGG GTGAACATCA C
```

This corresponds to the amino acid sequence <SEQ ID 1336; ORF 501.a>:

a501.pep

```
1 MVGRALTADA DIFVLLAAGG DGKVQHHFDG RVAFVKRFGY QAAVAVETEG
51 QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAQAVFA AFQAVFFQGF
101 DNGFGFAQSA DERNHDFNVG QPHFIADAFQ GFAFQGETVF EVVGDITRRT
151 TEAQHRVFFM RFVYVAADQV GVFGFVGVGH TDDGFTRINR CGQCRHAFGD
201 FIDVEVDRGR VTGDTAGNFR F*FVVLVVKF QQGFGVDTDL AVDDKFHTRQ
251 ADAFAGQVGE AECEFGIADV HHDFYRCFRH VVQSNIGNLY VQQAGVDEAG
301 IAFGTGYGNF LTVFQQFGCI AAADNGRNTQ FARDDGGVAG TSAPVGHDDG
351 SAFHHRFPIW VGHVGNQYVA GFDGIHLGSI FNQAYLALTD FLTDGAAFAQ
401 DGFFFAVDRKA AQVAAFFFLG FDGFGTGLQD VEFVAVQAVAS PFDVHRAAVV
451 FFDGQCVMRQ LGDFFVGNGE AVAVFFGDID VGYRFAGFCF VGKNHFDVF*
501 AHGFAQDGRF ACFQRGFEHI EFVGIDCALY DVFAQTVG*S DKDDLVTGTG
551 GIEGEHH
```

m501/a501 90.3% identity in 557 aa overlap

```
10 20 30 40 50 60
m501.pep MVGXALTADADIFVLLAAGGDGKVQHHFDGRVAFVKRFGYQAAVAVETEGQLGHVVRADG
|||
a501 MVGRALTADADIFVLLAAGGDGKVQHHFDGRVAFVKRFGYQAAVAVETEGQLGHVVRADG
10 20 30 40 50 60

70 80 90 100 110 120
m501.pep EAVEVLQELFRQYRVARQLAHNQAQAVFAAFQAVFFQGFQDNGFGFAQSADERNHDFNVG
|||||
a501 EAVEVLQELFRQYRVARQLAHNQAQAVFAAFQAVFFQGFQDNGFGFAQSADERNHDFNVG
70 80 90 100 110 120

130 140 150 160 170 180
m501.pep QPHFIADAFQGFQGETVFEVVGDTITRRTTEAQHRVFFMRVYVAADQVGVFGFVGVGH
|||||
a501 QPHFIADAFQGFQGETVFEVVGDTITRRTTEAQHRVFFMRVYVAADQVGVFGFVGVGH
130 140 150 160 170 180

190 200 210 220 230 240
m501.pep TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVVKFQQXFGVDTDL
|||||
a501 TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVVKFQQGFGVDTDL
190 200 210 220 230 240

250 260 270 280 290 300
m501.pep AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDFYRCFRHIVXGDIGNLYVQQTGIDKAG
|||||
a501 AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDFYRCFRHVQSNIGNLYVQQAGVDEAG
250 260 270 280 290 300

310 320 330 340 350 360
m501.pep IAFGTGYGNFLTVFQQFGCIAAADNGRNTQFARDDGGVAGTAAAVGNDGRSTFHHGFPIR
|||||
a501 IAFGTGYGNFLTVFQQFGCIAAADNGRNTQFARDDGGVAGTSAPVGHDDGGSFAFHHRFPIW
310 320 330 340 350 360
```

	370	380	390	400	410	420
m501.pep	IGHVGNQYVAGFDGIHLGSI FNQAH LALTD FLTDGA AFAXYGFVAVDGEAAQVAVALFLG					
a501	: : : : : : : : : : : :					
	370	380	390	400	410	420
	VGHVGNQYVAGFDGIHLGSI FNQAY LALTD FLTDGA AFADGFFAVDRKAAQVAAAFFLG					
	430	440	450	460	470	480
m501.pep	FYFGFTGLQDVEFAVQAVASPFDIHRAAVVFFDGCVMRQLSNFFVGNGEAVAVFLGDID					
a501	: : : : : : : : : :					
	430	440	450	460	470	480
	FDGFGFTGLQDVEFAVQAVASPFDVHRAAVVFFDGCVMRQLGDDFFVGNGEAVAVFFGDID					
	490	500	510	520	530	540
m501.pep	VGYGFTGFCFVGKNHFDVFXTHGFTQDGG LARFERGFEHKKFVRVDR TLYDVFAQTVRGG					
a501	: : : : : : : : : :					
	490	500	510	520	530	540
	VGYRFAGFCFVGKNHFDVFXAHGFAQDGRFACFQRGFEHIEFVGIDCALYDVFAQTVGXS					
	550	559				
m501.pep	NKDDLIVXGFGVEGEHHTX					
a501	: : :					
	DKDDLVTGFGIEGEHH					
	550					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1337>:

g502.seq

1	atgatgaaac	cgcacaacct	gttccaattc	ctcgccgttt	gctccctgac
51	cgtcgccgtc	gcttcgcgac	aggcggggcg	ggtggacgcg	ctcaagcaat
101	tcaacaacga	tgccgacggt	atcagcggca	gcttcaccca	aaccgtccaa
151	agcaaaaaga	aaacccaaac	cgcgcacggc	acgttcaaaa	tctgcgccc
201	gggcctcttc	aaatgggaat	acactttgcc	ctacagacag	actattgtcg
251	gcgacggcca	aaccgtttgg	ctctacgatg	ttgatttggc	acaagtgacc
301	aagtcgtccc	aagaccaggc	catcgccggc	agccccgccg	ccatcctgtc
351	gaacaaaacc	gccctcgaaa	gcagttacac	gctgaaagag	gacggttcgt
401	ccaacggcat	cgattatgtg	cggggcaacg	cccaaacgca	acaacgccgg
451	ctaccaatac	atccgcatcg	gcttcaaagg	cggcaacctc	gccgccatgc
501	agcttaa				

This corresponds to the amino acid sequence <SEQ ID 1338; ORF 502.ng>:

g502.pep

1	MMKPHNLFQF	LAVCSLTVAV	ASAQAGAVDA	LKQFNNDADG	ISGSFTQTQVQ
51	SKKKTQTAHG	TFKILRPGLF	KWEYTLPLYRQ	TIVGDGQTVW	LYDVDLAQVT
101	KSSQDQAIGG	SPAAILSNKT	ALESSYTLKE	DGSSNGIDYV	RNAQTQRRR
151	LPIHPHRLQR	RQPRRHAA*			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1339>:

m502.seq

1	atgatgaaac	cgcacaacct	gttccaattc	ctcgccgttt	gctccctgac
51	cgtcgccgtc	gcttcgcgac	aggcggggcg	ggttagacgcg	cttaagcaat
101	tcaacaacga	tgccgacggt	atcagcggca	gcttcaccca	amccgtccaa
151	wgcaaaaaga	aaacccaaac	cgcgcacggc	acgttcaaaa	tctgcgacc
201	gggccttttc	aaatgggaat	acaccaaact	t.acaggcaa	accatcgctc
251	gcgacggcca	aacygtttgg	ctmtacgatg	tygatctggc	acaagtgacc
301	aagtcgtccc	aagaccaggc	cataggcgsc	agccccgccg	ccatcctgtc
351	gaacaaarcc	gccctcgaaa	gcagctacac	gctgaaagag	gacggttcgt
401	ccaacggcat	cgattatgtg	ggcaacgccc	aaacgcaaca	acgccggcta
451	ccaatacatc	cgcacgcggt	tcaaaggcgg	caacctcgcc	gccatgcagc
501	tyaa				

This corresponds to the amino acid sequence <SEQ ID 1340; ORF 502.ng>:

m502.pep

1	MMKPHNLFQF	LAVCSLTVAV	ASAQAGAVDA	LKQFNNDADG	ISGSFTQXVQ
51	KKKKTQTAHG	TFKILRPGLF	KWEYTKLYRQ	TIVGDGQTVW	LYDVDLAQVT
101	KSSQDQAIGX	SPAAILSNKX	ALESSYTLKE	DGSSNGIDYV	GNAQTQRRRL
151	PIHPHRLQRR	QPRRHAAX			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 502 shows 95.8% identity over a 168 aa overlap with a predicted ORF (ORF 502.ng) from *N. gonorrhoeae*:

m502/g502

	10	20	30	40	50	60
m502 . pep	MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQXVQXKKKTQTAHG					
g502	MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQTVQSKKKKTQTAHG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m502 . pep	TFKILRPGLFKWEYTKLYRQTIIVGDGQTVWLYDVLDAQVTKSSQDQAIGXSPAAILSNKX					
g502	TFKILRPGLFKWEYTLPRYQTIIVGDGQTVWLYDVLDAQVTKSSQDQAIGGSPAAILSNKT					
	70	80	90	100	110	120
	130	140	150	160		
m502 . pep	ALESSYTLKEDGSSNGIDYV-GNAQTQQRRLPIHPHRLQRRQPRRHAA					
g502	ALESSYTLKEDGSSNGIDYVRGNAQTQQRRLPIHPHRLQRRQPRRHAA					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1341>:

a502 . seq

1	ATGATGAAAC	CGCACAACT	GTTCCAATC	CTCGCCGTTT	GCTCCCTGAC
51	CGTCTCCGTC	GCTTCCGCAC	AGGCGGGCGC	GGTGGACGCG	CTCAAGCAAT
101	TCAACAACGA	TGCCGACGGT	ATCAGCGGCA	GCTTCACCCA	AACCGTCCAA
151	AGCAAAAAGA	AAACCCAAAC	CGCGCACGGC	ACGTTCAAAA	TCCTGCGCCC
201	GGGCCTCTTT	AAATGGGAAT	ACACTTCGCC	TTACAAACAG	ACTATTGTCG
251	GCGACGGTCA	AACCGTTTGG	CTCTACGATG	TCGATTGTCG	ACAAGTGACC
301	AAGTCGTCCC	AAGACCAGGC	CATAGGCGGC	AGCCCCGCCG	CCATCCTGTC
351	GAACAAAACC	GCCCTCGAAA	GCAGCTACAC	GCTGAAAGAG	GACGGTTCGT
401	CCAACGGCAT	CGATTATGTG	GGCAACGCC	AAACGCAACA	ACGCCGGCTA
451	CCAATACATC	CGCATCGGCT	TCAAAGGCGG	CAACCTCGCC	GCCATGCAGC
501	TTAA				

This corresponds to the amino acid sequence <SEQ ID 1342; 502 217.a>:

a502 . pep

1	MMKPHNLFQF	LAVCSLTVS	ASAQAGAVDA	LKQFNNDADG	ISGSFTQTVQ
51	SKKKKTQTAHG	TFKILRPGLF	KWEYTSFYKQ	TIVGDGQTVW	LYDVLDAQVT
101	KSSQDQAIGG	SPAAILSNKT	ALESSYTLKE	DGSSNGIDYV	GNAQTQQRRL
151	PIHPHRLQRR	QPRRHAA*			

m502/a502 95.2% identity in 167 aa overlap

	10	20	30	40	50	60
m502 . pep	MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQXVQXKKKTQTAHG					
a502	MMKPHNLFQFLAVCSLTVSVAASQAGAVDALKQFNNDADGISGSFTQTVQSKKKKTQTAHG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m502 . pep	TFKILRPGLFKWEYTKLYRQTIIVGDGQTVWLYDVLDAQVTKSSQDQAIGXSPAAILSNKX					
a502	TFKILRPGLFKWEYTSFYKQTIIVGDGQTVWLYDVLDAQVTKSSQDQAIGGSPAAILSNKT					
	70	80	90	100	110	120
	130	140	150	160		
m502 . pep	ALESSYTLKEDGSSNGIDYVGNAQTQQRRLPIHPHRLQRRQPRRHAA					
a502	ALESSYTLKEDGSSNGIDYVGNAQTQQRRLPIHPHRLQRRQPRRHAA					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1343>:

g502-1.seq

```
1 ATGatGAAAc cgcaCaacct gttccaaTtc CTCGCCGTTT GCTCCCTGAC
51 CGTCGCCGTC GCTTCCGCAC AGGCGGGCGC GGTGGACGCG CTCAAGCAAT
101 TCAACAACGA TGCCGACGGT ATCAGCGGCA GCTTCACCCA AACCGTCCAA
151 AGCAAAAAGA AAACCCAAAC CGCGCACGGC ACGTTCAAAA TCCTGCGCCC
201 GGGCCTCTTC AAATGGGAAT ACACTTTGCC CTACAGACAG ACTATTGTCG
251 GCGACGGTCA AACCGTTGG CTCTACGATG TTGATTTGGC ACAAGTGACC
301 AAGTCGTCCC AAGACCAGGC CATCGGCGGC AGCCCCGCCG CCATCCTGTC
351 GAACAAAACC GCCCTCGAAA GCAGTTACAC GCTGAAAGAG GACGGTTCGT
401 CCAACGGCAT CGATTATGTG CGGGCAACGC CCAAACGCAA CAACGCCGGC
451 TACCAATACA TCCGCATCGG CTTCAAAGGC GGCAACCTCG CCGCCATGCA
501 GCTTAAAGAC AGCTTCGGCA ACCAAACCTC CATCAGTTTC GCGGTTTGA
551 ATACCAATCC CCAACTCTCG CGCGGCGCGT TCAAGTTTAC CCCGCCAAA
601 GCGTGGACG TGTGAGCAA CTGA
```

This corresponds to the amino acid sequence <SEQ ID 1344; ORF 502-1.ng>:

g502-1.pep

```
1 MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQTVQ
51 SKKKTQTAHG TFKILRPGLF KWEYTLPYRQ TIVGDGQTVW LYDVDLAQVT
101 KSSQDQAIGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV RATPKRNNAG
151 YQYIRIGFKG GNLAAMQLKD SFGNQTSISF GGLNTNPQLS RGAFKFTPPK
201 GVDVLSN*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1345>:

m502-1.seq

```
1 ATGATGAAAC CGCACAACT GTTCCAATTC CTCGCCGTTT GCTCCCTGAC
51 CGTCGCCGTC GCTTCCGCAC AGGCGGGCGC GGTAGACGCG CTTAAGCAAT
101 TCAACAACGA TGCCGACGGT ATCAGCGGCA GCTTCACCCA AACCGTCCAA
151 AGCAAAAAGA AAACCCAAAC CGCGCACGGC ACGTTCAAAA TCCTGCGACC
201 GGGCCTTTTC AAATGGGAAT ACACCAAACC TTACAGGCAA ACCATCGTCG
251 GCGACGGTCA AACCGTTGG CTCTACGATG TTGATCTGGC ACAAGTGACC
301 AAGTCGTCCC AAGACCAGGC CATAGCGGCG AGCCCCGCCG CCATCCTGTC
351 GAACAAAACC GCCCTCGAAA GCAGCTACAC GCTGAAAGAG GACGGTTCGT
401 CCAACGGCAT CGATTATGTG CTGGCAACGC CCAAACGCAA CAACGCCGGC
451 TACCAATACA TCCGCATCGG CTTCAAAGGC GGCAACCTCG CCGCCATGCA
501 GCTTAAAGAC AGCTTCGGCA ACCAAACCTC CATCAGTTTC GCGGTTTGA
551 ATACCAATCC CCAACTCTCG CGCGGCGCGT TCAAGTTTAC CCCGCCAAA
601 GCGTGGACG TGTGAGCAA CTGA
```

This corresponds to the amino acid sequence <SEQ ID 1346; ORF 502-1>:

m502-1.pep

```
1 MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQTVQ
51 SKKKTQTAHG TFKILRPGLF KWEYTKPYRQ TIVGDGQTVW LYDVDLAQVT
101 KSSQDQAIGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV LATPKRNNAG
151 YQYIRIGFKG GNLAAMQLKD SFGNQTSISF GGLNTNPQLS RGAFKFTPPK
201 GVDVLSN*
```

m502-1/g502-1 99.0% identity in 207 aa overlap

	10	20	30	40	50	60
m502-1.pep	MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQTVQSKKKTQTAHG					
g502-1	MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQTVQSKKKTQTAHG					
	10	20	30	40	50	60
m502-1.pep	TFKILRPGLFKWEYTKPYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGGSPAAILSNKT					
g502-1	TFKILRPGLFKWEYTLPYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGGSPAAILSNKT					
	70	80	90	100	110	120
m502-1.pep	ALESSYTLKEDGSSNGIDYVLRATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTSISF					
g502-1	ALESSYTLKEDGSSNGIDYVRATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTSISF					
	130	140	150	160	170	180

```

              190      200
m502-1.pep  GGLNTNPQLSRGAFKFTPPKGV DVL SNX
              |||
g502-1      GGLNTNPQLSRGAFKFTPPKGV DVL SNX
              190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1347>:

```

a502-1.seq
1  ATGATGAAAC CGCACAACTT GTTCCAATTC CTCGCCGTTT GCTCCCTGAC
51 CGTCTCCGTC GCTTCCGCAC AGGCGGGCGC GGTGGACGCG CTCAGCAAT
101 TCAACAACGA TGCCGACGGT ATCAGCGGCA GCTTCACCCA AACCGTCCAA
151 AGCAAAAAGA AAACCCAAAC CGCGCACGGC ACGTTCAAAA TCCTGCGCCC
201 GGGCCTCTTT AAATGGGAAT ACACTTCGCC TTACAAACAG ACTATTGTCG
251 GCGACGGTCA AACCGTTTGG CTCTACGATG TCGATTGGC ACAAGTGACC
301 AAGTCGTCCC AAGACCAGGC CATAGCGGCG AGCCCCGCG CCATCCTGTC
351 GAACAAAACC GCCCTCGAAA GCAGCTACAC GCTGAAAGAG GACGGTTCGT
401 CCAACGGCAT CGATTATGTG CTGGCAACGC CCAAACGCAA CAACGCCGGC
451 TACCAATACA TCCGCATCGG CTTCAAAGGC GGCAACCTCG CCGCCATGCA
501 GCTTAAAGAC AGCTTCGGCA ATCAAACCTC CATCAGTTTC GGCGGTTTGA
551 ATACCAATCC CCAACTCTCG CGCGGCGCGT TCAAGTTTAC CCCGCCAAA
601 GCGTGGACG TGTGAGCAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1348; ORF 502-1.a>:

```

a502-1.pep
1  MMKPHNLFQF LAVCSLTVSV ASAQAGAVDA LKQFNNDADG ISGSFTQTVQ
51 SKKKQTQAHG TFKILRPGLF KWEYTSYKQ TIVGDGQTVW LYDVLDAQVT
101 KSSQDQAIGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV LATPKRNNAG
151 YQYIRIGFKG GNLAAMQLKD SFGNQTISIF GGLNTNPQLS RGAFFKFTPPK
201 GVDVLSN*

```

a502-1/m502-1 98.6% identity in 207 aa overlap

```

              10      20      30      40      50      60
a502-1.pep  MMKPHNLFQFLAVCSLTVSVASAQAGAVDALKQFNNDADGISGSFTQTVQSKKKQTQAHG
              |||
m502-1      MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQTVQSKKKQTQAHG
              10      20      30      40      50      60

              70      80      90      100     110     120
a502-1.pep  TFKILRPGLFKWEYTSYKQTIIVGDGQTVWLYDVLDAQVTKSSQDQAIGGSPAAILSNKT
              |||
m502-1      TFKILRPGLFKWEYTKPYRQTIIVGDGQTVWLYDVLDAQVTKSSQDQAIGGSPAAILSNKT
              70      80      90      100     110     120

              130     140     150     160     170     180
a502-1.pep  ALESSYTLKEDGSSNGIDYVLATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTISIF
              |||
m502-1      ALESSYTLKEDGSSNGIDYVLATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTISIF
              130     140     150     160     170     180

              190     200
a502-1.pep  GGLNTNPQLSRGAFKFTPPKGV DVL SNX
              |||
m502-1      GGLNTNPQLSRGAFKFTPPKGV DVL SNX
              190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1349>:

```

g503.seq
1  atgtccgcgc cgtcggcatc ggtaatcatt ttgttccatg ccgcttcgat
51 ttcggcatcg agctgttcgg ggaagggcgt gtccaaaatc cattggcgga
101 tttctttgcc gacgcgtgcc agttcggaaa cgtcttcgac atccaatttt
151 gccagagcgg cggaaatgcg ttcgttcaga ccgttgtgtg cgagaaatgc
201 gcggttag

```

This corresponds to the amino acid sequence <SEQ ID 1350; ORF 503.ng>:

```

g503.pep
1  MSAPSASVII LFHAASISAS SCSGKGVSKI HWRISLPTRA SSETSSSTNF
51 ARAAEMRSFR PLCARNAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1351>:

1	atgtcgcgac	cgccgggcac	ggcaaccatt	ttgttccatg	ccgcttcgat
51	ttcggcatcg	agctgttcgg	ggaaaggcgt	atccaaaatc	cattggcgga
101	tttctttgcc	gacgcgtgcc	agttcggcaa	cgtcttcgac	atccaatatt
151	gccagtcgcg	cggaaatgcg	ttcgcctcaga	ccgttgtgtg	cgaggaatgc
201	gcacgtag				

m503.pep

1 MSAPPASATI LFHAASISAS SCSGKGVSKI HWRISLPTRA SSATSSTS NF
51 ASAAEMRSLR PLCARNAR*

Homology with a predicted ORF from *N. gonorrhoeae*

m503/g503

	10	20	30	40	50	60
m503.pep	MSAPPASATILFHAASISASSCSGKGVSKIHWRLSLPTRASSATSSTSNFASAAEMRSLR					
	:					
g503	MSAPSASVIILFHAASISASSCSGKGVSKIHWRLSLPTRASSETTSSTSNFARAAEMRSFR					
	10	20	30	40	50	60
	69					
m503.pep	PLCARNAR					
g503	PLCARNAR					

a503.seq

1	ATGTCCGCGC	CGCCGGCATC	GGCAACCATT	TTGTTCCATG	CCGCTTCGAT
51	TTCGGCATCG	AGCTGTTCCG	GGAAGGGCGT	GTCCAAAATC	CATTGGCGGA
101	TTTCTTTGCC	GACGCGTGCC	AGTTCGGCAA	CGTCTTCGAC	ATCTAATTTT
151	GCCAGTGC	CGGAAATGCG	TTCGCTCAGA	CCGTTGTGTG	CGAGGAATGC
201	GCGGTAG				

a503.pep

```

1  MSAPPASATI LFHAASISAS SCSGKGVSKI HWRISLPTRA SSATSSTSNF
51 ASAAEMRSLR PLCARNAR*

```

```

      10      20      30      40      50      60
m503.pep  MSAPPASATILFHAASISASSCSGKGVSKIHWRLSLPTRASSATSSSTSNFASAAEMRSLR
          |||||
a503      MSAPPASATILFHAASISASSCSGKGVSKIHWRLSLPTRASSATSSSTSNFASAAEMRSLR
          10      20      30      40      50      60

```

```

                                69
m503.pep      PLCARNARX
               |||||
a503          PLCARNARX

```

g503-1.seq

1	ATGGCGCGG	CGTTGTACAG	GGAGGCGAAA	ACGTGGCGCA	TCGCTTTTTT
51	AACGTTATCC	AAGCCATTGA	TATTCAAGTA	GGTTTCTCTG	TGGCCGGCAGA
101	ATGATGCGTC	GGGCAAGGTC	TCGGCGGTTG	CGGAAGAGCG	TACGGCAACG
151	GAAATTGTCG	CGCCGTCCGG	ATCGGTAATC	ATTTTGTTCC	ATGCCGCTTC
201	GATTTCGGCA	TCGAGCTGTT	CGGGGAAGGG	CGTGTCGAAA	ATCCATTGGC
251	GGATTCTCTT	CGCGACGCGT	CGCAGTTCGG	AAACGCTCTC	GACATCCAAT
301	TTTGCCAGAG	CGGCGGAAAT	GCGTTCGTTT	AGACCGTTGT	GTCCGAGAAA
351	TGCGCGGTAG				

```

1  MARSLYREAK TWRIAFLTSL KPLIFRKVSC WPANDASGRS SAVAERTAT
51 EMSAPSASVI ILFHAASISA SSCSGKGVSK IHWRLPLPTR ASSETSSTSN
101 FARAAEMRSE RPLCARNAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 1357>:

1	ATGGCACGGT	CGTTATACAG	GGAAAGCGAAT	ACATGGTGCA	TCGCTTCTTT
51	AACGGTATCC	AAGCCGTGTA	TGTTCAAGAA	GGTTTCTGT	TGTCCAGGGA
101	ATGATGATCG	CGGACGGTCT	TCGCGAGTTG	CGGAAGAACG	TACGGCAACG
151	GAAATGTCCG	CACCGCCGCG	ATCGGCAACC	ATTTTGTTC	ATGCCCGTTC
201	GATTTCCGCA	TCGAGCTGTT	CGGGGAAAGG	CGTATCCAAA	ATCCATTGGC
251	GGATTTCCTT	GCCGACGCGT	GCCAGTTCGG	CACGCTCTTC	GACATCCAAT
301	TTTGCACAGT	CGCGGGAAAT	GCGTTCGCTC	AGACCGTTGT	GTGCGAGGAA
351	TGCGCGGTAG				

This corresponds to the amino acid sequence <SEQ ID 1358; ORF 503-1>:

```

1  MARSLYREAN  TWCIALSTLS  KPLMFKKVSC  CPANDASGRS  SAVAERTAT
5  EMSAPPASAT  ILFHAASISA  SSCSGKGVSK  IHWRISLPTR  ASSATSSTSN
101 FASAAEMRSL  RPLCARNAR*

```

g503-1 / m503-1 89.9% identity in 119 aa overlap

	10	20	30	40	50	60
g503-1.pep	MARSLYREAKTWRIAFLTL	SKPLIFRKVSCWP	PANDASGRSSA	VAEERTATE	MSAPSASVI	
m503-1	MARSLYREANTWCIA	SLTL	SKPLMPFKVSCCP	PANDASGRSSA	VAEERTATE	MSAPPASAT
	10	20	30	40	50	60
	70	80	90	100	110	120
g503-1.pep	ILFHAASISASSCSG	KGVSKIHWRI	SLPTRASSET	SSTSNFARAA	EMRSFRPL	CARNARX
m503-1	ILFHAASISASSCSG	KGVSKIHWRI	SLPTRASSAT	SSTSNFASAA	EMRSLRPL	CARNARX
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 1359>:

1	ATGGCGCGGT	CGTTGTACAG	GGAGGCGAAT	ACATGGCGCA	TCGCTTCTTT
51	AACGTTTTC	AGGCCGTGTA	TATTCAGGAA	GGTTTCTCTG	TGGCCGGGCA
101	ATGATGTTCT	GAGCAGGTCT	TCGGCGGTTA	CGGAAGACGC	TACGGCAACG
151	GAATGTTCG	CGCCGCGCGC	ATCGGCAACC	ATTTTGTTC	ATGCCGCTTC
201	GATTTTCGCA	TCGAGCTGTT	CGGGCAAGGG	CGTGCTCAA	ATCCATTGCG
251	GGATTCTTTT	GCCGACGCGT	CGCAGTTCGG	CACGCTCTTC	GACATCTAAT
301	TTTGCAGTGC	CGGCAGGAAT	GCGTTCGCTC	AGACCGTTGT	GTGCGAGGAA
351	TGCGCGGTAG				

This corresponds to the amino acid sequence <SEO ID 1360; ORF 503-1.a>:

```

1  MARSLYREAN TWRIASLTFS KPLIFRKVSC WPANDASGRS SAVAEERTAT
51  EMSAPPASAT ILFHAASISA SSCSGKGVSK IHWRISLPTR ASSATSSTSN
101 FASAAEMRSL RPLCARNAR*

```

a503-1 / m503-1 95.8% identity in 119 aa overlap

	10	20	30	40	50	60
a503-1.pep	MARSLYREANTWRIASLTFSKPLIFRKVSCWPANDASGRSSAVAEERTATEMSAPPASAT					
m503-1	MARSLYREANTWCIASLTLSKPLMFKKVSCCPANDASGRSSAVAEERTATEMSAPPASAT					
	10	20	30	40	50	60
	70	80	90	100	110	120
a503-1.pep	ILFHAASISASSCSGKGVSKIHWRI	SLP	TRASSAT	SSTSNFASAAEMRSLRPLCARNARX		
m503-1	ILFHAASISASSCSGKGVSKIHWRI	SLP	TRASSAT	SSTSNFASAAEMRSLRPLCARNARX		
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1361>:

```
g504.seq
1  atgttggttc aggacttgcc ttttgaagtc aaactgaaaa aattccatat
51  cgatttttac aatacgggta tgccgcgcga ttttgccagc gatattgaag
101 taacggacaa ggcaaccggt gagaaactcg agcgcaccat ccgcgtgaac
151 catcctttga ccttgcacgg catcacgatt tatcaggcga gttttgccga
201 cggcggttcg gatttgacat tcaaggcgtg gaatttgagg gatgcttcgc
251 gcgaacctgt cgtgttgaag gcaacctcca tacaccagtt tccgttgga
301 atcggcaaac acaaatatcg tcttgagttc gatcagttca cttctatgaa
351 tgtggaggac atgagcagag gtgcggaacg ggaaaaaagc ctgaaatcca
401 ctctgaacga tgtccgcgcc gttactcagg aaggtaaaaa atacaccaat
451 atcggccctt ccattgtgta ccgcattccg gatgcggcag ggcaggcggt
501 cgaatataaa aactatatgc tgccgatttt gcaggacaaa gattattttt
551 ggctgaccgg cacgcgcagc ggcttgacgc agcaataacc ctggctgcgt
601 atccccttgg acaagcagtt gaaagcggac acctttatgg cattgcgtga
651 gtttttgaaa gatggggaag ggcgcaaacg tctggttgcc gacgcaacca
701 aagacgcacc tgccgaaatc cgcgaacaat tcatgctggc tgcggaaaaa
751 acgctgaata tctttgcgca aaaaggctat ttgggattgg acgaatttat
801 tacgtccaat atcccgaag ggcagcagga taagatgcag ggctatttct
851 acgaaatgct ttacggcgtg atgaacgctg ctttggtatg aaccatacgc
901 cggtagcggt tgcccgaatg gcagcaggat gaagcgcgga accgtttcct
951 gctgcacagt atggatgcct atacggggct gacggaatat cccgcgccta
1001 tgctgctcca gcttgacggg ttttccgagg tgcgttcctc aggtttgcag
1051 atgaccggtt cgccgggtgc gcttttggtc tatctcggtc cggatttggt
1101 ggttttgggt acagtattta tgttttatgt gcccaaaaaa cgggcgtggg
1151 tattgttttc aaacdgcata atccgttttg ctatgtcttc ggccgcagc
1201 gaacgggatt tgcagaagga atttcaaaa cacgtcgaga gcctgcaacg
1251 gctcggcaag gacttgaatc atgactga
```

This corresponds to the amino acid sequence <SEQ ID 1362; ORF 504.ng>:

```
g504.pep
1  MLVQDLPEFV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
51  HPLTLHGITI YQASFADGGS DLTFKAWNLR DASREPVVLK ATSIHQFPLE
101 IGKHKYRLEF DQFTSMNVED MSEGAREKS LKSTLNDVRA VTQEGKKYTN
151 IGPSIVYRIR DAAGQAVEYK NYMLPILODK DYFWLTGTRS GLQQQYRWLR
201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKDAPAEI REQFMLAAEN
251 TLNIFAQKGY LGLDEFITSN IPKGQDKMQ GYFYEMLYGV MNAALDETIR
301 RYGLPEWQOD EARNRFLLS MDAYTGLTEY PAPMLQLDG FSEVRSSGLQ
351 MTRSPGALLV YLGSVLLVLG TVFMFYVPPK RAWVLFSENKI RFAMSSARSE
401 RDLQKEFPKH VESLQRLGKD LNHD*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1363>:

```
m504.seq..
1  atattggttc aggacttgcc ttttgaagtc aaactgaaaa aattccatat
51  cgatttttac aatacgggta tgccgcgcga ttttgccagc gatattgaag
101 tgacggacaa ggcaaccggt gagaaactcg agcgcaccat ccgcgtgaac
151 catcctttga ccttgcacgg catcacgatt tatcaggcga gttttgccga
201 cggcggttcg gatttgacat tcaaggcgtg gaatttgagg gatgcttcgc
251 gcgagcctgt cgtgttgaag gcaacatcca tacaccagtt tccgttgga
301 attggcaaac acaaatatcg tcttgagttc gatcagttca cttctatgaa
351 tgtggaggac atgagcagag gcgcggaacg ggaaaaaagc ctgaaatcca
401 cgctgmmcga tgtccgcgcc gttactcagg aaggtaaaaa atacaccaat
451 atcggccctt ccattgttta ccgtatccg gatgcggcag ggcaggcggt
501 cgaatataaa aactatatgc tgccggtttt gcaggaaacg gattattttt
551 ggattaccgg cacgcgcagc ggcttgacgc agcaataacc ctggctgcgt
601 atccccttgg acaagcagtt gaaagcggac acctttatgg cattgcgtga
651 gtttttgaaa gatggggaag ggcgcaaacg tctggttgcc gacgcaacca
701 aaggcgcacc tgccgaaatc cgcgaacaat tcatgctggc tgcggaaaaa
751 acgctgaaca tctttgcaca aaaaggctat ttgggattgg acgaatttat
801 tacgtccaat atcccgaag agcagcagga taagatgcag ggctatttct
851 acgaaatgct ttacggcgtg atgaacgctg ctttggtatg aaccatacgc
901 cggtagcggt tgcccgaatg gcagcaggat gaagcgcgga atcgtttcct
951 gctgcacagt atggatgcgt acacgggttt gaccgaatat cccgcgccta
1001 tgctgctgca acttgatggg ttttccgagg tgcgttcctc gggtttgag
```

```

1051 atgacccggt ccccggtg gcttttggc tatctcggc cgggtgctgtt
1101 ggtattgggt acggtattga tgttttatgt gcgcgaaaaa cgggcgtggg
1151 tattgttttc agacggcaaa atccgttttg ccatgtcttc ggcccgacgc
1201 gaacgggatt tgcagaagga atttccaaaa cacgtcgaga gtctgcaacg
1251 gctcggcaag gacttgaatc atga

```

This corresponds to the amino acid sequence <SEQ ID 1364; ORF 504>:

m504.pep..

```

1  ILVQDLPEFEV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
51  HPLTLHGITI YQASFADGGS DLTFKAWNLG DASREPVVLK ATSIHQFPLE
101 IGKHKYRLEF DQFTSMNVED MSEGAREKS LKSTLXDVRA VTQEGKKYTN
151 IGPSIVYRIR DAAGQAVEYK NYMLPVLQEQ DYFWITGTRS GLQQQYRWLR
201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKGAPAEI REQFMLAAEN
251 TLNIFAQKGY LGLDEFITSN IPKEQQDKMQ GYFYEMLYGV MNAALDETIR
301 RYGLPEWQQD EARNRFLLS MDAYTGLTEY PAPMLQLDGF SEVRSSGLQ
351 MTRSPGALLV YLGSVLLVLG TVLMFYVREK RAWVLFSDGK IRFAMSSARS
401 ERDLQKEFPK HVESLQRLGK DLNHD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 504 shows 96.7% identity over a 425 aa overlap with a predicted ORF (ORF 504.ng) from *N. gonorrhoeae*:

m504/g504

	10	20	30	40	50	60
m504.pep	ILVQDLPEFEVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLERTIRVNHPLTLHGITI					
	:					
g504	MLVQDLPEFEVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLERTIRVNHPLTLHGITI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m504.pep	YQASFADGGSDLTFKAWNLDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED					
	:					
g504	YQASFADGGSDLTFKAWNLRDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED					
	70	80	90	100	110	120
	130	140	150	160	170	180
m504.pep	MSEGAREKSLKSTLXDVRAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKNYMLPVLQEQ					
	:					
g504	MSEGAREKSLKSTLNDVRAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKNYMLPILQDK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m504.pep	DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKGAPAEI					
	:					
g504	DYFWLTGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKDAPAEI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m504.pep	REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKEQQDKMQGYFYEMLYGVMNAALDETIR					
	:					
g504	REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKGQQDKMQGYFYEMLYGVMNAALDETIR					
	250	260	270	280	290	300
	310	320	330	340	350	360
m504.pep	RYGLPEWQQDEARNRFLLSMDAYTGLTEYPAPMLQLDGFSEVRSSGLQMTSPGALLV					
	:					
g504	RYGLPEWQQDEARNRFLLSMDAYTGLTEYPAPMLQLDGFSEVRSSGLQMTSPGALLV					
	310	320	330	340	350	360
	370	380	390	400	410	420
m504.pep	YLGSVLLVLGTVLMFYVREKRAWVLFSDGKIRFAMSSARSERDLQKEFPKHVESLQRLGK					
	:					

743

g504 YLGSVLLVLGTVFMFYVPPKKRAWVLFNSN-KIRFAMSSARSERDLQKEFPKHVESLQRLGK
 370 380 390 400 410

m504.pep DLNHD
 |||||
 g504 DLNHD
 420

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1365>:

a504.seq
 1 ATATTGGTTC AGGACTTGCC TTTTGAAGTC AAAGTAAAA AATTCCATAT
 51 CGATTTTAC AATACGGGTG TGCCGCGCGA TTTTGCCAGT GATATTGAAG
 101 TAACGGATAA GGCAACCGGT GAGAACTCG AGCGCACCAT CCGCGTGAAC
 151 CATCCTTTGA CCTTGACGCG CATCACGATT TATCAGGCGA GTTTTGCCGA
 201 CGGCGGTTCG GATTTGACAT TCAAGGCGTG GAATTTGGGT GATGCTTCGC
 251 GCGAGCCTGT CGTGTGAAG GCAACATCCA TACACCAGTT TCCGTTGGAA
 301 ATTGCCAAAC ACAATATCG TCTTGAGTTC GATCAGTTTA CTTCTATGAA
 351 TGTGGAGGAC ATGAGCGAGG GCGCGGAACG GGAAAAAAGC CTGAAATCCA
 401 CGCTGAACGA TGTCCGCGCC GTTACTCAGG AAGGTAAAAA ATACACCAAT
 451 ATCGGCCCTT CCATTGTTTA CCGTATCCGT GATGCGGCAG GGCAGGCGGT
 501 CGAATATAAA AACTATATGC TGCCGGTTTT GCAGGAACAG GATTATTTTT
 551 GGATTACCGG CACGCGCAGC GGCTTGACAG AGCAATACCG CTGGCTGCGT
 601 ATCCCCTTGG ACAAGCAGTT GAAAGCGGAC ACCTTTATGG CATTGCGTGA
 651 GTTTTTGAAA GATGGGGAAG GGCGCAAACG TCTGGTTGCC GACGCAACCA
 701 AAGGCGCACC TGCCGAAATC CGCGAACAAT TCATGCTGGC TGCCGAAAAAC
 751 ACGCTGAACA TCTTTGCACA AAAAGGCTAT TTGGGATTGG ACGAATTTAT
 801 TACGTCCAAT ATCCCGAAAG AGCAGCAGGA TAAGATGCAG GGCTATTTCT
 851 ACGAAATGCT TTACGGCGTG ATGAACGCTG CTTTGATGA AACCATACGC
 901 CCGTACGGCT TGCCCGAATG GCAGCAGGAT GAAGCGCGGA ATCGTTTCCT
 951 GCTGCACAGT ATGGATGCGT ACACGGGTTT GACCGAATAT CCCGCGCCTA
 1001 TGCTGCTGCA ACTTGATGGG TTTTCCGAGG TCGGTTCTGC GGGTTTGCAG
 1051 ATGACCCGTT CCCCGGGTGC GCTTTTGGTC TATCTCGGCT CCGTGCTGTT
 1101 GGTATTGGGT ACGGTATTGA TGTTTTATGT GCGCGAAAAA CGGGCGTGGG
 1151 TATTGTTTTC AGACGGCAA ATCCGTTTTG CCATGTCTTC GGCCGCGAGC
 1201 GAACGGGATT TGCAGAAGGA ATTTCCAAAA CACGTCGAGA GTCTGCAACG
 1251 GCTCGGCAAG GACTTGAATC ATGACTGA

This corresponds to the amino acid sequence <SEQ ID 1366; ORF 504.a>:

a504.pep
 1 ILVQDLPEFV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
 51 HPLTLHGITI YQASFADGGS DLTFKAWNLG DASREPVVLK ATSIHQFPLE
 101 IGKHKYRLEF DQFTSMNVED MSEGAREKS LKSTLNDVRA VTQEGKKYTL
 151 IGPSIVYRIR DAAGQAVEYK NYMLPVLQEQ DYFWITGTRS GLQQQYRWLR
 201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKGAPAEI REQFMLAAEN
 251 TLNIFAQKGY LGLDEFITSN IPKEQQDKMQ GYFYEMLYGV MNAALDETIR
 301 RYGLPEWQOD EARNRFLLSH MDAYTGLTEY PAPMLLQLDG FSEVRSSGLQ
 351 MTRSPGALLV YLGSVLLVLG TVLMFYVREK RAWVLFSDGK IRFAMSSARS
 401 ERDLQKEFPK HVESLQRLGK DLNHD*

m504/a504 99.8% identity in 425 aa overlap

	10	20	30	40	50	60
m504.pep	ILVQDLPEFVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLEERTIRVNHPLTLHGITI					
a504	ILVQDLPEFVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLEERTIRVNHPLTLHGITI					
	10	20	30	40	50	60
m504.pep	YQASFADGGSDLTFKAWNLDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED					
a504	YQASFADGGSDLTFKAWNLDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED					
	70	80	90	100	110	120
m504.pep	MSEGAREKSLKSTLXDVRVAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKNYMLPVLQEQ					
a504	MSEGAREKSLKSTLXDVRVAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKNYMLPVLQEQ					
	130	140	150	160	170	180
m504.pep						

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```

a504      |||||
MSEGAEREKSLKSTLNDVRAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKNYMLPVLQEQ
          130      140      150      160      170      180

          190      200      210      220      230      240
m504.pep  DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKGAPAEI
          |||||
a504      DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKGAPAEI
          190      200      210      220      230      240

          250      260      270      280      290      300
m504.pep  REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKEQQDKMQGYFYEMLYGVMNAALDETIR
          |||||
a504      REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKEQQDKMQGYFYEMLYGVMNAALDETIR
          250      260      270      280      290      300

          310      320      330      340      350      360
m504.pep  RYGLPEWQQDEARNRFLHSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTSPGALLV
          |||||
a504      RYGLPEWQQDEARNRFLHSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTSPGALLV
          310      320      330      340      350      360

          370      380      390      400      410      420
m504.pep  YLGSVLLVLGTVLMFYVREKRAWVLFSDGKIRFAMSSARSERDLQKEFPKHVESLQRLGK
          |||||
a504      YLGSVLLVLGTVLMFYVREKRAWVLFSDGKIRFAMSSARSERDLQKEFPKHVESLQRLGK
          370      380      390      400      410      420

m504.pep  DLNHDX
          |||||
a504      DLNHDX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1367>:

```

g505.seq
1  atgtttcggt tacaattcag gctgtttccc cctttgcgaa cgcctatgca
51  catcctgttg accgccctgc tcaaattgct ctccctgtcg tcgctttcct
101 gtcgtcacac gctgggaaac cggctcggac atctggcggt ttacctttta
151 aaggaagacc gcgcgcgcac cgtcgccaat atgcggcagg cgggtttgaa
201 ccccgacacg cagacgggtca aagccgtttt tgcggaaacg gcaaaatgcg
251 gtttggaact tgcccccgcg tttttcaaaa aaccggaaga catcgaaaca
301 atgttcaaag cggtagacacg ctgggaacac gtgcagcagg ctttggacaa
351 gggcgaaggg ctgctgttca tcacgccgca catcggcagg tacgatttgg
401 gcggacgcta catcagccag cagcttcctg tccacctgac cgccatgtac
451 aagccgccga aaatcaaagc gatagacaaa atcatgcagg cgggcagggt
501 gcgcggcaaa ggcaaaaccg cggccaccgg catacaaggg gtcaaacaaa
551 tcatcaaggc cctgcgcgcg ggcgaggcaa ccatcatcct gcccgaccac
601 gtcccttctc cgcaggaagg cggcggcggt tggcgaggatt ttttcggcaa
651 acctgcatac accatgacac tggcggcaaa attggcacac gtcaaaggcg
701 tgaaaaccct gtttttctgc tgcgaacgcc tgcccgacgg acaaggcttc
751 gtgttgacac tccgccccgt ccaaggggaa ttgaacggca acaaagccca
801 cgatgccgcc gtgttcaacc gcaataccga atattggata cgccgttttc
851 cgacgcagta tctgtttatg tacaaccgct ataaaacgcc gtaa

```

This corresponds to the amino acid sequence <SEQ ID 1368; ORF 505.ng>:

```

g505.pep
1  MFRLOFRLFP PLRTAMHILL TALLKCLSLI SLSCSLHTLGN RLGHIAFYLL
51  KEDRARIVAN MRQAGLNPDV QTVKAVFAET AKCGLELAPA FFKKPEDIET
101 MFKAHVHWEH VQALDKGEG LLFITPHIGS YDLGGYISQ QLPFHILTAMY
151 KPPKIKAIK IMQAGRVRGK GKTAPTGIQG VKQIIKALRA GEATIILPDH
201 VPSPQEGGGV WADFFGKPAY TMTLAAKLAH VKGVKTLFFC CERLPDGGGF
251 VLHIRPVQGE LNGNKAHDAA VFNRNTEYWI RRFPTQYLFM YNRYKTP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1369>:

m505.seq (partial)

```

1  GGCATGTTTC  GTTTACAATT  CAGGCTGTTT  CCCCCTTTGC  GAACCGCCAT
51  GCACATCCTG  TTGACCGCCC  TGCTCAAATG  CCTCTCCCTG  CTGCCGCTTT
101 CCTGTCTGCA  CACGCTGGGA  AACCGGCTCG  GACATCTGGC  GTTTTACCTT
151 TTAAAGGAAG  ACCGCGCGCG  CATCGTCGCC  AATATGCGGC  AGGCGGGTTT
201 GAACCCCGAC  CCCAAAACGG  TCAAAGCCGT  TTTTGCGGAA  ACGGCAAAAG
251 GCGGTTTGGA  ACTTGCCCCC  GCGTTTTTCA  GAAAACCGGA  AGACATAGAA
301 ACAATGTTCA  AAGCGGTACA  CGGCTGGGAA  CATGTGCAGC  AGGCTTTGGA
351 CAAACACGAA  GGGCTGCTAT  TCATCACGCC  GCACATCGGC  AGCTACGATT
401 TGGGCGGACG  CTACATCAGC  CAGCAGCTTC  CGTTCCTCGT  GACCGCCATG
451 TACAAACCGC  CGAAAATCAA  AGCGATAGAC  AAAATCATGC  AGGCGGGCAG
501 GGTTCGCGGC  AAAGGAAAAA  CCGCGCCTAC  CAGCATACAA  GGGGTCAAAC
551 AAATCATCAA  AGCCCTGCGT  TCGGGCGAGC  AACCATCGTC  CTGCCCGACC
601 ACGTCCCCTC  CCCTCAAGAA  GCGGGGGAAG  GCGTATGGGT  GGATTTCTTC
651 GGCAAACCTG  CCTATACCAT  GACGCTGGCG  GCAAATTG  CACACGTCAA
701 AGGCGTGAAG  ACCCTGTTTT  TCTGCTGCGA  ACGCCTGCCT  GGCGGACAAG
751 GTTTCGATTT  GCACATCCGC  CCCGTCCAAG  GGAATTGAA  CGGCGACAAA
801 GCCCATGATG  CCGCCGTGTT  CAACCGCAAT  GCCGAATATT  GGATACGCCG
851 TTTTCCGACG  CatATC....

```

This corresponds to the amino acid sequence <SEQ ID 1370; ORF 505>:

m505.pep (partial)

```

1  MFRLQFRLFP  PLRTAMHILL  TALLKCLSL  LPLSCLHTL  GNRLGHLAF  YLLKEDRA  RIVAN
51  KEDRARIVAN  MRQAGLNPD  PKTAVFAET  AKGGLLELA  PAFFRKPE  DIETMFK  AVHGW
101 MFKAVHGW  EH VQQALDK  HEG LLFITP  HIGSYDLG  GRYISQ  LPPFLT  AMY
151 KPPKIKAI  DKIMQAGR  VRGKGKT  APTSIOG  VKQIIKA  LRSGEAT  IVLPDH
201 VPSPOEG  GEGVWVD  FFGKPA  YTMTLA  AXLAHV  KGVKTL  FFCER  LPPGGQ
251 FDLHIRP  VQGELN  GDKAHD  AAVFN  RNAEY  WIRRF  PTHI...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 505 shows 93.7% identity over a 287 aa overlap with a predicted ORF (ORF 505.ng) from *N. gonorrhoeae*:

m505/g505

	10	20	30	40	50	60
m505.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
g505	MFRLQFRLFPPLRTAMHILLTALLKCLSLSLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505.pep	MRQAGLNPDPKTVKAVFAETAKGGLLELAPAFFRKPEDTETMFKAVHGWVQQALDKHEG					
g505	MRQAGLNPDQTVKAVFAETAKGGLLELAPAFFRKPEDTETMFKAVHGWVQQALDKHEG					
	70	80	90	100	110	120
m505.pep	MRQAGLNPDPKTVKAVFAETAKGGLLELAPAFFRKPEDTETMFKAVHGWVQQALDKHEG					
g505	MRQAGLNPDQTVKAVFAETAKGGLLELAPAFFRKPEDTETMFKAVHGWVQQALDKHEG					
	70	80	90	100	110	120
m505.pep	LLFITPHIGSYDLGGYISQQLPPFLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTSIQG					
g505	LLFITPHIGSYDLGGYISQQLPPFLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTSIQG					
	130	140	150	160	170	180
m505.pep	LLFITPHIGSYDLGGYISQQLPPFLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTSIQG					
g505	LLFITPHIGSYDLGGYISQQLPPFLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTSIQG					
	130	140	150	160	170	180
m505.pep	VKQIIKALRSGEATIVLPDHVPSPOEGGEGVWVDFFGKPAYTMTLAAXLAHVKGKTLFF					
g505	VKQIIKALRSGEATIVLPDHVPSPOEGGEGVWVDFFGKPAYTMTLAAXLAHVKGKTLFF					
	190	200	210	220	230	240
m505.pep	VKQIIKALRSGEATIVLPDHVPSPOEGGEGVWVDFFGKPAYTMTLAAXLAHVKGKTLFF					
g505	VKQIIKALRSGEATIVLPDHVPSPOEGGEGVWVDFFGKPAYTMTLAAXLAHVKGKTLFF					
	190	200	210	220	230	240
m505.pep	CCERLPGGQGFDLHIRPVQELNGDKAHDAAVFNRNAEYWIRRFPTHI					
g505	CCERLPGGQGFVLHIRPVQELNGDKAHDAAVFNNTTEYWIRRFPTQYLFMYNRYKTP					
	240	250	260	270	280	290

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1371>:

a505.seq

```

1   ATGTTTCGTT TACAATTCAG GCTGTTTCCC CCTTTGCGAA CCGCCATGCA
51  CATCCTGTTG ACCGCCCTGC TCAAATGCCT CTCCCTGCTG CCGCTTTCCT
101 GTCTGCACAC GCTGGGAAAC CGGCTCGGAC ATCTGGCGTT TTACCTTTTA
151 AAGGAAGACC GCGCGCGCAT CGTCGCCAAT ATGCGTCAGG CAGGCATGAA
201 TCCCGACCCC AAAACGGTCA AAGCCGTTTT TGCGGAAACG GCAAAAGGCG
251 GTTTGGAAGT TGCCCCCGCG TTTTTCAGAA AACCGGAAGA CATAGAAACA
301 ATGTTCAAAG CGGTACACGG CTGGGAACAT GTGCAGCAGG CTTTGGACAA
351 ACACGAAGGG CTGCTATTCA TCACGCCGCA CATCGGCAGC TACGATTGTT
401 GCGGACGCTA CATCAGCCAG CAGCTTCCGT TCCCGCTGAC CGCCATGTAC
451 AAACCGCCGA AAATCAAAGC GATAGACAAA ATCATGCAGG CGGGCAGGGT
501 TCGCGGCAAA GGAAAAACCG CGCCTACCAG CATACAAGGG GTCAAACAAA
551 TCATCAAAGC CCTGCGTTTC GCGGAAGCAA CCATCGTCCT GCCCGACCAC
601 GTCCCTCCC CTCAAGAAGG CGGGAAGGC GTATGGGTGG ATTTCTTCGG
651 CAAACCTGCC TATACCATGA CGCTGGCGGC AAAATTGGCA CACGTCAAAG
701 GCGTGAAAC CCTGTTTTTC TGCTGCGAAC GCCTGCCTGG CGGACAAGGT
751 TTCGATTGTC ACATCCGCCC CGTCCAAGGG GAATTGAACG GCGACAAAGC
801 CCATGATGCC GCCGTGTTCA ACCGCAATGC CGAATATTGG ATACGCCGTT
851 TTCCGACGCA GTATCTGTTT ATGTACAACC GCTACAAAAT GCCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1372; ORF 505.a>:

a505.pep

```

1   MFRLLQFRLFP PLRTAMHILL TALLKCLSL PLSLHLTLGN RLGHIAFYLL
51  KEDRARIVAN MRQAGMNPDP KTVKAVFAET AKGGLLELAPA FFRKPEDIET
101 MFKAHVHGEH VQALDKHEG LLFITPHIGS YDLGGYISQ QLPFPLTAMY
151 KPPKIKAIK IMQAGRVRGK GKTAPTSIQG VKQIIKALRS GEATIVLPDH
201 VPSPQEGGEG VWVDFGKPA YMTLAAKLA HVKGVKTLFF CCERLPGGQG
251 FDLHIRPVQG ELNGDKAHDA AVFNRNAEYW IRRFPTQYLF MYNRYKMP*

```

m505/a505 99.0% identity in 287 aa overlap

m505.pep	10	20	30	40	50	60
	MFRLLQFRLFPPLRTAMHILLTALLKCLSLPLSLHLTLGNRLGHIAFYLLKEDRARIVAN					
a505	MFRLLQFRLFPPLRTAMHILLTALLKCLSLPLSLHLTLGNRLGHIAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505.pep	70	80	90	100	110	120
	MRQAGLNPDPKTVKAVFAETAKGGLLELAPFAFRKPEDIETMFKAHVHGEHVQALDKHEG					
a505	MRQAGMNPDPKTVKAVFAETAKGGLLELAPFAFRKPEDIETMFKAHVHGEHVQALDKHEG					
	70	80	90	100	110	120
m505.pep	130	140	150	160	170	180
	LLFITPHIGSYDLGGYISQQLPFPLTAMYPKPPKIKAIKIMQAGRVRGKGKTAPTSIQG					
a505	LLFITPHIGSYDLGGYISQQLPFPLTAMYPKPPKIKAIKIMQAGRVRGKGKTAPTSIQG					
	130	140	150	160	170	180
m505.pep	190	200	210	220	230	240
	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFGKPAYMTLAAXLAHVKGKTLFF					
a505	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFGKPAYMTLAAXLAHVKGKTLFF					
	190	200	210	220	230	240
m505.pep	250	260	270	280		
	CCERLPGGQGFDLHIRPVQGEELNGDKAHDAVFNRNAEYWIIRFPPTHI					
a505	CCERLPGGQGFDLHIRPVQGEELNGDKAHDAVFNRNAEYWIIRFPPTQYLFMYNRYKMPX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1373>:

m505-1.seq

```
1  ATGTTTCGTT TACAATTCAG GCTGTTTCCC CCTTTGCGAA CCGCCATGCA
51  CATCCTGTTG ACCGCCCTGC TCAAATGCCT CTCCTGCTG CCGCTTTCCT
101 GTCTGCACAC GCTGGGAAAC CGGCTCGGAC ATCTGGCGTT TTACCTTTTA
151 AAGGAAGACC GCGCGCGCAT CGTCGCCAAT ATGCGGCAGG CGGGTTTGAA
201 CCCCGACCCC AAAACGGTCA AAGCCGTTT TCGGAAACG GCAAAAGGCG
251 GTTTGGAECT TGCCCCGCG TTTTCAGAA AACCGGAAGA CATAGAAACA
301 ATGTTCAAAG CGGTACACGG CTGGGAACAT GTGCAGCAGG CTTTGACAA
351 ACACGAAGGG CTGCTATTCA TCACGCCGCA CATCGGCAGC TACGATTGG
401 GCGGACGCTA CATCAGCCAG CAGCTTCCGT TCCCGCTGAC CGCCATGTAC
451 AAACCGCCGA AAATCAAAGC GATAGACAAA ATCATGCAGG CGGGCAGGGT
501 TCGCGGCAAA GGA AAAACCG CGCCTACCAG CATAAAGGG GTCAAACAAA
551 TCATCAAAGC CTGCGTTCG GCGGAAGCAA CCATCGTCTT GCCCGACCAC
601 GTCCTCTCCC CTCAAGAAGG CGGGGAAGGC GTATGGGTGG ATTTCTTCGG
651 AAACCTGCCA TATACCATGA CGCTGGCGGC AAAATTGGCA CACGTCAAAG
701 GCGTGA AAAC CCTGTTTTTC TGCTGCGAAC GCCTGCCTGG CGGACAAGGT
751 TTCGATTTGC ACATCCGCCC CGTCCAAGGG GAATTGAACG GCGACAAAGC
801 CCATGATGCC GCCGTGTTCA ACCGCAATGC CGAATATTGG ATACGCCGTT
851 TTCCGACGCA GTATCTGTTT ATGTACAACC GTCACAAAT GCCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1374; ORF 505-1>:

m505-1.pep

```
1  MFRLQFRLFP PLRTAMHILL TALLKCLSL LPLSCLHTLGN RLGHlafyLL
51  KEDRARIVAN MRQAGLNPD P KTVKAVFAET AKGGLLELAPA FFRKPEDiet
101 MFKAHVHWEH VQALDKHEG LLFITPHIGS YDLGGYISQ QLPFPLTAMY
151 KPPKIKAIK IMQAGRVRGK GKTAPTSIOG VKQIIKALRS GEATIVLPDH
201 VPSPQEGGEG VWVDFFGKPA YMTLAAKLA HVKGVKTLFF CCErLPGGQG
251 FDLHIRPVQG ELNGDKAHDA AVFNrNAEYW IRRFPTQYLF MYNRYKMP*
```

m505-1/g505 94.3% identity in 298 aa overlap

```

      10      20      30      40      50      60
m505-1.pep MFRLQFRLFPPLRTAMHILLTALLKCLSL LPLSCLHTLGNRLGHlafyLLKEDRARIVAN
          |||
g505      MFRLQFRLFPPLRTAMHILLTALLKCLSL LSLSCLHTLGNRLGHlafyLLKEDRARIVAN
          |||
      10      20      30      40      50      60

      70      80      90     100     110     120
m505-1.pep MRQAGLNPD PKTVKAVFAETAKGGLLELAPAFFRKPEDietMFKAHVHWEHVQALDKHEG
          |||
g505      MRQAGLNPD TQTVKAVFAETAKGGLLELAPAFFKKPEDietMFKAHVHWEHVQALDKGEG
          |||
      70      80      90     100     110     120

      130     140     150     160     170     180
m505-1.pep LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTSIOG
          |||
g505      LLFITPHIGSYDLGGYISQQLPFPLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTGIQG
          |||
      130     140     150     160     170     180

      190     200     210     220     230     240
m505-1.pep VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFFGKPAYTMTLAAKLAHVKGVKTLFF
          |||
g505      VKQIIKALRAGEATIILPDHVPSPQEGG-GVWADFFGKPAYTMTLAAKLAHVKGVKTLFF
          |||
      190     200     210     220     230

      250     260     270     280     290     299
m505-1.pep CCErLPGGQGF DLHIRPVQGE LNNGDKAHDA AVFNrNAEYW IRRFPTQYLFMYNRYKMPX
          |||
g505      CCErLPGGQGF V LHIRPVQGE LNNGNKAHDA AVFNrNTEYW IRRFPTQYLFMYNRYKTPX
          |||
      240     250     260     270     280     290
```

m505-1/a505 99.7% identity in 298 aa overlap

```

      10      20      30      40      50      60
m505-1.pep MFRLQFRLFPPLRTAMHILLTALLKCLSL LPLSCLHTLGNRLGHlafyLLKEDRARIVAN
          |||
a505      MFRLQFRLFPPLRTAMHILLTALLKCLSL LPLSCLHTLGNRLGHlafyLLKEDRARIVAN
          |||
      10      20      30      40      50      60

      70      80      90     100     110     120
```

```

m505-1.pep  MRQAGLNPDPKTVKAVFAETAKGGLELAPAFFRKPEDMETMFKAVHGWEHVQQALDKHEG
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a505          MRQAGMNPDPKTVKAVFAETAKGGLELAPAFFRKPEDMETMFKAVHGWEHVQQALDKHEG
              70      80      90      100     110     120

              130     140     150     160     170     180
m505-1.pep  LLFITPHIGSYDLGGRYISQQLPFPLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTSTIQQ
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a505          LLFITPHIGSYDLGGRYISQQLPFPLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTSTIQQ
              130     140     150     160     170     180

              190     200     210     220     230     240
m505-1.pep  VKQIIKALRSGEATIVLPDHVPSPOEGGEGVWVDFFGKPAYTMTLAAKLAHVKGVKTLFF
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a505          VKQIIKALRSGEATIVLPDHVPSPOEGGEGVWVDFFGKPAYTMTLAAKLAHVKGVKTLFF
              190     200     210     220     230     240

              250     260     270     280     290     299
m505-1.pep  CCERLPGGGQFDLHIRPVQGELNGDKAHDAAVFNRNAEYWIRRFPTQYLFMYNRYKMPX
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a505          CCERLPGGGQFDLHIRPVQGELNGDKAHDAAVFNRNAEYWIRRFPTQYLFMYNRYKMPX
              250     260     270     280     290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1375>:

```

g506.seq
1   ATGGCGGTAT TGTATGAAGT CGGGCGCATC GCCCATGGCT GCGGCGGTGT
51  TGTCAAACAA AGCCTGTTTC TGCGCGTCGT TCATCAGGTT GAACAAGGCG
101 CGCGGTTGGC TGAAGTAGTC GTCATCGTCT TGCGGTTAGT CCCAGTGTGC
151 CGCGTCGCCG TTGATTTTCA AAGGCGGTTT GCGGAAGTCG GGTGTGTGCT
201 GCCATTGGCC GAAGCTGTTG GGTTCGTAGT GCGGCAGGCT GCCGTAGTTG
251 CCGTCGGCGC GGCCTTGTCG GTCGCGCTGG TTGCTGTGAA CAGGGCAACG
301 CGGACGATTG ACGGGGATTT GCGCGAAGTT CACACCCAAG CGGTAACGTT
351 GCGCGTCGGC GTAATTGAAC AAACGGGCTT GCAACATTTT ATCCGGGCTC
401 GCGCCGATAC CGGGAACGAG GTTGCTCGGT GCGAAGCGCG ATTGTTCCAC
451 ATCGGCGAAG AAGTTTTTCG GATTGCGGTT CAACTCGAAT TCGCCCACTT
501 CAATCAGCGG ATAGTCTTTT TTCGGCCAAA CTTTGGTCAA GTCAAACGGA
551 TGATAAGGCA CTTTTTCGGC ATCGGCTTCA GGCATGACTT GGATGTACAT
601 CGTCCATTTT GGGAACTCGC CGCGCTCGAT GGCTTCGTAC AGGTCGCGCT
651 GATGGCTTTT GCGGTCGTCG GCGATGATTT TTGCAGCTTC TTCGTTGGTC
701 AGGTTTTTAA TCCCTTGCTG GCTGCGGAAA TGAATTTTCA CCCAAAAACG
751 TTCGCCCGCT TCGTTCCAGA AGCTGTAGGT ATGCGAACCG AAGCCGTGCA
801 TATGGCGGTA GCTGGCGGGA ATACCGCGGT CGCTCATCAC GATGGTAACT
851 TGGTGCAGGG CTTGCGGCAG CAGCGTCCAG AAGTCCAGT TGTGTGTGGC
901 GGAACGCATA TTGGTGCGCG GATCGCGTTT GACGGCTTTG TTCAGGTCGG
951 GGAATTTGCG CGGGTCGCGC AGGAAGAACA CGGGCGTGTT GTTGCCGACC
1001 ACATCCAGT TGCCTTCTTC GGTATAGAAT TTCAACGCAA AACCGCGGAT
1051 GTCGCGTTCC GCATCGGCTG CGCCGCGCTC GCCTGCCACG GTGGTGAAAC
1101 GGGCGAACAT CTCGGTTTTT TTGCCGACTT CGCTGAAAAT TTTGGCGCGG
1151 GTGTATTTGG TGATGTCGTG TGTTACGGTA AACGTACCGA ACGCGCCCGA
1201 ACCTTTGGCG TGCATACGGC GTTCGGGGAT GACTTCGCGC ACGAAGTCGG
1251 CGAGTTTTTC ATTACGCCAC AAATCTTGCG TCAGCAGGGG GCCGCGCGGG
1301 CCGGCGGTCA GGCTGTTTTG ATTGTGCGCA ACGGGCGCGC CGTTGTTTCA
1351 GGTACAGATG GTTACGGGGC ATTTGGAGGT AGTCATCGCT CTGTTCCTT
1401 TTCTCAGGTT GGTCAAATGG GGGGCAAACG GCTTACAGTA CGATTGGCG
1451 GAAAGCGTAT TCGTAACCGG TTTCTTGATT GTAATAAATT TCTTGAATCG
1501 ACATTTTATT TTCCTTTTGC AAAAATATG GATGCGATTA TACGCCAAGA
1551 TTTTCGTTAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 1376; ORF 506.ng>:

```

g506.pep
1   MAVFDEVGRI AHGCGGVVKQ SLFLRVVHQQ EQGARLAEVV VIVLAVVPVC
51  RVAVDFQRRF GEVGLLLPLA EAVGFVVRQA AVVAVGAALS VALVAVNRRAT
101 RTIDGLAEV HTQAVTLRVG VIEQTGLQHF IRARADTGNE VARCEGGLFH
151 IGEFVGIAV QLEFAHFNQR IVFFRPNFGQ VKRMIRHFFG IGFRHDLDDVH

```


201 RPFRELAALD GFVQVALMAF AVVGDDDFCSF FVGQVFNPLL AAEMEFHPKT
 251 FARFVPEAVG MRTEAVHMAV AGGNTAVAHH DGNLVQGFQ QRPEVPVVC
 301 GTHIGARIAF DGFVQVGEFA RVAQEEHGRV VADHIPVAFF GIEFQKRTAD
 351 VAFRIGCAAL ACHGGETGEH LGFFADFAEN FGAGVFGDVV CYGKRTERAR
 401 TFGVHTAFGD DFAHEVGEFF IQPQILRQQG AARAGGQAVL IVGNGRAVVH
 451 GQMGYGAFFG SHRSCSFSQV GQMGGKRLTV RFGGKRIRNR FLDCNKFLES
 501 TFYFPFAKTM DAIIRQDFRY *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1377>:

m506.seq

1 ATGGCGGTAT TTGATGAAGT CGGGCGCGTC GCCCATTGCG GCGGCGGTGT
 51 TGCCGAACAA TGCCTGTTTC TCGCGTCGT TCATCAGGTT GAACAGGGCG
 101 CGCGGTTGGC TGAAATAGTC GTCATCGTCT TGGCGGTAGT CCCAGTGTGC
 151 CGCGTCGCCG TTGATTTTCA AAGGCGGTTT GCGCAATCG GGTGTGTGCT
 201 GCCATTGGCC GAAGCTGTyG GGTTCGTAGT GCGGCAGGCT GCCGyAGTTG
 251 CCGTCGGCGC GGCCTTGCCC GTyGCGsTgr TTgCTGTgAA CAsGGCAACG
 301 CGGACGATTG ACGGGAATTT GCGGGAAGTT TACGCCCAA CCGTAGCGTT
 351 GTGCGTCGGC GTAATTGAAC AAACGCGCTT GCAGCATTTT ATCTsGGCTG
 401 GCGCCGACAC CGGGAACGAG GTTGCTCGGT GCGAAGGCGG ATTGTTCCAC
 451 ATCGGCGAAG AAGTTTTTCG GATTGCGGTT CTCAAACGGA TGATAAGGTA
 501 CTTTTTCCGC GTCTGCTTCA GGCATGACTT GGATGTACAT CGTCCATTTC
 551 GGAAACTCGC CGCGTTCGAT GGCTTCsTAT AAGTCGCGCT GATGGCTTTC
 601 GCGGTCGTCG GCGATGATTT TGGCGGCTTC TTCGTTGGTC AGGTTTTTAA
 651 TGCCTTGTTG GGTGCGGAAA TGGAAATTTCA CCCAAAACG CTCGCTGCT
 701 TCGTTCAGAG AGCTGTAGGT ATGCGAACCG AAGCCGTGCA TATGGCGGTA
 751 GCCGCGGGG ATGCCGCGGT CGCTCATCAC GATGGTAACT TGGTGCAGTG
 801 CTTGCGGAG CAGCGTCCAG AAGTCCCAGT TGTGTGTGGC AGAGCGCATA
 851 TTGGTGCAGG GGTGCGGTTT GACGGCTTTG TTCAGGTCGG GGAACCTACG
 901 CGGTCGCGC AGGAAGAACA CGGGCGTGTT GTTGCCGACC ACATCCAGT
 951 TGCCTTCTTC GGTATAAAAT TTCAAGGCAA AACCGCGGAT GTCGCGTTCT
 1001 GCATCGGCTG CGCCGCGTTC GCCTGCCACG GTGGTGAAAC GGGCGAACAT
 1051 CTCGGTTTTT TTGCCGACTT CGCTGAAGAT TCCTTTGGCG TGCATACGGC
 1101 GTTCGGGAT GACTTCGCGC ACGAAGTCGG CGAGTTTTTC AGTCATCGCT
 1151 CTTGTTCTT TTCTCAGGTT GGTCAAATGG GGTAAACGG CTTACAGTAC
 1201 GATTTGGCGG AAAGCGTATT CGTAACCGGT TTCTTGATTG CAATAAATTT
 1251 CTTGAATCGA CATTTTATTT CCCTTTTGTA AAAACTATGG ATGCGACTAT
 1301 ACGCCAAGAT TTTCGCTATT AA

This corresponds to the amino acid sequence <SEQ ID 1378; ORF 506>:

m506.pep

1 MAVFDEVGRV AHCGGGVAEQ CLFLRVVHGV EQGARLAEIV VIVLAVVPVC
 51 RVAVDFORRF GESGLLLPLA EAVGFVVRQA AXVAVGAALP VAXXAVNXAT
 101 RTIDGNLAEV YAQTVALCVG VIEQTRLQHF IXAGADTGNE VARCEGLLFH
 151 IGEEVFGIAV QLEFAHFNQR IVFFRPNFGQ VKRMIRYFFR VCFRHDLDVH
 201 RPFRLAAFD GFXXVALMAF AVVGDDFGGF FVGQVFNALL GAEMEFHPKT
 251 LACFVPEAVG MRTEAVHMAV AGGDAVAHH DGNLVQCFQ QRPEVPVVC
 301 RAHIGARVAF DGFVQVGELT RVAQEEHGRV VADHIPVAFF GIKFQKRTAD
 351 VAFICGAAAF ACHGGETGEH LGFFADFAED FGAGVFGDVV RYGKRTERAR
 401 TFGVHTAFGD DFAHEVGEFF IQPQILRQQR AARTGGQAVL IVGNRRRAVVH
 451 GQMGYRAFFG SHRSCSFSQV GQMGGKRLTV RFGGKRIRNR FLDCNKFLES
 501 TFYFPFVKTM DATIRQDFRY *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 506 shows 89.2% identity over a 520 aa overlap with a predicted ORF (ORF 506.ng) from *N. gonorrhoeae*:

m506/g506

	10	20	30	40	50	60
m506.pep	MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDFORRF					
	:: :: :: :: :: :: ::					
g506	MAVFDEVGRIAHGCGGVVKQSLFLRVVHQVEQGARLAEVVIVLAVVPVCRVAVDFORRF					
	10	20	30	40	50	60

750

	70	80	90	100	110	120
m506.pep	GESGLLLPLAEAVGFVVRQAAXVAVGAALPVAXXAVNXATRTIDGNLAEVYAQTVALCVG					
g506	GEVGLLLPLAEAVGFVVRQAADVAVGAALSVALVAVNRATRTIDGDLAEVHTQAVTLRVG					
	70	80	90	100	110	120
m506.pep	VIEQTRLQHFIXAGADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
g506	VIEQTGLQHFIRARADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
	130	140	150	160	170	180
m506.pep	VKRMIRYFFRVCFRHDLVHRPFRKLAAFDGFXXVALMAFAVVGDDFGGFFVGVQVFNALL					
g506	VKRMIRHFFGIGFRHDLVHRPFRCLAALDGFVQVALMAFAVVGDDFCFFVGVQVFNPLL					
	190	200	210	220	230	240
m506.pep	GAEMEFHPKTLACFVPEAVGMRTEAVHMAVAGGDAVAHHDGNLVQCFGQQRPEVPVVC					
g506	AAEMEFHPKTFARFVPEAVGMRTEAVHMAVAGGNTAVAHHDGNLVQCFGQQRPEVPVVC					
	250	260	270	280	290	300
m506.pep	RAHIGARVAFDGFVQVGEFARVAQEEHGRVVADHIPVAFFGKIFQKGTADVAFCIGCAAF					
g506	GTHIGARIAFDGFVQVGEFARVAQEEHGRVVADHIPVAFFGKIEFQKGTADVAFRIGCAAL					
	310	320	330	340	350	360
m506.pep	ACHGGETGEHLGFFADFAEDFGAGVFGDVVRYGKRTERARTFGVHTAFGDDFAHEVGEFF					
g506	ACHGGETGEHLGFFADFAENFGAGVFGDVVCYGKRTERARTFGVHTAFGDDFAHEVGEFF					
	370	380	390	400	410	420
m506.pep	IQPQILRQQAARTGGQAVLIVGNRRVAVHGMGYRAFGGSHRSCSFSQVGMGGKRLTV					
g506	IQPQILRQQAARAGGQAVLIVGNRAVAVHGMGYGAFGGSHRSCSFSQVGMGGKRLTV					
	430	440	450	460	470	480
m506.pep	RFGGKRIRNRFLDCNKFLESTFYFPFVKTMDATIRODFRY					
g506	RFGGKRIRNRFLDCNKFLESTFYFPFAKTMDAIRQDFRY					
	490	500	510	520		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1379>:

a506.seq

```

1  ATGGCGGTAT TTGATGAAGT CGGGCGCGTC GCCCATTGCG GCGGCGGTGT
51  TGCCGAACAA TGCCTGTTTC TGC CGTCGT TCATCAGGTT GAACAGGGCG
101 CGCGGTGGC TGAAATAGTC GTCATCGTCT TGGCGGTAGT CCCAGTGC GC
151 CGCGTCGCCG TTGATTTTCA AAGGCGGTTC GCGGAAGTCG GGCTGCTGCT
201 GCCATTGGCC GAAGCTGTTG GGTTCGTAGT GCGGCAGGCT GCCGTAGTTG
251 CCGTCGGCGC GTCCTTGTCG GTCGCGCTGG TTGCTGTGAA CAGGGCAACG
301 CGGACGGTTG ACAGGGATTT GCGGGAAGTT CACGCCCAAG CGGTAGCGTT
351 GCGCGTCGGC GTAATTGAAC AAACGCGCCT GCAACATTTT ATCTGGGCTG
401 GCGCCGACAC CGGGAACGAG GTTGCTCGGT GCGAAGGCGG ATTGTTCCAC
451 ATCGGCGAAG AAGTTTTCGG GATTGCGGTT CAACTCGAAT TCGCCCACTT
501 CAATCAGCGG ATAGTCTTTT TTCGGCCAAA CTTTGGTCAA GTCAAACGGA
551 TGATACGCA CTTTTTCCGC ATCGGCTTCA GGCATGACTT GGATGTACAT
601 CGTCCATTTC GGAACTCGC CGCGCTCGAT GGCTTCGTAC AGGTGCGCT

```

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651 GATGGCTTTC ACGGTCGTCG GCGATGATTT TGGCGGCTTC TTCGTTGGTC
701 AGGTTTTTAA TGCCTTGTTC GGTGCGGAAA TGGAAATTTCA CCCAAAAACG
751 CTCGCCTGCT TCGTTCAGTA AGCTGTAGGT ATGCGAACCG AAGCCGTGCA
801 TATGGCGGTA GCCGCGGGG ATGCCGCGGT CGCTCATCAC GATGGTAACT
851 TGGTGCACTG CTTGCGGCAG CAGCGTCCAG AAGTCCCAGT TGTGTTGGC
901 AGAGCGCATA TTGGTGCGCG GGTGCGGTTT GACGGCTTTG TTCAGGTCGG
951 GGAACCTACG CGGGTCGCGC AGGAAGAACA CGGGCGTGTT GTTGCCGACC
1001 ACATCCCAGT TGCCTTCTTC GGTATAGAAC TTCAACGCAA AACCCGCGAT
1051 GTCGCGTTCT GCATCGGCTG CGCCGCGTTC GCCTGCCACG GTGGTGAAAC
1101 GGGCGAACAT CTCGGTTTTT TTGCCGACTT CGCTGAAGAT TTTGGCGCGG
1151 GTGTATTTGG TGATGTCGTG CGTTACGGTA AACGTACCGA ACGCGCCCGA
1201 ACCTTTGGCG TGCATACGGC GTTCGGGGAT GACTTCGCGC ACGAAGTCGG
1251 CGAGTTTTTC ATTCAGCCAC AAATCCTGCG CCAGCAGAGG GCCGCGAGGA
1301 CCGGCGGTCA GGCTGTTTTG ATTGTCGGCA ACAGGCGCGC CGTTGTCAT
1351 GGTCAGATGG GTTACAGGGC ATTTGGAGGT ANTCATCGCT CTTGTTCTT
1401 TTCTCAGGTT GGTCAAAT.G GGGGTAACG GCTTACAGTA CGATTGGCG
1451 GAAAGCGTAT TCGTAACCGG TTTCTTGATT GCAATAAATT TCTTGAATCG
1501 ACATTTTATT TCCCTTTTGT AAAAATATG GATGCGACTA TACGCCAAGA
1551 TTTTCGCTAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 1380; ORF 506.a>:

```

a506.pep
  1 MAVFDEVGRV AHCGGGVAEQ CLFLRVVHGV EQGARLAEIV VIVLAVVPVR
  51 RVAVDFOQRRF GEVGLLLPLA EAVGFVVRQA AVVAVGASLS VALVAVNRAT
 101 RTVDRDLAEV HAQAVALRVG VIEQTRLQHF IWAGADTGNE VARCEGGLFH
 151 IGEEVFGIAV QLEFAHFNQR IVFFRPNFGQ VKRMIRHFFR IGFRHDLVDH
 201 RPFRLAALD GFVQVALMAF TVVGDDFGGF FVGQVFNALL GAEMEFHPKT
 251 LACFVPEAVG MRTEAVHMAV AGGDAVAHH DGNLVQCFGQ QRPEVPVVC
 301 RAHIGARVAF DGFVQVGELT RVAQEEHGRV VADHIPVAFF GIELQRKTAD
 351 VAFICIGAAF ACHGGETGEH LGFFADFAED FGAGVFGDVV RYGRKTERAR
 401 TFGVHTAFGD DFAHEVGEFF IQPQILRQQR AARTGGQAVL IVGNRRRAVVH
 451 GQMGYRAFGG XHRSCSFSQV GQXGKRLTV RFGGKRIRNR FLDCNKFLES
 501 TFYFPFVKTM DATIRQDFRY *

```

m506/a506 94.8% identity in 520 aa overlap

```

          10      20      30      40      50      60
m506.pep  MAVFDEVGRVAHCGGGVAEQCLFLRVVHVEQGARLAEIVVIVLAVVPVCRVAVDFOQRRF
          |||
a506      MAVFDEVGRVAHCGGGVAEQCLFLRVVHVEQGARLAEIVVIVLAVVPVRRVAVDFOQRRF
          10      20      30      40      50      60

          70      80      90      100     110     120
m506.pep  GESGLLLPLAEAVGFVVRQAAXVAVGAALPVAXXAVNXATRTIDGNLAEVYAQTVALCVG
          |||
a506      GEVGLLLPLAEAVGFVVRQAAXVAVGASLSVALVAVNRATRTVDRDLAEVHAQAVALRVG
          70      80      90      100     110     120

          130     140     150     160     170     180
m506.pep  VIEQTRLQHFIWAGADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ
          |||
a506      VIEQTRLQHFIWAGADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ
          130     140     150     160     170     180

          190     200     210     220     230     240
m506.pep  VKRMIRYFFRVCFRHDLVDHVPFRKLAADFDFGXVALMAFAVVGDDFGGFFVGQVFNALL
          |||
a506      VKRMIRHFFRIGFRHDLVDHVPFRKLAADFDFVQVALMAFTTVVGDDFGGFFVGQVFNALL
          190     200     210     220     230     240

          250     260     270     280     290     300
m506.pep  GAEMEFHPKTLACFVPEAVGMRTEAVHMAVAGGDAVAHHDGNLVQCFGQQRPEVPVVC
          |||
a506      GAEMEFHPKTLACFVPEAVGMRTEAVHMAVAGGDAVAHHDGNLVQCFGQQRPEVPVVC
          250     260     270     280     290     300

```

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	310	320	330	340	350	360
m506.pep	RAHIGARVAFDGFVQVGELTRVAQEEHGRVVADHIPVAFFGIKFQGKTADVAFCIGCAAF					
a506	RAHIGARVAFDGFVQVGELTRVAQEEHGRVVADHIPVAFFGIELQRKTADVAFCIGCAAF					
	310	320	330	340	350	360
	370	380	390	400	410	420
m506.pep	ACHGGETGEHLGFFADFAEDFGAGVFGDVVRYGKRTERARTFGVHTAFGDDFAHEVGEFF					
a506	ACHGGETGEHLGFFADFAEDFGAGVFGDVVRYGKRTERARTFGVHTAFGDDFAHEVGEFF					
	370	380	390	400	410	420
	430	440	450	460	470	480
m506.pep	IQPQILRQORAARTGGQAVLIVGNRRRAVVHGMGYRAFGGSHRSCSFSQVGOMGGKRLTV					
a506	IQPQILRQORAARTGGQAVLIVGNRRRAVVHGMGYRAFGGXHRSCSFSQVGQXGKRLTV					
	430	440	450	460	470	480
	490	500	510	520		
m506.pep	RFGGKRIRNRFLDCNKFLESTFYFPFVKTMDATIRQDFRYX					
a506	RFGGKRIRNRFLDCNKFLESTFYFPFVKTMDATIRQDFRYX					
	490	500	510	520		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1381>:

g507.seq

```

1  ATGCTCTTGC CGGCTTTGCA ACAAGGCGGC GGCTTCCTGA GCGGCGGCGG
51  TTTCGGCCTC GTCGGGCAGG TTCAGGGCTT GGTTTTCTTG CTTAGACGG
101 CCTTTGCGCT CTTGCTGCTT GGCAACGTT TGTTCGGCAT GGGCAAGCTG
151 CTGCTGCTTC AACGCCAGTT CGCGGCGGAT GCGGTTTGCC TCGTCCTGCT
201 GGGTTTGGAA GGCAGCGTTG AGCGTGGCTT GGAATTCTTC CAATTCGGGC
251 AGACGCTCTT CGTGTTCGCG AACCTGCATC GCCCATTCCT CCAATTCGGT
301 TTGCTTTTCT TCGACCTGCA ACTCGTTTTT CTCAAGCTGC ACGCGGATTT
351 GCTGCTGCTC CTGCCGATG CGTTGCAACT GCGCCTGCGC TGCCTGCTTG
401 TCGCGTTCGA TCGGTTGGTG CAGGTTTTGC CGGTGGCGGA TTTGTTCTTC
451 CAAACGGGCA ATCTGCTCGC GCAACACGCC GCGTTTGTG CTCAATTCGT
501 GTACTGCCTG CTGCTGCGAC TGTTCGGCAG TCTGCAAGGC GTGTACTTCG
551 TTATTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1382; ORF 507.ng>:

g507.pep

```

1  MLLPALQQGG GFLSGGGFGL VGQVQGLVFL LQTAFALFVL GNGLFGMGKL
51  LLLRQFAAD AVCLVLLGLE GSVERGLDFF QFGQTLFVFG NLHRPFRQFG
101 LLFPDLQLVF LKLHADLLL LPDALQLRLR CLLVAFDALV QVLPVADLFF
151 QTGNLLAQHA AFVAQFVYCL LLRLFGSLQG VYFVI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1383>:

m507.seq

```

1  ATGCTCTTGC TGACTTTGCA ACAAGGCGGC TGCTTCCTGC GCGGCGGCGG
51  TTTCGGCTTC GTCGGGCAGG TTTAAGGCTT GGTTTTCTTG TTTCAGACGA
101 CCTTTGCGCT CTTGCTGCTT GGCAATCGTT TGTTCGGCAT GGGCAAGCTG
151 CTGCTGCTTC AACGCCAGTT CGCGGCGGAT GCGGTTTGCC TCGTCCTGCT
201 GGGTTTGGAA GGCAGCGTTG AGCGTGGCTT GGGCTTCTTC CAATTCGGGC
251 AGACGCTCCT CGTGTTCGCG AACCTGCATC GCCCATTCCT CCAGCTCGGT
301 TTGTTTTTCT TCGACCTGCA ACTCGTTTTT TTCAAGCTGC ACGCGGATTT
351 GCTGCTGCTC TTGATGAATG CGTTGTAAC TCGCCTGCGC TGCCTGCTTG
401 TCGCGTTCGA TCGGTTGGTG CAGGTTTTGC TGATGGCGGA TTTGTTCTTC
451 CAAACGGGCA ATCTGCTCGC GCAACACGCC GCGCTTGTG CTCAATTCAT
501 GCACTGCCTG CTGCTGCGAC TGTTCGGCAG TCTGCAAGGC GTGTACTTCG
551 TCGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1384; ORF 507>:

m507.pep

```

1  MLLLTQQGG CFLRGGGFGF VGQVXGLVFL FQTTFALFVL GNRLFGMGKL

```

m507/g507

	10	20	30	40	50	60
m507.pep	MLLLTLQGGGCFLRGGGFGFVGVQVXGLVFLFQTTTFALFVLGNRLFIMGKLLLLLQRFQFAAD					
	: :					
a507	MLLLALQGGGSFLRGGGFGFVRQIQGLVFLFQTTTFALFVLGNLFGMGKLLLLLQRFQFAAD					
	10	20	30	40	50	60
	70	80	90	100	110	120

754

```

m507.pep    AVCLVLLGLEGGVERGLGFFQFGQTLVFGNLHRPFRQLGLFFFDLQLVFFKLHADLLLL
             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a507        AVCLVLLGLEGGIECGLGFFQFGQTLFVFGNLHRPFRQFGLLFFRLQLVFFKLHADLLLL
             70      80      90      100     110     120

             130      140      150      160      170      180
m507.pep    LMNALXLRRLRCLLVAFDALVQVLLMADLFFQTGNLLAQHAALVAQFMHCLLLRLFGSLQG
             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a507        LMDALHLRLRLRLVAFDALVQVLLMADLFFQTGNLFAQHAAFVAQFVHRLLLRLFGSLQG
             130      140      150      160      170      180

m507.pep    VYFVFX
             |||||
a507        VYFVFX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1387>:

```

g508.seq
1  ATGGTAGCGT TTGGCGTTGA TCAGGGCCTC CTGCTGCTGC AACAGGGCGG
51 TTTGGGTGGC GGCCTGAAGC TGCGGCAGCT TGGTTTGACG GGTTTGTACG
101 CGGGCGTATT GCTCCCTGCC CTGTTCTCTGA ATCTGCGCGA GTTTTCTCTG
151 CACGGCGATG TATTCTTCGT CCAGCGTGTG TACGGTTTCG GTCAACTCGT
201 CGAGCTTGAT GTGCTGCTCG TCGTTTTGGA ACTCGGTTTC ATAGGCGAGG
251 GCAAGCTCTT GCCGGCGTTC CTGCCAGTCC AGGGTTTGCT GTTCGAGCCG
301 GCGGATTTCG TGCCGGTAGT TTTGTTTTTG CGGGTTGAGT TTGTGGACGG
351 CGACTTCGGC AAGCCCGTAT TGGCGGTTGG CTTCCAACAG GGCAAGCTGC
401 GCCTGTTTCA GACGGCCTTG CTGCTCTTGG CGGCTGTGCG CGGTGGTTTG
451 CTGCTGGTGT TCGAGTTCGG CGGCGGCTTC CTGCAAAGTA GCGATGTCGT
501 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1388; ORF 508.ng>:

```

g508.pep
1  MVAFGVDQGL LLLQQGGLGG GLKLRLGLQ GLYAGVLLPA LFLNLRFFFL
51 HGDVFFVQRV YGFGQLVELD VLLVVLELGF IGEKLLPAF LPVQGLLPFP
101 GDLLPVVLFL RVEFVDGDFG KPVLA VGFGQ GKRLRFOTAL LLLAAVRGGL
151 LLVFEFGGGF LQSSDVV

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1389>:

```

m508.seq
1  ATGGTAGCGT TTGGCGTTGA TCAGGGCTTC CTGCTGCTGC AACAGGGCGG
51 TTTGGGTGGC GGCCTGAAGC TGCGGCAGCT TGGTTTGACG GGTTTGCACT
101 TTAGCGTATT GCTCCCTGCC CTGTTCTCTGA ATCTGCGCGA GTTTCTCTTG
151 CACAACAATA TATTCTTCGT CCAAGGTCTG TACGGCTTCG CTTAATTCTT
201 CAAGCTTGAT GTGCTGCTCG TCGTTTTGGA ACTCGGTTTC ATAGGCGAGG
251 GCAAGCTCTT GCTGGCGTTC CTGCCAGTCG AGGGTTTGCT GTTCAAGCTG
301 GCGGATTTCG TGCCGGTAGT TTTGTTTTTG CTGGTTGAGT TTGTGGACGG
351 CGACTTCGGC AAGCCCGTAT TGGCGGTTGG CTTCCAACAG GGCAAGCTGC
401 GCCTGTTTCA GACGGCCTTG CTGCTCTTGG CGGCTGTGCG CGGTGGTTTG
451 CTGCTGGTGT TCGAGTTCGG CGGCGGCTTC CTGCAAGGTA ACGATGTCGT
501 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1390; ORF 508.ng>:

```

m508.pep
1  MVAFGVDQGF LLLQQGGLGG GLKLRLGLQ GLHFSVLLPA LFLNLRFFFL
51 HNNIFFVQGL YGFAXFFKLD VLLVVLELGF IGEKLLLA FLPVEGLLFKL
101 GDLLPVVLFL LVEFVDGDFG KPVLA VGFGQ GKRLRFOTAL LLLAAVRGGL
151 LLVFEFGGGF LQGNDDV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 508 shows 86.8% identity over a 167 aa overlap with a predicted ORF (ORF 508.ng) from *N. gonorrhoeae*:

m508/g508

755

	10	20	30	40	50	60
m508 . pep	MVAFGVDQGFLLLLQQGGGLGGGLKLRQLGLQGLHFSVLLPALFLNLREFLLHNNIFFVQGL					
g508	MVAFGVDQGFLLLLQQGGGLGGGLKLRQLGLQGLYAGVLLPALFLNLREFLLHGDVFFVQVRV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m508 . pep	YGFAXFFKLDVLLVVLELGFIGEGKLLLAFLPVEGLLFKLGDLLPVVLFLLVEFVDGDFG					
g508	YGFQQLVELDVLLVVLELGFIGEGKLLPAFLPVQGLLFEPGDLLPVVLFLLVEFVDGDFG					
	70	80	90	100	110	120
	130	140	150	160		
m508 . pep	KPVLA VG FQQGKLR L FQTALLLLAAVRGGLLLVFEFGGGFLQGNDVV					
g508	KPVLA VG FQQGKLR L FQTALLLLAAVRGGLLLVFEFGGGFLQSSDVV					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1391>:

```

a508 . seq
1   ATGGTAGCGT TTGGCGTTGA TCAGGGCTTC CTGCTGCTGC AACAGGGCGG
51  TTTGGGTGGC GGCCTGAAGC TGCGGCAGCT TGGTTGTCAG GGTTCGTACG
101 CGGGCGTATT GTTCCCTACC CTGCTCCTGA ATCTGCGCGA GTTCTCTCTG
151 TACGACAATA TATTCTTCGT CCAACTCTG TACGGCTTCG CTCAACTCTT
201 CGAGCTTGAT GTGCTGCTCG TCGTTTTGGA ACTCGTTTC ATAGGCGAGG
251 GCAAGCTCTT GCTGGCGTTC CTGCCAATCG AAGGTTTGTG GTTCAAGCTG
301 GGCAATTTGC TGTGTTAGT TTTGTTTTTG CTGGTTGAGC TTGTGGACGG
351 CGACTTCGGC AAGCCCGTAT TGGCGGTTGG CTTCCAACAG GGCAAGCTGC
401 GCCTGTTTCA GACGACCTTG CTGCTCTTGG CGGCTGTGCG CGGCGGTTTG
451 CTGCTGGTGT TCGAGTTCGG CGGCGGCTTC CTGCAAAATG GCGATGTCGT
501 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1392; ORF 508.a>:

```

a508 . pep
1   MVAFGVDQGF LLLQQGG LGG GLKLRQLGLQ GLYAGVLFPT LLLNLREFLL
51  YDNIFVQTL YGFAQLFELD VLLVVLELGF IGEGKLLLAFL LPIEGLLFKL
101 GNLLLVLEFL LVELVDGDFG KPVLA VG FQQ GKLRL FQTTL LLLAAVRGGL
151 LLVFEFGGGF LQNGDVV*

```

m508/a508 88.6% identity in 167 aa overlap

	10	20	30	40	50	60
m508 . pep	MVAFGVDQGFLLLLQQGGGLGGGLKLRQLGLQGLHFSVLLPALFLNLREFLLHNNIFFVQGL					
a508	MVAFGVDQGFLLLLQQGGGLGGGLKLRQLGLQGLYAGVLFPTLLNLREFLLYDNIFVQTL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m508 . pep	YGFAXFFKLDVLLVVLELGFIGEGKLLLAFLPVEGLLFKLGDLLPVVLFLLVEFVDGDFG					
a508	YGFAQLFELDVLVLELGFIGEGKLLLAFLPIEGLLFKLGNNLLVVLFLLVELVDGDFG					
	70	80	90	100	110	120
	130	140	150	160		
m508 . pep	KPVLA VG FQQGKLR L FQTALLLLAAVRGGLLLVFEFGGGFLQGNDVVX					
a508	KPVLA VG FQQGKLR L FQTALLLLAAVRGGLLLVFEFGGGFLQNGDVVX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1393>:

g509 . seq

```

1   atggtcgctg tatgtgatga acgggctgta cagcggacgt tgggtggccca
51  attcgcgcaa caaggcggct tgtttttgct cttcggttcag gctgttgtag
101 tcttccaagc ctgctgtgtg gaaaagctcg gcaaccacat cggcgtgttt
151 gcctgcgtgt tggcgagggt cgagcggcat catgtggaag ccgaacacgg
201 acacggaacg gatgaggtct gccaaacggc cttcggcaag caggcggctg
251 ccgttgtcga taagggaacg ttgcaatttt ttcaaatacat cgagaaattt
301 ttgggcccga gcataaggct cgagaaagcc gaattttgcag cccatgcccc
351 aaccgagcga gcgcgctttg cccatagcgc gcgccataat gtaggcaatg
401 gcgcggcggt aaggttcttc ggtgcgggcg atttcttcgt caggcgagag
451 ggctgccagt gccattacgt cgtcgttgac tttgacgcgg cggatggaaa
501 gcggcagttc gcggtaaagt ttgtcaggtt cgctgcggtt aaaacggaac
551 acggcatcgg cgtggcggcg gaaggcaaa cgcagggttt cggcagaaac
601 aaacggattg ccgtcgcggg cgcgcggcat ccagccggcg attttaagga
651 tattcggaac gcggacatcg ggataggccg tctgaaagtc gtgttccatc
701 ttgcggtaga gtttgggagc ggcttcaaaa aagctcatcg ggaagatgga
751 cagcccggtt ttgatttcgt cgttgacgct gagtttgtgg cggcgcggtt
801 cgctggtctg ccacaagccc agaagcacgg tgtcgatttc gcggcgacgc
851 cgtgccagcg cgtcggcatt ggtgcagcgt tcgcgttgcg gcagcagcgc
901 gcggatgcgg cggttgaaat tcaaaacggg ttggcgttgc acttcggtcg
951 ggtgcgcggg caaaacggcg gtaacggacg tattgtccaa ctgccgctgc
1001 accgatttgc cgtcggcttt ccccgctttg agcctgcgga cggtttccgt
1051 caggctgcct tctgctgcgt tgtggccggc atcttcgtgg atttggcggc
1101 ggcgttcgtg gtgcacgtct tcggcgatat tcagaatctg ggcgaacagc
1151 gcgcaggcaa gcgtcagatc gtaggtctgc cgttcgtcca attgcggcaa
1201 tactttttca atcaatgccg cgctgtcgtc ggaagtggac aagagtttga
1251 ccgttttcgac aaccaacggc gaggcttctt cgtgcaggag gttgaacagg
1301 gactgtttca aaaattccgc gtccgccgcc aaagccgcgt ccttcggatt
1351 gttcaggata tgcagttgca tgattttcct ctcattgccg taaatactgt
1401 aaatgtacct caaatgccgc atccgtgcc aaccgttcac actttaacca
1451 ctcatgtccc gaaatgccgt ctgaagttga acgccgccc acggcgcggt
1501 tacaatcgcc cgcaactggt tttttccgaa catcatcatg accgcgaccg
1551 aacacgacaa cgacgacgca ctccctgctg ggtacagccg ccacatcctc
1601 ttggacgaaa tcggcatcga agggcagcag aagctttccg ccgcgcatat
1651 tttggtcgtc ggctgcggcg gattgggcgc cgccgcccc gccctatctc
1701 gccgcctcgg gggtcggcac gctga

```

This corresponds to the amino acid sequence <SEQ ID 1394; ORF 509.ng>:

g509.pep

```

1   MVAVCDERAV QRTLVQFAQ QGGLFLLFVQ AVVVFQACVL EKLGNHIGVF
51  ACVLAQVERH HVEAEHGHGT DEVCQTAFGK QAAAVVDKGT LQFFQIIEKF
101 LGRSIRLEKA EFAAHAQTER ARFAHSARHN VGNGAAVRFF GAGDFFVRRE
151 GCQCHYVVD FDAADGKRQF AVKFVEFAAV KTEHGIGVAA EGKAQGFARN
201 KRIAVAVAAD PAADFKDIRN ADIGIGRLKV VFHLAVEFGQ GFKKAHREDG
251 HAVVDFVVD EFVAARFAGL PQAQKHGVDF AAQPCQRVGI GAAAFALROOR
301 ADAAVEIQNG LALHFGRVRG QNGGNRIVQ LPLHRFAVGF PRFEPADGFR
351 QAAFCCVAG IFVDLAAAFV VHVFGDIQNL GEQPAGKRQI VGLPFVQLRQ
401 YFFNQCRVV GSGQEFDRFD NQRRGFFVQE VEQGLFOKFR VRRQSRVLRI
451 VQDMQLHDFP LIAVNTVNVP QMPHPCQTVH TLTHVPHKCR LKLNAARRRR
501 YNRPLFFSE HHHDRDRTRQ RRRTPAAVQP PHPLGRNRHR RAAEAFRRAY
551 FGRRLLRRIGR RRPCIPSPR GSAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1395>:

m509.seq

```

1   ATGGTCGCTG TATGTGATAA ACGGGCTGTA CAGAGGACGT TGATGGCTCA
51  ATTCGCGCAA CAGGGCGGTT TGTTTTGTCT CTTGTTTCAG GCGGTTGTAG
101 TCTTCCAAGC CTGCGTGTGT GAAAAGCTCG GCAACCACAT CGGCGTGTGT
151 GCCTGCGTGT TGGCGCAAGT CGAGCGGCAT CATGTGAAAG CCGAACACGG
201 ATACGGAACG GATGAGGTCT GCCAAACGGC CTTGCGCAAG CAGACGGCTG
251 CCGTTGTCTG TAAGGGAACG TTGCAATTTT TTCAAATCAT CCAGAACTC
301 TTGTGCCGAA GCATAAGGCT CGAGAAAGCC GAATTTGCAG CCCATACCCA
351 AACCAGACGC GCGCGCTTTG CCCATAGCGC GCGCCATAAT GTAGGCGATG
401 GCGCGCGGTT AGGGTTCTTC GGCGCGGGCG ATTTCTTCGT CGGGCGATTT
451 GTCGGACAAC GCCGTTACAT CGCCGTTGAC TTTGACGCGG CGGATGGAGA
501 GCGGCAGTTC GCGGTAGAGT TTGTGAGATT CGCCGCGATA GAAGCGGAAC

```



```
551 ACGGCATCGG CGTGGCGGCG GAAGGCAAAG CGCAGGGTTT CGGCAGAAAC
601 AAACGGATTG CCGTCGCGGT CGCCGCCGAT CCAGCCGCCG ATTTTGAGGA
651 TGTCCGGAAC GCGGACGCCG GGATAGGCCG TCTGAAAGTC GTGTTCCATC
701 TTGCGGTAGA GCTTGGGCAG GGCTTCGAAA AAGCTCATCG GGAAGATGGA
751 CACGCCGTG TTGATTTCTG CGTTGACGCT GAGTTTGTGG CGGCGCGTTT
801 CGCTGGTCTG CCACAAGCCC AGCAGGATAG TGTCGATTtC GCgGCGCAGC
851 CGTGCCAGCG CGTCGGCATT GGTGCAGCGT TCgCGTTGCG GCAACAGTGC
901 GCGGATGCGG CGGTTGAAGC TTAAGACGGT TTGGCGTTGC ACTTCGGTCG
951 GGTGCGCGGT CAAAACGGCG GTAACGGACG TATTGTCCAA CTGCCGCTGC
1001 ACCGATTGTC CGTCGGCTTT CCCCCTTTTG AGCCTGCGGA CGGTTTCCGT
1051 CAGGCTGCC TCCGCGCCGC CGCGTCCGGC TTCTTCGTGG ATTTGGCGGC
1101 GCGGTTTCGT GTGCACGTCT TCGGCGATGT TCAAAATCTG GGCGAACAGG
1151 CCGCAGGCCA AGGTTAAATC GTGGGTTTGT TGTTCTGTTCA ATTGCGGCAG
1201 TACTTTTTCA ATCAATGCCG CGCTGTCGTC GGAAGTGGAC AAGAGTTTGA
1251 CTGTTTTGAC AACCAACGGC GAGGCTTCTT CGTGCAGGAG GTTGAACAGG
1301 GATTGTTTCA GAAATTCCGC GTCCGCCGCC AAAGCCGCGT CCTTTGGATT
1351 GTTCAGAATA TGCAGTTGCA TGATTTTTCT CTCTCGTCTG CCGTAAATAT
1401 TGTAATGTA CCCCAAATGC CGCATCCGTG CCAAACCGTT CACACTTTAA
1451 CCGCCCGTGT CCGGAAATGC CGTCTGAAGT TGAACGCCGC CCGACGGCAG
1501 CGTTACAATC GCCCGCAACT GTTTTTtTTCC GAACATCATC ATGACCACGA
1551 CCGAACACGA CAACGACGAT GCATTCTGTC TGCGGTACAG CCGCCACATC
1601 CTCTTGACG AAATCGGCAT CGAAGGGCAG CAGAAACTTT CCGCCGCGCA
1651 TATTTTGTC GTCGGCTGCG GCGGTTTGGG TGCCGCCGCA CT.GCCCTAC
1701 CTTGCCGCTT CGGGTGTCTCG CACGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 1396; ORF 509>:

```
m509.pep
  1 MVAVCDKRAV QRTLMAQFAQ QGGLFLLFVQ AVVVFQACVL EKLGNHIGVF
 51 ACVLAQVERH HVKAEHGYGT DEVCQTAFGK QTAAVVDKGT LQFFQIIQKL
101 LCRSIRLEKA EFAAHTQTER ARFAHSARHN VGDGAAVGFF GAGDFFVGRF
151 VGQRRYIAVD FDAADGERQF AVEFVEFAAI EAEHGIGVAA EGKAQGFGRN
201 KRIAVAVAAD PAADFEDVRN ADAGIGRLKV VFHLAVELGQ GFKAHREDG
251 HAVVDFVVD AEFVAARFAGL PQAQQDSVDF AAQPCQRVGI GAAAFALRQC
301 ADAAVEAXDG LALHFRVRG QNGGNGRIVQ LPLHRFAVGF PRFEPADGFR
351 QAAFRAAASG FFVDLAAAFV VHVFGDVQNL GEQAAGQGXI VGLLFVQLRQ
401 YFFNQCRVV GSGQEFDCFD NQRRGFFVQE VEQGLFQKFR VRRQSRVLWI
451 VQNMQLHDFS LSSAVNIVNV PQMPHPCQTV HTLTARVPKC RLKLNAAARRQ
501 RYNRPQLFFS EHHHDHDRTR QRRCIPAAVQ PPHPLGRNRH RRAAETFRR
551 YFGRRLRRFG CRRTXPTLPL RVSAR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 509 shows 87.8% identity over a 575 aa overlap with a predicted ORF (ORF 509.ng) from *N. gonorrhoeae*:

m509/g509

```
          10          20          30          40          50          60
m509.pep  MVAVCDKRAVQRTLMAQFAQQGGLFLLFVQAVVVFQACVLEKLGNHIGVVFACVLAQVERH
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g509       MVAVCDERAVQRTLVAQFAQQGGLFLLFVQAVVVFQACVLEKLGNHIGVVFACVLAQVERH
          10          20          30          40          50          60

          70          80          90          100         110         120
m509.pep  HVKAEHGYGTDEVCQTAFGKQTAAVVDKGT LQFFQIIQKLLCRSIRLEKA EFAAHTQTER
          ||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g509       HVEAEHGHGTDEVCQTAFGKQAAAVVDKGT LQFFQII EKFLGRSIRLEKA EFAAHTQTER
          70          80          90          100         110         120

          130         140         150         160         170         180
m509.pep  ARFAHSARHN VGDGAAVGFFGAGDFFVGRFVGQRRYIAVDFDAADGERQFAVEFVEFAAI
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g509       ARFAHSARHN VNGAAVRFFGAGDFFVRRREGCQCHYVVVDFDAADGKRQFAVKFVEFAAV
          130         140         150         160         170         180
```

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	190	200	210	220	230	240
m509.pep	EAEHGIGVAAEGKAQGFGRNKRIAVAVAADPAADFEDVRNADAGIGRLKVVFHLAVELGQ					
g509	KTEHGIGVAAEGKAQGFARNKRIAVAVAADPAADFDIRNADIGIGRLKVVFHLAVEFGQ					
	190	200	210	220	230	240
	250	260	270	280	290	300
m509.pep	GFKAHREDGHAVVDFVDAEFVAARFAGLPQAQQDSVDFAAQPCQRVGIGAAFALRQQC					
g509	GFKKAHREDGHAVVDFVDAEFVAARFAGLPQAQKHGVDFAAQPCQRVGIGAAFALRQQR					
	250	260	270	280	290	300
	310	320	330	340	350	360
m509.pep	ADAAVEAXDGLALHFGRVRGQNGNGRIVQLPLHRFAVGFPFRFEPADGFRQAAFRAAASG					
g509	ADAAVEIQNGLALHFGRVRGQNGNGRIVQLPLHRFAVGFPFRFEPADGFRQAAFCCVVG					
	310	320	330	340	350	360
	370	380	390	400	410	420
m509.pep	FFVDLAAAFVVHVFGDVQNLGEQAAGQGXI VGLLFVQLRQYFFNQCRVVGSGQEFDCFD					
g509	IFVDLAAAFVVHVFGDIQNLGEQPAKQRQIVGLPFVQLRQYFFNQCRVVGSGQEFDRFD					
	370	380	390	400	410	420
	430	440	450	460	470	480
m509.pep	NQRGFFVQVEVEQGLFQKFRVRQSRVLWIVQNMQLHDFSLSSAVNIVNVPQMPHPCQTV					
g509	NQRGFFVQVEVEQGLFQKFRVRQSRVLRIQDMQLHDFPLI -AVNTVNVNVPQMPHPCQTV					
	430	440	450	460	470	
	490	500	510	520	530	540
m509.pep	HTLTARVPKCRCLKLNAARRQRYNRPQLFFSEHHHDHRTQRRCIPAAVQPPHPLGRNRH					
g509	HTLTTHVPKCRCLKLNAARRRRYNRPQLFFSEHHHDDRTRQRRRTPAAVQPPHPLGRNRH					
	480	490	500	510	520	530
	550	560	570			
m509.pep	RRAAETFRRAYFGRRLLRRFGCRRTCPTLPLRV SAR					
g509	RRAAEAFRRAYFGRRLLRRIGRRRPCISP PRGSAR					
	540	550	560	570		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1397>:

```

a509.seq
1   ATGGTCGCTG TATGTGATGA ACGGACTGTA CAGTGGACGT TGATGGCTCA
51  ATTTCGCGCAA CAGGCGCGCT TGTTTTGTCT CTTCGTTGAG GCTGTTGTAG
101 TCTTCCAAGC CTGCGTGTG GAAAAGCTCG GCAACCACAT CGGCGTGTGT
151 GCCTGCGTGT TGGCGCAGGT CGAGCGGCAT CATGTGGAAG CCGAACACGG
201 ATACGGAACG GATGAGGTCT GCCAAACGGC CTTCGGCAAG CAGGCGGCTG
251 CCGTTGTCTGA TAAGGGAATG TTGCAATTTT TTCAAATCAT CGAGAAATTC
301 TTGTGCCGAA GCATAAGGCT CGAGAAAGCC GAATTTGCAG CCCATACCCA
351 AACCGAGCGC GCGCGCTTTG CCCATAGCGC GCGCCATAAT GTAGGCAATG
401 GCGCGACGGT AGGGTTCTTC GGCGCGGGCG GTTCTTCGT CGGGCGATTT
451 GTCGGACAAC GCCATCACAT CGCCGTTGAC TTTGACGCGG CGGATGGAGA
501 GCGGCAGTTC GCGGTAGAGT TTGTCGAGTT CGCCACGGTA AAAACGGAAC
551 ACGGCATCGG CGTGGCGGCG GAAGGCAAAA CGCAAGGTTT CGGCAGAAAC
601 GAACGGATTG CCGTCCGCGT CGCCGCCGAT CCAGCCGCGG ATTTTGAGGA
651 TGTCCGGAAC GCGGACATCG GGATAGGCCG TCTGAAAGTC GTGTCCATC
701 TTGCGGTAGA GCTTGGGCAG GGCTTCAAAA AAGCTCATCG GAAAGATGGA
751 CACGCCGTTG TTGATTTCTG CGTTGACGCT GAGTTTGTGG CGGCGCGTTT
801 CGCTGGTCTG CCACAAGCCC AGCAGGATAG TGTCGATTTC GCGCGCAGC
851 CGTGCCAGCG CGTCCGCATT GGTACAGCGT TCGCGTTGCG GCAGCAGCGC

```

a509.pep	1	MVAVCDERTV	QWTLMAQFAQ	QGGLFLLFVE	AVVVVFQACVL	EKLGNHIGVF
	51	ACVLAQVERH	HVEAEHGYGT	DEVCGTAFGK	QAAAVVDKGM	LQFFQIIEKF
	101	LCRSIRLEKA	EFAAHTQTER	ARFAHSARHN	VGNATGVGFF	GAGGFFVVRG
	151	VGQRHHIAVD	FDAADGERQF	AVEFVEFATV	KTEHGIGVAA	EGKTOGGFGRN
	201	ERIAVAVAAD	PAADFEDVRN	ADIGIGRLKV	VFHLAVELGQ	GFKKAHRKDG
	251	HAVVDFVDDA	EFVAERFAGL	PQAQQDSVDF	AAQPCQRVGI	GTAFALRQQR
	301	ADAAVEITDQ	LALHFRGVRG	QNGGNGRIVQ	LPLHRFAVGF	PRFEPADGFR
	351	QAAFAAAASG	FFVDLAAAFV	VHVFGDVQNL	GEQAAGQG*I	VGLLFFVLQRLQ
	401	YFFNQCRRAV	GSQGQEFDRD	NQRRGFFVQE	VEQGLFQKFR	VRRQSRVLWI
	451	VQNMQLHDFS	LIAVNTVNPV	QMPHPCQTVH	TLTARVPKCR	LKLNAARRQR
	501	YNRPQLFXSE	HHHDHDRTRQ	RCRCPAAVQP	PHPLGRNWHR	RAAETFRRAY
	551	FGRRLRRFGC	RXPCEISPLP	ASAR*		

	10	20	30	40	50	60
m509.pep	MVAVCDKRAVQRTLMAQFAQQGGLFLLFVQAVVVVQACVLEKLGNHIGVFACVLAQVERH					
a509	MVAVCDERTVQWTLMAQFAQQGGLFLLFVEAVVVVQACVLEKLGNHIGVFACVLAQVERH					
	10	20	30	40	50	60
m509.pep	HVKAEHGYGTDEVCQTAFGKQTAAVVDKGTLOFFQIIQKLLCRSIRLEKAEEFAAHTQTER					
a509	HVEAEHGYGTDEVCQTAFGKQAAAVVDKGMLOFFQIIIEKFLCRSIRLEKAEEFAAHTQTER					
	70	80	90	100	110	120
m509.pep	ARFAHSARHNVGDGAAGVFFGAGDFFVGRFVGQRRYIAVDFDAADGERQFAVEFVEFAAI					
a509	ARFAHSARHNVGNATVGGFFGAGGFFVGRFVGQRHHIAVDFDAADGERQFAVEFVEFATV					
	130	140	150	160	170	180
m509.pep	EAEHGIGVAAEGKAQGGFRNKRIAVAVAADPAADFEDVRNADAGIGRLKVVFHLAVELGQ					
a509	KTEHGIGVAAEGKTQGGFRNERIAVAVAADPAADFEDVRNADIGIGRLKVVFHLAVELGQ					
	190	200	210	220	230	240
m509.pep	GFEKAHREDGHAVVDFVVDAAEFVAARFAGLPQAQQDSVDFAAQPCQRVGIGAAFALRQQC					
a509	GFKKAHRKDDGHAVVDFVVDAAEFVAARFAGLPQAQQDSVDFAAQPCQRVGIGTAFALRQQR					
	250	260	270	280	290	300
m509.pep						
a509						
	310	320	330	340	350	360

```

m509.pep      ADAAVEAXDGLALHFGRVRGQNGNGRIVQLPLHRFAVGFRPFEPADGFRQAAFRAAASG
a509          ADAAVEIQDGLALHFGRVRGQNGNGRIVQLPLHRFAVGFRPFEPADGFRQAAFRAAASG
              310      320      330      340      350      360

              370      380      390      400      410      420
m509.pep      FFVDLAAAFVHVFGDVQNLGEQAAGQGXIIVGLLFVQLRQYFFNQCRVVGSGQEFDCFD
a509          FFVDLAAAFVHVFGDVQNLGEQAAGQGXIIVGLLFVQLRQYFFNQCRVVGSGQEFDRFD
              370      380      390      400      410      420

              430      440      450      460      470      480
m509.pep      NQRRGFFVQVEVEQGLFQKFRVRQRSLVWIVQNMQLHDFSLSSAVNIVNVPQMPHPQCQTV
a509          NQRRGFFVQVEVEQGLFQKFRVRQRSLVWIVQNMQLHDFSLI-AVNTVNVVPQMPHPQCQTV
              430      440      450      460      470

              490      500      510      520      530      540
m509.pep      HTLTARVPKCRLKLNAAARRQRYNRPQLFFSEHHHDHDRTRQRRICIPAAVQPPHPLGRNRH
a509          HTLTARVPKCRLKLNAAARRQRYNRPQLFXSEHHHDHDRTRQRRICIPAAVQPPHPLGRNWH
              480      490      500      510      520      530

              550      560      570
m509.pep      RRAAETFRRAYFGRRLRRFGCRRTXPTLPLRV SARX
a509          RRAAETFRRAYFGRRLRRFGCRXPCPISPLPASARX
              540      550      560      570

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1399>:

```

g510.seq
1   atgccttcgc ggacaccgca gggaaaaagg ggttattcct gccccaaagcg
51  ggatagtgcc ttttggcagg cgttgtccat atcggttatt ttacgcgcaa
101 aatcgccgat tgccaaatcg ccgccgttca gggagggttt caataggctcg
151 tggacgacgt tgagcgcggc cataatgacg attttttcgc tgtccgcgac
201 gcggccgcct tcgcgatgg cttcggttt gccgttgagc attccgactg
251 cctgcaacag tgtgtctttt tcttctgccg gcgtgttgac agtcagccgg
301 ggcgtgcatg acttcgatgt agacttggtc gatgttcac ctttaatcct
351 tattgctgcg tttcctgccg ttgggggagg cgcgctgcca gtgcgctga

```

This corresponds to the amino acid sequence <SEQ ID 1400; ORF 510.ng>:

```

g510.pep
1   MPSRTPQGKR GYSCPKRDSA FWQALSISVI LRAKSPIAKS PPFREVFNRS
51  WTTLSAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLTISR
101 GVHDFDVLDF DVHPLILIAA FPAVGGGALP VR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1401>:

```

m510.seq
1   ATGCCTTCGC GGACACCGCA GGGnAAAAGG GGTTATTCCT GCGCCAAGCG
51  GGATAGTGCT TTTTGGCAGG CGTTGTCCAT ATCGGCTATT TTACGCGCAA
101 AATCGCCGAT TGCCAAATCG CCGCGTTCA GGGAGGTTT CAACAGGTGCG
151 TGGACGACGT TGAGCGCGGC CATAATGACG ATTTTTCGC TGTCCGCGAC
201 GCGTCCGCCT TCGCGGATGG CTTGGCTTT GCCGTGAGC ATTCCGACTG
251 CCTGCAACAG TGTGTCTTTT TCTTCTGCCG GCGTGTGAC GGTGAGCCGG
301 GCGGTGCAwG ACTTCsAtGT GGAATTGTTT GATGTTTCATC CTTTAATCCT
351 TATTGCTGCG TTTCTGCCA TTGGGGGAGG CCGCTGCCA GTGCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1402; ORF 510>:

```

m510.pep
1   MPSRTPQGKR GYSCAKRDSA FWQALSISAI LRAKSPIAKS PPFREVFNRS
51  WTTLSAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLTISR
101 GVXDFXVDLF DVHPLILIAA FPAIGGGALP VR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 510 shows 96.2% identity over a 132 aa overlap with a predicted ORF (ORF 510.ng) from *N. gonorrhoeae*:

m510/g510

```

      10      20      30      40      50      60
m510.pep  MPSRTPQGKRGYSCAKRDSAFWQALSISAILRAKSPIAKSPPFREVFNRSWTTLAAIMT
          |||||
g510      MPSRTPQGKRGYSCPKRDSAFWQALSISVILRAKSPIAKSPPFREVFNRSWTTLAAIMT
          |||||
      70      80      90     100     110     120
m510.pep  IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRGVXDFXVDLFDVHPLILIAA
          |||||
g510      IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRGVHDFDVLFDVHPLILIAA
          |||||
      70      80      90     100     110     120

      130
m510.pep  FPAIGGGALPVRX
          |||:|||||
g510      FPAVGGGALPVRX
          |||||
      130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1403>:

```

a510.seq
  1  ATGCCTTCGC GGACACCGCA GGGAAAAAGG GGTTATTCCT GCGCCAAGCG
 51  GGATAGTGCT TTTTGGCAGG CGTTGTCCAT ATCGGCTATT TTACGCGCAA
101  AATCGCCGAT TGCCAAATCG CCGCCGTTCA GGGAGGTTT CAACAGGTCG
151  TGGACGACGT TGAGCGCGGC CATAATGACG ATTTTTCGCG TGTCCGCGAC
201  GCGTCCGCCT TCGCGGATGG CTTGCGCTTT GCCGTTGAGC ATTCCGACTG
251  CCTGCAACAG TGTGTCTTTT TCTTCTGCCG GCGTGTGAC GGTGAGCCGG
301  G. CGTGCATG ACTTCGATGT GGA CTGTTC GATGTTTCATC CTTTAATCCT
351  TATTGCTGCG TTCTCTGCCG TTGGGGGAGG CGCGCTGCCA GTGCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1404; ORF 510.a>:

```

a510.pep
  1  MPSRTPQGKR GYSCAKRDSA FWQALSISAI LRAKSPIAKS PPFREVFNR
 51  WTTLAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLTVSR
101  XVHDFDVLDF DVHPLILIAA FPAVGGGALP VR*

```

m510/a510 97.0% identity in 132 aa overlap

```

      10      20      30      40      50      60
m510.pep  MPSRTPQGKRGYSCAKRDSAFWQALSISAILRAKSPIAKSPPFREVFNRSWTTLAAIMT
          |||||
a510      MPSRTPQGKRGYSCAKRDSAFWQALSISAILRAKSPIAKSPPFREVFNRSWTTLAAIMT
          |||||
      10      20      30      40      50      60

      70      80      90     100     110     120
m510.pep  IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRGVXDFXVDLFDVHPLILIAA
          |||||
a510      IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRXVHDFDVLFDVHPLILIAA
          |||||
      70      80      90     100     110     120

      130
m510.pep  FPAIGGGALPVRX
          |||:|||||
a510      FPAVGGGALPVRX
          |||||
      130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1405>:

```

g512.seq
  1  atgaaagtgc ttgttttagg tgcgggtgtt gccggcgat cctccgtgtg

```

g512.pep

1	<u>MKVLVLGAGV</u>	AGVSSVWYLA	EAGHEVTVID	RTEGVAMETS	FANAGQLSYG
51	YTPPWAAPI	PTKALKRLFK	SHPPLLFRPD	GGLYQIEWLW	RMLQNCTATR
101	YQINKERMVR	ISEYSREMFR	RFEAQDTDMNF	EGRKKGTLQI	FRQTEEVEAA
151	KQDIAVLERY	GVPPYRLKPE	ECAEFEPALA	RVTAKIVGGL	HLPADATGDC
201	RLFTENLYKL	QCEKGVRIFY	NOTISRIDHN	GLRIKAVETK	QGGLKQMPLS
251	ARSAASAGLC	WRSWISICPE	IPSKAIP*		

```
m512.seq (partial)
1  ..GTTTTGGAAC GCTACGGCGT GCCGTACCGC CGTCTGAAAC CCGAAGAATG
51  TGCAGAAATT GAGCCTGCGC TGGCACGCGT TACCGCCAAA ATTGCCGGCG
101 GCCTGCACCT GCCTGCAGAT GCGACCGGCG ACTggCGCCT CTTCACTGAA
151 AACCTATACA AATTGTGTCA GGAAAAGGGC GTACGGTTTC ATTTCAACCA
201 AAACATCAGC CGCATCGACC ACAACGGGCT GCGCATCAA ACCGTTGAAA
251 CCAAAACAGG CGGTTTGAAG CAGATGCCGT TGTCTGCGCG CTCGGTTGCT
301 TCAGCAGGAC GGTTTTGGCG CAGTTGGATC TCAATCTGCC CATTTATCCC
351 GTCAAAGGCT ATTCCTTGA
```

```
m512.pep      (partial)
1      ..VLERYGVPIR RLPKEECAEF EPALARVTAK IAGGLHLPAD ATGDWRLFTE
51     NLYKLCQKEG VRHFHNQNIS RIDHNGLRIR TVETKQGGGLK QMPLSARVA
101    SAGREFWRSWI SICPEIPSKA IP*
```

ORF 512 shows 93.4% identity over a 122 aa overlap with a predicted ORF (ORF 512.ng) from *N. gonorrhoeae*:

```

                                10      20      30
m512.pep                      VLERYGVPYRRLKPEECAEFEPALARVTAK
                                |||||
g512      TDMNFEGRRKKGTLQIFRQTEEVEAAKQDIAVLERYGVPYRRLKPEECAEFEPALARVTAK
              130      140      150      160      170      180

                                40      50      60      70      80      90
m512.pep      IAGGLHLPADATGDWRLFTENLYKLCQEKGVRFHFNQNISRIDHNGLRIKTVETKQGGLK
              |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g512      IVGGLHLPADATGDCRLFTENLYKLCQEKGVRFYFNQTI SRIDHNGLRIKAVETKQGGLK
              190      200      210      220      230      240

                                100      110      120
m512.pep      QMPLSARSVASAGRFWRSWISICPFIPSKAIP
              |||||:|||||
g512      QMPLSARSAASAGLCWRSWISICPFIPSKAIP

```

250

260

270

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1409>:

```
a512.seq
  1 ATGAAAGTGC TTGTTT TAGG TGCTGGTGT GCCGGCGTAT CTTCCGCGTG
  51 GTATCTGGCA GAGGCAGGAC ATGAAGTAAC GGTCATCGAC CGCGCCGAGG
 101 GCGTGGCGAT GGAAACCACT TTTGCCAACG CAGGCCAGCT TTCTTACGGC
 151 TATACCACGC CTTGGGCTGC ACCCGGTATT CCGACCAAAG CACTGAAATG
 201 GCTGTTTAAA AGCCATCCGC CTTTGCTGTT TCGCCCCGAC GGCAGCCTGT
 251 ATCAAATCGA ATGGCTGTGG CAGATGCTGC AACACTGCAC GGCAGCGCGC
 301 TATCAAATCA ATAAAGAGCG CATGGTCAGG ATGTCCGAAT ACAGCCGTGA
 351 AATGTTCCGC CGTTTTGAAG CGCAAACCGG CATGAATTTT GAGGGACGCA
 401 AAAAAGGGAC GTTGCAGATT TTCCGCCAAA CCAAAGAAGT CGAAGCGGCA
 451 AAACAAGACA TTGCCGTTTT GGAACGCTAC GGCGTGCCGT ACCGCCGTCT
 501 GAAGCCCGAA GAATGCGCAG AATTCGAGCC TGCGCTGGCA CGCGTTACCG
 551 CCAAAATTGC CGGCGGCGTG CACCTGCCCG CAGACGCGAC CGGCGACTGC
 601 CGCCTCTTCA CTGAAAACCT GTACAAATTG TGTCAGGAAA AGGGCGTACG
 651 GTTTCATTTC AACCAAACCA TCAGCCGCAT CGACCACAAC GGGCTGCGCA
 701 TCAAAACCGT TGAAACGAAA CAGGCGGGT TGAAGCAGAT GCCGTTGTCT
 751 GCGCGCTCGG CTGCTTCAGC AGGACGGTTT TGGCGCAAGT GGATCTCAAT
 801 CTGCCGATTT ATCCCGTCAA AGGCTATTCC TTGA
```

This corresponds to the amino acid sequence <SEQ ID 1410; ORF 512.a>:

```
a512.pep
  1 MKVLVLGAGV AGVSSAWYLA EAGHEVTVID RAEGVAMETS FANAGQLSYG
  51 YTPPWAAPGI PTKALKWLFK SHPPLLFPRD GSLYQIEWLW QMLQHCTAAR
 101 YQINKERMVR MSEYSREMFV RFEAQTGMNF EGRKKGTLOI FRQTKEVEAA
 151 KQDIAVLERY GVPYRRLKPE ECAEFEPALA RVTAKIAGGL HLPADATGDC
 201 RLFTENLYKL CQEKGVRFHF NQTISRIDHN GLRIKTVETK QGGLKQMPLS
 251 ARSAASAGRF WRKWISICRF IPSKAIP*
```

m512/a512 95.9% identity in 122 aa overlap

```
m512.pep                                10      20      30
                                VLERYGVPYRRLKPEECAEFEPALARVTAK
a512                                TGMNFEGRKKGTLOIFRQTKEVEAAKQDIAVLERYGVPYRRLKPEECAEFEPALARVTAK
                                130      140      150      160      170      180

                                40      50      60      70      80      90
m512.pep                        IAGGLHLPADATGDWRLFTENLYKL CQEKGVRFHFNQNISRIDHNGLRIKTVETKQGGLK
a512                        IAGGLHLPADATGDCRLFTENLYKL CQEKGVRFHFNQTISRIDHNGLRIKTVETKQGGLK
                                190      200      210      220      230      240

                                100      110      120
m512.pep                        QMPLSARSVASAGRFWRWSWISICPFIPSKAIPX
a512                        QMPLSARSAASAGRFWRKWISICRFIPSKAIPX
                                250      260      270
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1411>:

```
g513.seq
  1 ATGGGTTC CGCCGAACGC CGCCGCCGCC GCCGAAGTGA AACACCCTGT
  51 TTCGCAAGGT ATGATTCAA TGCTGGGCGT GTTGTCGAT ACCATCATCG
 101 TTTGTTCTTG CACCGCCTTC ATCATCTTGA TTTACCAACA GCCTTATGGC
 151 GATTTGAGCG GTGCGGCGCT GAcgcAGGCG GCGATTGTCA GCCAAGTGGG
 201 GCAATGGGGC GCGGGTTTCC TCGCCGTCAT CCTGTTTATG TTGCTTTT
 251 CCACCGTTAT CGGCAACTAT GCCTATGCCG AGTCCAACGT CCAATTCATC
 301 AAAAGCCATT GGCTGATTAC CGCCGTTTTC CGTATGCTGG TTTTGGCGTG
 351 GGTCTATTTC GCGCGGGTTC CCAATGTGCC TTTGGTCTGG GATATGGCGG
 401 ATATGGCGAT GGGCATCATG GCGTGGATCA ACCTCGTCGC CATCTGCTG
 451 CTCTCGCCat TGGCGTTTAT GCTGCTGCGC GATTACACCG CCAAGCTGAA
```

501 AATGGGCAAA GACCCCGAGT TCAAACCTTc cgAACATCCG GGCCTGAAAC
 551 GCCGCATCAA ATCCGATGTT TGGTAA

This corresponds to the amino acid sequence <SEQ ID 1412; ORF 513.ng>:

g513.pep

1 MGSAPNAAAA AEVKHPVSQG MIQMLGVFVD TIIVCSCTAF IILIYQQPYG
 51 DLSGAALTQA AIVSQVGQWG AGFLAVILFM FAFSTVIGNY AYAESNVQFI
 101 KSHWLITAVF RMLVLAWVYF GAVANVPLVW DMADMAMGIM AWINLVAILL
 151 LSPLAFMLLR DYTAKLKMKG DPEFKLSEHP GLKRRIKSDV W*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1413>:

m513.seq

1 ATGGGTTCCG CGCCGAACGC CGCCGCCGCC GCCGAAGTGA AACACCCTGT
 51 TTCGCAAGGT ATGATTCAAA TGCTGGGCGT GTTGTGCGAT ACCATCATCG
 101 TTTGTTCTTG CACCGCCTTC ATCATCTTGA TTTACCAACA GCCTTATGGC
 151 GATTTGAGCG GTGCGGCGCT GAcgcAGGCG GCGATTGTCA GCCAAGTGGG
 201 GCAATGGGGC GCGGGTTTCC TCGCCGTCAT CCTGTTTATG TTTGCCTTTT
 251 CCACCGTTAT CGGCAACTAT GCCTATGCCG AGTCCAACGT CCAATTCATC
 301 AAAAGCCATT GGCTGATTAC CGCCGTTTTT CGTATGCTGG TTTTGGCGTG
 351 GGTCTATTTT GCGCGGTTTG CCAATGTGCC TTTGGTCTGG GATATGGCGG
 401 ATATGGCGAT GGGCATCATG GCGTGGATCA ACCTCGTCGC CATCCTGCTG
 451 CTCTCGCCat TGGCGTTTAT GCTGCTGCGC GATTACACCG CCAAGCTGAA
 501 AATGGGCAAA GACCCCGAGT TCAAACCTTc cgAACATCCG GGCCTGAAAC
 551 GCCGCATCAA ATCCGATGTT TGGTAA

This corresponds to the amino acid sequence <SEQ ID 1414; ORF 513>:

m513.pep

1 MGSAPNAAAA AEVKHPVSQG MIQMLGVFVD TIIVCSCTAF IILIYQQPYG
 51 DLSGAALTQA AIVSQVGQWG AGFLAVILFM FAFSTVIGNY AYAESNVQFI
 101 KSHWLITAVF RMLVLAWVYF GAVANVPLVW DMADMAMGIM AWINLVAILL
 151 LSPLAFMLLR DYTAKLKMKG DPEFKLSEHP GLKRRIKSDV W*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 513 shows 99.5% identity over a 191 aa overlap with a predicted ORF (ORF 513.ng) from *N. gonorrhoeae*:

m513/g513

m513.pep	10	20	30	40	50	60
	MGSAPNAAAAAEVKHPVSQGM IQMLGVFVD TIIVCSCTAF IILIYQQPYG DLSGAALTQA					
g513	MGSAPNAAAAAEVKHPVSQGM IQMLGVFVD TIIVCSCTAF IILIYQQPYG DLSGAALTQA					
	10	20	30	40	50	60
m513.pep	70	80	90	100	110	120
	AIVSQVGQWGAGFLAVILFM FAFSTVIGNY AYAESNVQFI KSHWLITAVFRMLVLAWVYF					
g513	AIVSQVGQWGAGFLAVILFM FAFSTVIGNY AYAESNVQFI KSHWLITAVFRMLVLAWVYF					
	70	80	90	100	110	120
m513.pep	130	140	150	160	170	180
	GAVANVPLVWDMADMAMGIMAWINLVAILLSPLAFMXLRD Y TAKLKMKG DPEFKLSEHP					
g513	GAVANVPLVWDMADMAMGIMAWINLVAILLSPLAFMLLRD Y TAKLKMKG DPEFKLSEHP					
	130	140	150	160	170	180
m513.pep	190					
	GLKRRIKSDVW					
g513	GLKRRIKSDVW					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1415>:

a513.seq


```
1 ATGAACGAGA ACTTTACCGA ATGGCTGCAC GGCTGGGTCTG GCGCCATCAA
51 CGATCCGATG TGGTCATACT TGGTTTATNT GCTTTTGGGT ACGGGGCTTT
101 TCTTACCAGT AACCACGGGC TTTGTCCAAT TCCGCCTGTT CGGGCGCAGC
151 ATCAAAGAAA TGCTCGGCGG CCGCAAACAG GGGGACGACC CTCACGGCAT
201 CACGCCGTTT CAGGCATTTG TAACCGGCCT TGCCAGCCGC GTGGGCGTGG
251 GCAATATCGC GGGCGTGGCC ATCGCCATCA AAGTCGGCGG ACCGGGCGCG
301 GTGTTTTGGA TGTGGGTAAC CGCCTTAATC GGTATGAGTT CGGCGTTTGT
351 CGAATCTTCG CTGGCGCAGC TCTTTAAAGT CCGCGACTAC GACAACCACC
401 ATTTCCGGGG CGGCCCTGCC TACTACATCA CTCAGGGGCT GGGGCAGAAA
451 TGGCTGGGCG TGTTGTTCGC CCTGAGCCTG ATTTTCTGTT TCGGCTTTGT
501 GTTTGAAGCG GTTCAGACCA ATACCATTGC CGATACCGTC AAAGCGGCGT
551 GGGGTTGGGA GCCTCATTAT GTCGGCGTCG CCCTGGTGAT TTTAACCGCG
601 CCGATTATCT TCGGCGGCAT CAGGCGCATA TCTAAAGCGG CGGAAATCGT
651 CGTCCCCTG ATGGCGGTTT TGTACCTCTT TATCGCGCTT TTCATCATTT
701 TGACCAATAT TCCGATGATT CCGGACGTGT TCGGTCAGAT TTTTTCGGGC
751 GCGTTCAAAT TCGACGCGGC AGCAGGCGGC TTAATCGGCG GTCTGATTTT
801 GCAAACGATG ATGATGGGCA TCAAACGCGG CCTGTATTCC AACGAGGCGG
851 GTATGGGTTT CCGCGCGAAC GCGCGCGCCG CCGCCGAAGT GAAACACCCT
901 GTTTCGCAAG GTATGATTCA AATGCTGGGC GTGTTTGTCT ATACCATCAT
951 CGTTTGTCT TGCACCGCCT TCATCATCTT GATTTACCAA CAGCCTTACG
1001 GCGATTGAG CCGTGCGGCG CTGACGCAGG CGGCGATTGT CAGCCAAGTG
1051 GGGCAATGGG GCGCGGCGCT CCTCGCCGTC ATCCTGTTTA TGTTTGCCTT
1101 TTCCACCGTT ATCGGCAACT ATGCCTATGC CGAGTCCAAC GTCCAATTCA
1151 TCAAAAGCCA TTGGCTGATT ACCGCGGTTT TCCGTATGCT GGTTTTGGCG
1201 TGGGTCTATT TCGGCGCGGT TGCCAATGTG CCTTTGGTCT GGGATATGGC
1251 GGATATGGCG ATGGGCATTA TGGCGTGGAT CAACCTTGTC GCCATCCTGC
1301 TGCTCTCGCC CTTGGCGTTT ATGCTGCTGC GCGATTACAC CGCCAAGCTG
1351 AAAATGGGCA AAGACCCCGA GTTCAAACCT TCCGAACATC CGGGCCTGAA
1401 ACGCCGTATC AAATCCGACG TTTGGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1416; ORF 513.a>:

```
a513.pep
1 MNENFTEWLH GWVGAINDEP WSYLVYXLLG TGLFFTVTTG FVQFRLFGRS
51 IKEMLGGRKQ GDDPHGITPF QAFVTGLASR VGVGNIAGVA IAIKVGGPGA
101 VFWMWVTALI GMSSAFVESH LAQLFKVRDY DNHHFRGGPA YYITQGLGQK
151 WLGVLFLSL IFCFGVFEEA VQNTIADTV KAAWGWEPHY VGVALVILTA
201 PIIFGGIRRI SKAAEIVVPL MAVLYLFIAL FIILTNIPMI PDVFGQIFSG
251 AFKFDAAAGG LLGLISQTM MMGIKRGlys NEAGMGSAPN AAAAAEVKHP
301 VSQGMQMLG VFVDTIIVCS CTAFIILIYQ QPYGDLGSA LTQAAIVSQV
351 QQWAGFLAV ILFMFAFSTV IGNYAYAESN VQFIKSHWLI TAVFRMLVLA
401 WYFYGAVANV PLVWDMADMA MGIMAWINLV AILLLSPLAF MLLRDYAKL
451 KMGKDPEFKL SEHPGLKRRI KSDVW*
```

m513/a513 100.0% identity in 191 aa overlap

```
m513.pep
10 20 30
MGSAPNAAAAAEVKHPVSQGMQMLGVFVD
|||||
a513
260 270 280 290 300 310
DAAAGLLGLISQTM MMGIKRGlysNEAGMGSAPNAAAAAEVKHPVSQGMQMLGVFVD

40 50 60 70 80 90
TIIVCSCTAFIILIYQQPYGDLGSAALTQAAIVSQVQWAGFLAVILFMFAFSTVIGNY
|||||
a513
320 330 340 350 360 370
TIIVCSCTAFIILIYQQPYGDLGSAALTQAAIVSQVQWAGFLAVILFMFAFSTVIGNY

100 110 120 130 140 150
AYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMADMAMGIMAWINLVAILL
|||||
a513
380 390 400 410 420 430
AYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMADMAMGIMAWINLVAILL

160 170 180 190
LSPLAFMLLRDYTAKLKMKGKDPFKLSEHPGLKRRIKSDVWX
|||||
```

a513

LSPLAFMLLRDY TAKLMGKDPEFKLSEHPGLKRRIKSDVWX
 440 450 460 470

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1417>:

g515.seq

```

1   atggttcaaa tacaggttgt gcgcgcgcgc ggcgttgccc gtggtctgca
51  ttccgagttt gcgcgcgcgc taactgccga ggaaatagcc ttcgacaatg
101 ccgttttgaa tcacgaagcg cggcgcgcgc gcaacacctt ccgcatacaa
151 atagctgctg cggaaagagc gggggatgtg cgttctctcg cgcaggttga
201 ggaaatcggg caggactttt ttgccgatgc tgcgatcag gaaactgctt
251 tggcggtaga gcgcgcgcgc ggagagtgtg ccgacgaggt gtccgatcag
301 cccgcccga acggtggtat cgaagaggac ggggtagctg cctgtcggga
351 tgctgcggct gccgagtcgg cgcaaagtgc ggcgggcggc ggtttgaccg
401 atggtttcgg ggctgtccat atccggatgg cggcagggcg aatcgtacca
451 ttagtcgcgc tgcattccgt ttctgtcggc ggcgacgacg ctgcaggaaa
501 tgctgtggtg cgtgctttgc cgtgtgctgc caaaaccgtg ggtgttgccg
551 taaacgtatt ggtactgtcc gggtttgcac gccgcgcctt cggagttttc
601 gatgcggctg tccgtgtcca acgtgtcctg ttgcattgtt ttgccaagc
651 cgacggcggc ttccgtatcc aaatcccatt cgtggttaaag gtcggggctg
701 ccgatgtgtt gcgccatcaa ctccgggtcg gcaagtccgg cgcaaccgtc
751 ttccggcggg tggcgggcga tgcggcgccg ggcgcggacg gtgtcgcgca
801 gggcttggtt ggagaagtgc gcggtgccgg cgcggccttt gcgtttgccg
851 acgtaaacgg taatgtcca cgtttgttgc tgcgtgaact cgatttgttc
901 gatttcgccc aagcgcacgc tgacgctttg tccgagcgat tgcgtgaagt
951 cggcttcggc ggcggtcgcg cccgctgctt ttgccaagtc gagcgtgcgg
1001 cggcagaggt cgaggagtgc ggaagcgggt tggttgaaca gcataacaat
1051 ctttcttggt ggagcgttgt ggcattttta

```

This corresponds to the amino acid sequence <SEQ ID 1418; ORF 515.ng>:

g515.pep

```

1   MVQIQVVRAA GVARGLHSEF ARAVTAEIEA FDNAVLNHEA RRGNTFRIK
51  IAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERAA GECADSVSDQ
101 PARNGGIEED GVAACRDAEA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHSVFVG GDAAAGNAV V RALPVCCKTV GVAVNVLVLS GLHRRAFGVF
201 DAAVRVQRCL FALFCQADGG FRIQIPFVVK VGVADVLRHQ LGVGKSGATV
251 FGGVAGDVGG GADGVAQGLF GEVGGAGAAF AFADVNGNVQ RFVLLLELDLF
301 DFAQAHADAL SERFAEVGFG GGRARCFCQV ERAAAEVEEF GSGVVEQHNN
351 LSWWSVVAF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1419>:

m515.seq (partial)

```

1   ..GGAAAGAGCG GGGGATGTGC GTTCTTCGCG CAGGTTGAGG AAATCGGGCA
51  GGACTTTTCT GCCGATGCTG TCGATCAGGA AACTGCTTTG GCGGTAGAGC
101 GCGCCGCCCG AGAGTGCGCC GACGAGGTGT CCGATAAGAC CGCCCGAAAC
151 GGTGGTATCG AAGAGGACGG GGTAGCTGCC TGTCGGGATG CTGCGGCTGC
201 CGAGTCGGCG CAAAGTGCGG CGGGCGGCGG TTTGACCGAT GGTTTCGGGG
251 CTGTCCATAT CCGGATGGCG GCAGGCGGAA TCGTACCAGT AGTCGCGCTG
301 CATGCCGTTT TCGTCGGCGG CAACGACGCT GCAGGAAATG CTGTGGTGCG
351 TGCCTTGCCG GTGTGCGGCA AAACCGTGGG TGTGCGGTA AACGTATTGG
401 TAATGGCCCG TTTGCACCGC CGCGCCTTCG GAGTTTTCGA TCGGCTCATC
451 CTCGTTACAG GCGGCTTGTT CGCATTGTTT TGCCAAGCCG ACGGCGGCTk
501 CCGTATCCAA ATCCCATTCG TGGTAAAGGT CGGGGTCGCC GATGTGTTTT
551 GCCATCAGAC AGGCATCGGC AAGTCCGGCG CAACCGTCTT CGGCGGTGTG
601 GCGGGCGATG TCGATGGCGG CTTTGACGGT GTCTTGACAG GCTTTTTCGG
651 AGAAGTCGGC AGTACTGGCG CGGCCTTTGC GTTTGCCGAC GTAAACGGTA
701 ATGTCCAGCG ACTTGCTCTG CTGGAACGCG ATTTGTTsGA TTTsGCCCAG
751 CCGCACGCTG ACGCTTTGTC CCAATGATTC GCTGAAATCG GCTTCGGCGG
801 CGGTTGCGCC CGTCGCTTTT GCCAAGTCGA GCGTGCGGCG GCAGAGGTCTG
851 AGGAGTTCGG AAGCGGTGTG GTTgAACAGC ATAGAAATCT TTCTTGATGA
901 TGCTTTGCGG CATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1420; ORF 515>:

m515.pep (partial)

```

1  .GKSGGCAFFA QVEEIGQDFS ADAVDQETAL AVERAAGECA DEVSDKTARN
51  GGIEEDGVAA CRDAAAESA QSAAGGGLTD GFGAVHIRMA AGGIVPVVAL
101 HAVFVGGNDA AGNAVVRALP VCGKTVGVAV NVLVMAGLHR RAFGVFDALI
151 LVQGLFALF CQADGGXRIQ IPFVVKVGVA DVFCHQTGIG KSGATVFGGV
201 AGDVGDFDG VLQFFGEVG STGAFAFAD VNGNVQRLVL LELDLXDXAQ
251 PHADALSQXF AEIGFGGGCA RRFCQVERAA AEVEEFGSGV VEQHRNLSXX
301 CFAAF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 515 shows 85.9% identity over a 304 aa overlap with a predicted ORF (ORF 515.ng) from *N. gonorrhoeae*:

m515/g515

```

m515.pep          10          20          30
                  GKSGGCAFFA QVEEIGQDFS ADAVDQETALA
                  ::| | | | | | | | | | | | | | | | | |
g515              AEEIAFDNAV LNHEARRGGNTFRIKIAAERAGDV RFFA QVEEIGQDFFADA VDQETALA
                  30      40      50      60      70      80

m515.pep          40          50          60          70          80          90
                  VERAAGECADEVSDKTARNGGIEEDGVAACRDAAAESAQSAAGGGLTDGFGAVHIRMAA
                  | | | | | | | | | | : | | | | | | | | | | | | | | | | | | | | | | | |
g515              VERAAGECADEVSDQPARNGGIEEDGVAACRDAAAESAQSAAGGGLTDGFGAVHIRMAA
                  90      100     110     120     130     140

m515.pep          100         110         120         130         140         150
                  GGIVPVVALHAVFVGGNDAAGNAVVRALPVCGKTVGVAVNVLMAGLHRRAFGVFDALIL
                  | | | | | | | | : | | | | : | | | | | | | | | | | | | | | | : | | | | | |
g515              GGIVPVVALHSVFVGGDDAAGNAVVRALPVCGKTVGVAVNVLVLSGLHRRAFGVFDAAVR
                  150     160     170     180     190     200

m515.pep          160         170         180         190         200         210
                  VQGLFALFCQADGGXRIQIPFVVKVGVAADV FCHQTGIGKSGATVFGGVAGDVGDFDG
                  | | | | | | | | | | | | | | | | : | | : | | | | | | | | | | | | | |
g515              VQRCFLALFCQADGGFRIQIPFVVKVGVAADVLRHQLGVGKSGATVFGGVAGDVGGGADGV
                  210     220     230     240     250     260

m515.pep          220         230         240         250         260         270
                  LQFFGEVGSTGAFAFADVNGNVQRLV LLELDLXDXAQPHADALSQXFAEIGFGGGCAR
                  | | : | | | | : | | | | | | | | | | : | | | | | | | | | | : | | | | | |
g515              AQGLFGEVGGAGAAFAFADVNGNVQRFV LLELDLDFDAQAHADALSERFAEVGFGGGRAR
                  270     280     290     300     310     320

m515.pep          280         290         300
                  RFCQVERAAA EVEEFGSGVVEQHRNLSXXCFAAF
                  | | | | | | | | | | | | | | | | | | : | |
g515              CFCQVERAAA EVEEFGSGVVEQHNNLSWWSVAF
                  330     340     350

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1421>:

```

a515.seq
1  ATGGTTCAAA TAAAGGTTGT GCGCGCCGCC GCGGTTGCC CTTGGTCTGCA
51  TTCCGAGTTT GCGCGCGCTG TAACTGCTGA GGAAATAGCC TTCGACAATG
101 CCGTTTTGAA TCACGAAGCG CGGTGCGGTG GCAACGCCTT CCGCATCAAA
151 ATAGCTGCTG CCGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTGCATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCTCCGCC GGAGAGTGCG CCGACGAGGT GTCCGATAAG
301 ACCGCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGTTG CCTGTCCGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GCGGGGCGGC GGTGTTGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CCGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATGCCGT TTTCGTCGGC GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTCG CGGTGTGCGG CAAAACCGTA GGTGTTGCCG

```

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```

551 TAAACGTATT GGTAATGGCC GGTTCGACC GCCGCGCCTT CGGAGTTTTT
601 GATGCGCTCA TCCTCGTTCA GGGCGGCTTG TTCGCATTGT TTTGCCAAGC
651 CGACGGCGGC TTCCGTATCC AAATCCCATC CGTGGTAAAG GTCGGGGTCG
701 CCGATGTGTT GCGCCATCAA CTCGGGGTCG GCAAGTCCGG CGCAACCGTC
751 TTCGGCGGTG TGGCGGGCGA TGTCNNNNGC GCGCGGACG GTGTCGCGCA
801 GGGCTTGTTT GGAGAAATCG GCGGTGCCGG CGCGGCCTT GCGTTTGCCG
851 ACGTAAACGG TAATGTCCAG CACTTGTCC TGCTGAACT CGATTTGTTC
901 GATTCGCCC AGCCGCACGC TGACGCTTG TCCCAATGAT TCGCTGAAAT
951 CGGCTTCGGC GCGGTTGCG CCCGTCGCTT TTGCCAAGTC GAGCGTGCGG
1001 CGGCAGAGGT CGAGGAGTTC GGAAGCGGTG TGGTTGAACA GCATAGAAAT
1051 CTTTCTTGAT GATGCTTTGC GGCATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1422; ORF 515.a>:

```

a515.pep
1  MVQIKVVRAA  GVARGLHSEF  ARAVTAEIEA  FDNVLNHEA  RCGGNAFRIK
51  IAAERAGDV  RFFAQVEEIG  QDFFADAVDQ  ETALAVERSA  GECADVSDK
101 TARNGGIEED  GVVACRDAAA  AESAQSAAGG  GLTDGFGAVH  IRMAAGGIVP
151 VVALHAVFVG  GNDAAGNAV  RALPVCCKTV  GVAVNVLMMA  GLHRRAFGVF
201 DALILVQGG  FALFCQADGG  FRIQIPFVVK  VGVADVLRHQ  LGVGKSGATV
251 FGGVAGDVXX  GADGVAQGLF  GEIGGAGAAF  AFADVNGNVQ  RLVLKLDLF
301 DFAQPHADAL  SQ*FAEIGFG  GGCARRFCQV  ERAAAEVEEF  GSGVVEQHRN
351 LS**CFAAF*

```

m515/a515 92.1% identity in 304 aa overlap

```

m515.pep                                10      20      30
                                         GKSGGCAFFAQVEEIGQDFESADAVDQETALA
                                         ::|  |||||  |||||  |||||
a515      AEEIAFDNAVLNHEARCGGNAFRIKIAAAERAGDVRFFAQVEEIGQDFFADAVIDQETALA
           30      40      50      60      70      80

m515.pep      40      50      60      70      80      90
VERAAGECADEVSDKTARNGGIEEDGVAACRDAAAESAQSAAGGGLTDGFGAVHIRMAA
|||:|||||  |||||  |||||  |||||  |||||  |||||
a515      VERSAGECADEVSDKTARNGGIEEDGVVACRDAAAESAQSAAGGGLTDGFGAVHIRMAA
           90     100     110     120     130     140

m515.pep      100     110     120     130     140     150
GGIVPVVALHAVFVGNDAGNAVVRALPVCCKTVGVAVNVLMAGLHRRAFGVFDALIL
|||||  |||||  |||||  |||||  |||||  |||||
a515      GGIVPVVALHAVFVGNDAGNAVVRALPVCCKTVGVAVNVLMAGLHRRAFGVFDALIL
           150     160     170     180     190     200

m515.pep      160     170     180     190     200     210
VQGGFLFALFCQADGGXRIQIPFVVKVGVDVFCQHTGIGKSGATVFGGVAGDVGGFDGV
|||||  |||||  |||||  |||||  |||||  |||||
a515      VQGGFLFALFCQADGGFRIQIPFVVKVGVDVLRHQLGVGKSGATVFGGVAGDVXXGADGV
           210     220     230     240     250     260

m515.pep      220     230     240     250     260     270
LQFFGEVVGSTGAFAFADVNGNVQRLVLLDLXDXAQPHADALSQXFAEIGFGGCGAR
||:||||:  |||||  |||||  |||||  |||||  |||||
a515      AQGLFGEIGGAGAAFAFADVNGNVQRLVLLKLDLDFDFAQPHADALSQXFAEIGFGGCGAR
           270     280     290     300     310     320

m515.pep      280     290     300
RFCQVERAAAEVEEFGSGVVEQHRNLSXXCFAAFX
|||||  |||||  |||||  |||||  |||||  |||||
a515      RFCQVERAAAEVEEFGSGVVEQHRNLSXXCFAAFX
           330     340     350     360

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1423>:

g515-1.seq

```

1  ATGGTTCAAA TACAGGTTGT GCGCGCCGCC GCGGTTGCCC GTGGTCTGCA

```

```

51  TTCCGAGTTT GCGCGCGCTG TAACTGCCGA GGAAATAGCC TTCGACAATG
101 CCGTTTTGAA TCACGAAGCG CGGCGCGGTG GCAACACCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCGCCGCC GGAGAGTGTG CCGACGAGGT GTCCGATCAG
301 CCGCGCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGCTG CCTGTCGGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GCGGGGCGGC GGTTTGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CCGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATTCCGT TTTCGTCGGC GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CGGTGTGCGG CAAAACCGTG GGTGTTGCCG
551 TAAACGTATT GGTAGTGTCG GGTTTGCACC GCCGCGCCTT CGGAGTTTTC
601 GATGCGGCTG TCCGTGTCCA ACGCTGCCTG TTCGATTGT TTTGCCAAGC
651 CGACGGCGGC TTCCGTATCC AAATCCCATT CGTGGTAAAG GTCGGGGTCG
701 CCGATGTGTT GCGCCATCAA CTCGGGGTCG GCAAGTCCGG CGCAACCGTC
751 TTCGGCGGTG TGGCGGGCGA TGTCGGCGGC GCGCGGACG GTGTGCGCA
801 GGGCTTGTTT GGAGAAGTCG GCGGTGCCGG CCGCGCCTTT GCGTTGCCG
851 ACGTAAACGG TAATGTCCAG CGATTGTGTC TGCTGGAACG CGATTGTTC
901 GATTTCGCCC AAGCGCACGC TGACGCTTTG TCCGAGCGAT TCGCTGAAGT
951 CGGCTTCGGC GCGGTCGCG CCCGCTGCTT TTGCCAAGTC GAGCGTGC GG
1001 CGGCAGAGGT CGAGGAGTTC GGAAGCGGTG TGGTTGAACA GCATAACAAT
1051 CTTCTTGGT GGAGCGTTGT GGCATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1424; ORF 515-1.ng>:

g515-1.pep

```

1  MVQIQVVRAA GVARGLHSEF ARAVTAEIEA FDNVLNHEA RRGNTFRIK
51  IAAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERAA GECADSVSDQ
101 PARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHVSFVG GNDAAAGNAV RALPVCCKTV GVAVNVLVVS GLHRRAFGVF
201 DAAVRVQRCL FALFCQADGG FRIQIPFVVK VGADVLRHQ LGVGKSGATV
251 FGGVAGDVGG GADGVAQGLF GEVGGAGAAF AFADVNGNVQ RFVLELDLF
301 DFAQAHADAL SERFAEVGFG GGRARCFCQV ERAAAEVEEF GSGVVEQHNN
351 LSWWSVVAFA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1425>:

m515-1.seq

```

1  ATGGTTCAAA TACAGTTTGT GCGCGCCGCC GCGGTTGCCG GTGGTCTGCA
51  TACCGAGTTT GCGCGCGCTG TAACTGCTGA GGAAATAGCC TTCGACAATG
101 CCGTTTTGAA TCACGAAGCG CGGTGCGGTG GCAACGCCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCGCCGCC GGAGAGTGTG CCGACGAGGT GTCCGATAAG
301 ACCGCCCCGA ACGGTGGTAT CGAAGAGGAC GGGGTAGCTG CCTGTCGGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GCGGGGCGGC GGTTTGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CCGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATGCCGT TTTCGTCGGC GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTCG CGGTGTGCGG CAAAACCGTG GGTGTTGCCG
551 TAAACGTATT GGTAAATGGC GGTTCGACC GCCGCGCCTT CGGAGTTTTC
601 GATGCGCTCA TCCTCGTTCA GGGCGGCTTG TTCGATTGT TTTGCCAAGC
651 CGACGGCGGC TTCCGTATCC AAATCCCATT CGTGGTAAAG GTCGGGGTCG
701 CCGATGTGTT TTGCCATCAG ACAGGCATCG GCAAGTCCGG CGCAACCGTC
751 TTCGGCGGTG TGGCGGGCGA TGTCGATGCG GGCTTTGACG GTGTCTTGCA
801 GGGCTTTTTC GGAGAAGTCG GCAGTACTGG CCGCGCCTTT GCGTTGCCG
851 ACGTAAACGG TAATGTCCAG CGACTTGTCC TGCTGGAACG CGATTGTGTC
901 GATTTGCGCC AGCCGCACGC TGACGCTTGG TCCCAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1426; ORF 515-1>:

m515-1.pep

```

1  MVQIQVVRAA GVARGLHTEF ARAVTAEIEA FDNVLNHEA RCGGNAFRIK
51  IAAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERAA GECADSVSDK
101 TARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHVSFVG GNDAAAGNAV RALPVCCKTV GVAVNVLVMA GLHRRAFGVF
201 DALILVQGLL FALFCQADGG FRIQIPFVVK VGADVFC HQ TGIGKSGATV
251 FGGVAGDVGG GFDGVLQGFF GEVGSTGAFF AFADVNGNVQ RLVLLELDLF
301 DFAQPHADAL SQ*

```

m515-1/g515-1 91.7% identity in 312 aa overlap

```

          10      20      30      40      50      60
g515-1.pep  MVQIQVVRAAGVARGLHSEFARAVTAEIEAFDNVLNHEARRGNTFRIKIAAAERAGDV
              |||
m515-1      MVQIQVVRAAGVARGLHTEFARAVTAEIEAFDNVLNHEARCGGNAFRIKIAAAERAGDV
          10      20      30      40      50      60

```

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	70	80	90	100	110	120
g515-1.pep	RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDQPARNGGIEEDGVAACRDAAA					
m515-1	RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDKTARNNGGIEEDGVAACRDAAA					
	70	80	90	100	110	120
	130	140	150	160	170	180
g515-1.pep	AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHSVFGGNDAAAGNAVVRALPVCCKTV					
m515-1	AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHAVFVGGNDAAAGNAVVRALPVCCKTV					
	130	140	150	160	170	180
	190	200	210	220	230	240
g515-1.pep	GVAVNVLVVSGLHRRAFGVFDAAVRVQRCLFALFCQADGGFRIQIPFVVKVGVADVLRHQ					
m515-1	GVAVNVLVMAGLHRRAFGVFDALILVQGGFLFALFCQADGGFRIQIPFVVKVGVADVLFCHQ					
	190	200	210	220	230	240
	250	260	270	280	290	300
g515-1.pep	LGVGKSGATVFGGVAGDVGGADGVAQGLFGEVGGAGAAFAFADVNGNVQRFVLELDLF					
m515-1	TGIGKSGATVFGGVAGDVGGFDGVLQGGFGEVGGSTGAFAFADVNGNVQRLVLELDLF					
	250	260	270	280	290	300
	310	320	330	340	350	360
g515-1.pep	DFAQAHADALSERFAEVFGGGRARCFQVERAAAEEVEFGSGVVEQHNNLSWWSVVAFX					
m515-1	DFAQPHADALSQX					
	310					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1427>:

a515-1.seq

```

1  ATGGTTCAAA TAAAGTTGT GCGCGCCGCC GCGGTTGCCC GTGGTCTGCA
51  TTCCGAGTTT GCGCGCGCTG TAACTGCTGA GGAATAGCC TTCGACAATG
101 CCGTTTTGAA TCACGAAGCG CGGTGCGGTG GCAACGCCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCTCCGCC GGAGAGTGCG CCGACGAGGT GTCCGATAAG
301 ACCGCCCCGA ACAGTGCTAT CGAAGAGGAC GGGGTAGTTG CCTGTCGGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GCGGGCGGCG GGTTCGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CCGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATGCCGT TTTCGTCCGC GGCAACGACG CTCGAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CGGTGTGCGG CAAAACCGTA GGTGTGCGCG
551 TAAACGTATT GGTAATGGCC GGTTCGACC GCCGCGCCTT CGGAGTTTTC
601 GATGCGCTCA TCCTCGTTCA GGGCGGCTTG TTCGCATTGT TTTGCCAAGC
651 CGACGGCGCG TCCTGTATCC AAATCCCAT CGTGGTAAAG GTCGGGGTCG
701 CCGATGTGTT GCGCCATCAA CTCGGGGTCG GCAAGTCCGG CGCAACCGTC
751 TTCGGCGGTG TGGCGGGCGA TGTCGGCGGC GCGCGGACG GTGTCGCGCA
801 GGGCTTGTTT GGAGAAATCG GCGGTGCCGG CCGGCGCTTT GCGTTTGCCG
851 ACGTAAACGG TAATGTCCAG CGACTTGTC TGCTGAACT CGATTTGTTC
901 GATTCGCCCC AGCCGCACGC TGACGCTTG TCCCAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1428; ORF 515-1.a>:

a515-1.pep

```

1  MVQIKVVRAA GVARGLHSEF ARAVTAEEIA FDNAVLNHEA RCGGNAFRIK
51  IAAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERSA GECADEVSDK
101 TARNGGIEED GVVACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHAVFVG GNDAAAGNAV RALPVCCKTV GVAVNVLVMA GLHRRAFGVF
201 DALILVQGGF FALFCQADGG FRIQIPFVVK VGVADVLRHQ LGVGKSGATV
251 FGGVAGDVGG GADGVAQGLF GEIGGAGAAF AFADVNGNVQ RLVLLKLDLF
301 DFAQPHADAL SQ*

```

m515-1/a515-1 94.9% identity in 312 aa overlap

	10	20	30	40	50	60
a515-1.pep	MVQIKVVRAAGVARGLHSEFARA VTAEEIAFDNAVLNHEARCGGNAFRIKIAAAERAGDV					
m515-1	MVQIQVVRAAGVARGLHTEFARA VTAEEIAFDNAVLNHEARCGGNAFRIKIAAAERAGDV					
	10	20	30	40	50	60
	70	80	90	100	110	120
a515-1.pep	RFFAQVEEIGQDFFADAVDQETALAVERSAGECADEVSDKTARNNGGIEEDGVVACRDAAA					

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```

m515-1      RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDKTARNGGIEEDGVAACRDAAA
              70      80      90      100     110     120

              130     140     150     160     170     180
a515-1.pep  AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTV
              |||||
m515-1      AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTV
              130     140     150     160     170     180

              190     200     210     220     230     240
a515-1.pep  GVAVNVLVMAGLHRRAFGVFDALILVQGGFLALFCQADGGFRIQIPFVVKVGADVLRHQ
              |||||
m515-1      GVAVNVLVMAGLHRRAFGVFDALILVQGGFLALFCQADGGFRIQIPFVVKVGADVLRHQ
              190     200     210     220     230     240

              250     260     270     280     290     300
a515-1.pep  LGVGKSGATVFGGVAGDVGGGADGVAQGLFGEIGGAGAAFAFADVNGNVQRLVLLKLDLF
              |:|||||
m515-1      TGIGKSGATVFGGVAGDVGGGDFGLQGFFGEVVGSTGAFAFADVNGNVQRLVLELDF
              250     260     270     280     290     300

              310
a515-1.pep  DFAQPHADALSQX
              |||||
m515-1      DFAQPHADALSQX
              310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1429>:

```

g516.seq
1   atgttggttc gtaaaacgac cgccgccggt ttggcggcaa ccttgatact
51  gaacggctgt acgatgatgt tgcgggggat gaacaacccg gtcagccaaa
101 caatcacccg caaacacggt gacaaagacc aaatccgcgc cttcgggtgtg
151 gttgccgaag acaatgccca attggaaaag ggcagcctgg tgatgatggg
201 cgggaaatac tggttcgccg tcaatcccgga agattcggcg aagctgacgg
251 gccttttgaa ggccgggttg gacaagccct tccaaatagt tgaggatacc
301 ccgagctatg cccgccacca agccctgccc gtcaaattcg aagcgcccg
351 cagccagaat ttcagtaccg gaggtccttg cctgcgctat gataccggca
401 gacctgacga catcgccaag ctgaaacagc ttgagtttaa agcggtcaaa
451 ctcgacaatc ggaccattta cacgcgctgc gtatccgcca aaggcaaata
501 ctacgccacg ccgcaaaaac tgaacgccga ttatcatttt gagcaaagtg
551 tgcccgccga tatttattat acggttactg aaaaacatac cgacaaatcc
601 aagctgtttg gaaatatctt atatacgccc cccttgttga tattggatgc
651 ggccggccgc gtgctggtct tgcctatggc tctgattgca gccgcgaatt
701 cctcagacaa atga

```

This corresponds to the amino acid sequence <SEQ ID 1430; ORF 516.ng>:

```

g516.pep
1   MLFRKTTAAV LAATLILNGC TMMLRGMNPN VSQTITRKHV DKDQIRAFGV
51  VAEDNAQLEK GSLVMMGGKY WFAVNPEDSA KLTGLLKAGL DKPFQIVEDT
101 PSYARHQALP VKFEAPGSQN FSTGGCLCLRY DTGRPDIAK LKQLEFKAVK
151 LDNRTIYTRC VSAKGYYAT PQKLNADYHF EQSVPADIYY TVTEKHTDKS
201 KLFGNILYTP PLLILDAAA VLVLPALIA AANSSDK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1431>:

```

m516.seq
1   ATGTTGTTCC GTAAAACGAC CGCCGCCGTT TTGGCGGCAA CCTTGATGCT
51  GAACGGCTGT ACGTTGATGT TGTGGGGAAT GAACAACCCG GTCAGCGAAA
101 CAATCACCCG CAAACACGTT GACAAAGACC AAATCCGCGC CTCGGGTGTG
151 GTTGCCGAAG ACAATGCCCA ATTGGAAGG GGCAGCCTGG TGATGATGGG
201 CGGAAAATAC TGGTTCGTCG TCAATCCCGA AGATTCGGCG AAGCTGACGG
251 GCATTTTGAA GGCAGGGCTG GACAAACCCT TCCAAATAGT TGAGGATACC
301 CCGAGCTATG CTCGCCACCA AGCCCTGCCG GTCAAACCTG AATCGCCTGG
351 CAGCCAGAAT TTCAGTACCG AAGGCCTTTG CCTGCGCTAC GATACCGACA
401 AGCCTGCCGA CATCGCCAAG CTGAAACAGC TCGGGTTTGA AGCGGTCAAA
451 CTCGACAATC GGACCATTTA CACGCGCTGC GTATCCGCCA AAGGCAAATA

```

501 CTACGCCACA CCGCAAAAC TGAACGCCGA TTACCATTTT GAGCAAAGTG
 551 TGCTGCCGA TATTTATTAC ACGGTTACTG AAGAACATAC CGACAAATCC
 601 AAGCTGTTTG CAAATATCTT ATATACGCC CCCTTTTGA TACTGGATGC
 651 GCGGGCGCG GTACTGGCT TGCCTGCGG GGCTCTGGT GCGGTCGTGG
 701 ATGCCGCCCG CAAATGA

This corresponds to the amino acid sequence <SEQ ID 1432; ORF 516>:

m516.pep

1 MLFRKTTAAV LAATLMLNGC TLMLWGMNPN VSETITRKHV DKDQIRAFGV
 51 VAEDNAQLEK GSLVMMGGKY WFFVNPEDSA KLTGILKAGL DKPFQIVEDT
 101 PSYARHQALP VKLESPGSQN FSTEGCLRLY DTDKPADIAK LKQLGFEAVK
 151 LDNRTIYTRC VSAKGYYAT PQKLNADYHF EQSVPADIYY TVTEEHTDKS
 201 KLFANILYTP PFLILDAAGA VLALPAAALG AVVDAARK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 516 shows 90.0% identity over a 231 aa overlap with a predicted ORF (ORF 516.ng) from *N. gonorrhoeae*:

m516/g516

	10	20	30	40	50	60
m516.pep	MLFRKTTAAVLAATLMLNGCTLMLWGMNPNVSETITRKHVDKDQIRAFGVVAEDNAQLEK					
	: : :					
g516	MLFRKTTAAVLAATLILNGCTMLRGMNPNVSQTITRKHVDKDQIRAFGVVAEDNAQLEK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m516.pep	GSLVMMGGKYWFFVNPEDSAKLTGILKAGLDKPFQIVEDTPSYARHQALPVKLESPGSQN					
	: : :					
g516	GSLVMMGGKYWFAVNPEDSAKLTGILLKAGLDKPFQIVEDTPSYARHQALPVKFEAPGSQN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m516.pep	FSTEGCLRLYDTDKPADIAKLKQLGFEAVKLDNRTIYTRCVSAKGYYATPQKLNADYHF					
	: : :					
g516	FSTGGLCLRYDTGRPDDIAKLKQLEFKAVKLDNRTIYTRCVSAKGYYATPQKLNADYHF					
	130	140	150	160	170	180
	190	200	210	220	230	239
m516.pep	EQSVPADIYYTVTEEHTDKSKLFANILYTPPFLILDAAGAVLALPAAALGAVVDAARK					
	: : :					
g516	EQSVPADIYYTVTEKHTDKSKLFGNILYTPPLILDAAGAVLALPAAALGAVVDAARK					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1433>:

a516.seq

1 ATGTTGTTCC GTAAAACGAC CGCCGCCGTT TTGGCGGCAA CCTTGATGTT
 51 GAACGGCTGT ACGGTAATGA TGTGGGGTAT GAACAGCCCG TTCAGCGAAA
 101 CGACCGCCCG CAAACACGTT GACAAGGACC AAATCCGCGC CTTCCGGTGTG
 151 GTTGCCGAAG ACAATGCCCA ATTGGAAAAG GGCAGCCTGG TGATGATGGG
 201 CGGGAAATAC TGGTTCGTCG TCAATCCTGA AGATTCGCGC AAGCTGACGG
 251 GCATTTTGAA GGCCGGGTG GACAAGCAGT TTCAAATGGT TGAGCCCAAC
 301 CCGCGCTTTG CCTACCAAGC CCTGCGGTC AACTCGAAT CGCCGCCAG
 351 CCAGAATTTT AGTACCGAAG GCCTTGCCT GCGCTACGAT ACCGACAGAC
 401 CTGCCGACAT CGCCAAGCTG AACAGCCTTG AGTTTGAAGC GGTGGAAGTC
 451 GACAATCGGA CCATTTACAC GCGCTGCGTC TCCGCCAAAG GCAAATACTA
 501 CGCCACACCG CAAAACTGA ACGCCGATTA TCATTTTGAG CAAAGTGTGC
 551 CTGCCGATAT TTATTACACG GTTACGAAAA AACATACCGA CAAATCCAAG
 601 TTGTTTGAAG ATATTGCATA TACGCCACC ACGTTGATAC TGGATGCCGT
 651 GGGCGCGGTG CTGGCCTTGC CTGTCGCGGC GTTGATTGCA GCCACGAATT
 701 CCTCAGACAA ATGA

This corresponds to the amino acid sequence <SEQ ID 1434; ORF 516.a>:

a516.pep

773

```

1 MLFRKTTAAV LAATLMLNGC TVMMWGMNSP FSETTARKHV DKDQIRAFGV
51 VAEDNAQLEK GSLVMMGGKY WVVNPNEDSA KLTGILKAGL DKQFQMVEPN
101 PRFAYQALPV KLESPASQNF STEGLCLRYD TDRPADIACL KQLEFEAVEL
151 DNRTIYTRCV SAKGKYATP QKLNADYHFE QSVADIYYT VTKKHTDKSK
201 LFENIAYTPT TLILDAVGAV LALPVAALIA ATNSSDK*

```

m516/a516 86.1% identity in 238 aa overlap

```

              10      20      30      40      50      60
m516.pep      MLFRKTTAAVLAATLMLNGCTLMLWGMNPNVSETITRKHVDDKDQIRAFGVVAEDNAQLEK
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a516           MLFRKTTAAVLAATLMLNGCTVMMWGMNSPFSETTARKHVDDKDQIRAFGVVAEDNAQLEK
              10      20      30      40      50      60

              70      80      90      100     110     120
m516.pep      GSLVMMGGKYWVVNPNEDSAKLTGILKAGLDKPFQIVEDTPSYARHQALPVKLESPGSON
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a516           GSLVMMGGKYWVVNPNEDSAKLTGILKAGLDKQFQMVEPNPRFA-YQALPVKLESPASQN
              70      80      90      100     110

              130     140     150     160     170     180
m516.pep      FSTEGCLCLRYDTPADIAKLKQLGFEAVKLDNRTIYTRCVSAKGKYATPQKLNADYHF
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a516           FSTEGCLCLRYDTPADIAKLKQLEFEAVELDNRTIYTRCVSAKGKYATPQKLNADYHF
              120     130     140     150     160     170

              190     200     210     220     230     239
m516.pep      EQSVADIYYTVTEEHTDKSKLFANILYTPPFLILDAAGAVLALPAAALGAVVDAARKX
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a516           EQSVADIYYTVTKKHTDKSKLFENIAYTPTTLILDAVGAVLALPVAALIAATNSSDKX
              180     190     200     210     220     230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1435>:

```

g517.seq
1 atgcatcggg ttccagacgg cattggagtg tcagtcgtgt tctgccgatt
51 cgtaggcttc gacgattttt tgcaccagag gatgccggac aacgtcttcg
101 ccggtgaagg tatggaaata cagtcctgcc acgccgtgca gtttctcagc
151 tgcgtctttc aatccccgatt tgatgttttt gggcaggctg atttggctgg
201 tgcgcgggt aatgacggct ttcgcgccga agccgatgcg ggtcaggaac
251 attttcattt gtccggcgct ggtgttttgc gcttcgtcga ggatgatgta
301 tgcgcgggt agcgtcctgc cgcgcatata ggcgagcggg gcgatttcaa
351 tcaggccttt ttcaatcagc ttggttacac ggtcaaagcc catcagggtca
401 tagagggcat cataaagcgg acggaggtag ggtcgactt tttgggtcag
451 gtctccgggc aggaagccca gtttctcacc ggcttcgacg gcaggccgaa
501 ctaa

```

This corresponds to the amino acid sequence <SEQ ID 1436; ORF 517.ng>:

```

g517.pep
1 MHRVSDGIGV SVVFCRFVGF DDFLHQMPD NVFAGEGMEI QSCHAVQFLT
51 CVFQSRFDVF GQVDLAGVAG NDGFRAEADA GQEHFHLFGR GVLRFVEDDV
101 CAVERPAAHI GERGDFNQAF FNQLGYTVKA HQVIEGIIKR TEVGVDFLQG
151 VSGQEAQFLT GFDGRPN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1437>:

```

m517.seq
1 ATGCATCGGG TTTCAGACGG CATTGGAATG TCAGTCGTGT TCTGCCGATT
51 CGTAGGCTTC GACGATTTT TGCACCAAAG GATGCCGGAC AACGTCTTCG
101 CCGGTAAAGG TGTGAAATA CAGCCCTTCC ACGTTGTGCA GTTTCTCACG
151 CGCATCTTTT AATCCCCGATT TGATGTTTTT GGGCAGGTGCG ATTTGGCTGG
201 TGTCGCCGGT AATGACGGCT TTCGCGCCGA AGCCGATGCG GGTCAGGAAC
251 ATTTTCATTT GTTCGGCGGT GGTGTTTTGC GCTTCGTCGA GGATGATGTA
301 TGCGCCGTTG AGCGTCCTGC CGCGCATATA GGCAGCGGG GCGATTTCAA
351 TCAGGCCTTT TTCAATCAGC TTGTTTACAC GGTCAAAGCC CATCAGGTCA
401 TAGAGGGCAT CATAAAGCGG ACGAAGGTAG GGATCGACTT TCTGGGTCAG

```

451 GTCTCCGGGC AGGAAGCCCA GTTCTCGCC GGCTTCGACG GCTGgGCGCA
501 CTAA

This corresponds to the amino acid sequence <SEQ ID 1438; ORF 517>:

m517.pep
1 MHRVSDGIGM SVVFCRFVGF DDFLHQMPD NVFAGKGVEI QPFHVQFLT
51 RIFXSRFDVF GOVDLAGVAG NDGFRAEADA GOEHFHLFGR GVLRFVEDDV
101 CAVERPAAHI GERGDFNQAF FNQLGYTVKA HQVIEGIIKR TKVGIDFLGQ
151 VSGQEAQFLA GFDGWAH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 517 shows 92.7% identity over a 164 aa overlap with a predicted ORF (ORF 517.ng) from *N. gonorrhoeae*:

m517/g517

m517.pep	10	20	30	40	50	60
	MHRVSDGIGMSVVFCRFVGFDDFLHQMPD NVFAGKGVEIQPFHVQFLTRIFXSRFDVF					
	: : : : :					
g517	10	20	30	40	50	60
	MHRVSDGIGMSVVFCRFVGFDDFLHQMPD NVFAGEGMEIQSCHAVQFLTCVFQSRFDVF					
m517.pep	70	80	90	100	110	120
	GOVDLAGVAGNDGFRAEADAGOEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGDFNQAF					
	: : : : :					
g517	70	80	90	100	110	120
	GOVDLAGVAGNDGFRAEADAGOEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGDFNQAF					
m517.pep	130	140	150	160		
	FNQLGYTVKAHQVIEGIIKRTKVGIDFLGQVSGQEAQFLAGFDGWAH					
	: : : :					
g517	130	140	150	160		
	FNQLGYTVKAHQVIEGIIKRTKVGIDFLGQVSGQEAQFLTGFDGRPN					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1439>:

a517.seq
1 ATGCATCGGG TTTCAGACGG CATTGGAATG TCAGTCGTGT TCTGCCGATT
51 CGTAGGCTTC GACGATTTT TGCACCAAAG GATGCCGGAC AACGTCTTCG
101 CCGGTAAAGG TGTGGAATA CAGCCCTTCC ACGCCGTGCA GTTCTCACG
151 CGCATCTTTT AATCCCGATT TGATGTTTTT GGGCAGGTCG ATTTGGCTGG
201 TGTCGCCGGT AATGACGGCT TTCGCGCCGA AGCCGATGCG GGTACAGAAC
251 ATTTTCATT GTTCGGGCGT GGTGTTTTGC GCTTCGTGCA GGATGATGTA
301 TGCGCCGTTG AGCGTCCTGC CGCGCATATA GGCGAGCGGG GCAATCTCAA
351 TCAGACCTTT TTCAATCAGC TTGGTGACAC GGTCAAGCC CATCAGGTCA
401 TAGAGGCGAT CATAAGCGG ACGAAGGTAG GGATCGACTT TCTGGGTCAG
451 GTCACCGGGC AGAAAACCCA GTTCTCGCC GGCTTCGACG GCAGGCCGCA
501 CTAA

This corresponds to the amino acid sequence <SEQ ID 1440; ORF 517.a>:

a517.pep
1 MHRVSDGIGM SVVFCRFVGF DDFLHQMPD NVFAGKGVEI QPFHAVQFLT
51 RIF*SRFDVF GOVDLAGVAG NDGFRAEADA GOEHFHLFGR GVLRFVEDDV
101 CAVERPAAHI GERGNLQTF FNQLGDTVEA HQVIEGIIKR TKVGIDFLGQ
151 VTGQKTQFLA GFDGRPH*

m517/a517 93.4% identity in 167 aa overlap

m517.pep	10	20	30	40	50	60
	MHRVSDGIGMSVVFCRFVGFDDFLHQMPD NVFAGKGVEIQPFHVQFLTRIFXSRFDVF					
	: : : : :					
a517	10	20	30	40	50	60
	MHRVSDGIGMSVVFCRFVGFDDFLHQMPD NVFAGKGVEIQPFHAVQFLTRIFXSRFDVF					
m517.pep	70	80	90	100	110	120
	GOVDLAGVAGNDGFRAEADAGOEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGDFNQAF					
	: : : : :					
a517	70	80	90	100	110	120
	GOVDLAGVAGNDGFRAEADAGOEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGNLQTF					

	70	80	90	100	110	120
m517.pep	130	140	150	160		
	FNQLGTYVKAHQVIEGIIKRTKVGIDFLGQVSGQEAQFLAGFDGWAHX					
a517	130	140	150	160		
	FNQLGDTVEAHQVIEGIIKRTKVGIDFLGQVTGQKTQFLAGFDGRPHX					

```
g518.seq
1  atgacgtttt  cggcgggcaaa  gctcaacatt  tcggcactga  tgttgtgtct
51  ttcggcagga  atgaccgttt  tactttccgc  ttttttactg  ctccgaccgg
101 aaggcagcat  cttattcaac  cattttttca  gcataaatat  tctgaccgga
151 agagcggcat  ctccacgggc  aaccgtgttc  agactgcata  aggcggtacg
201 attccacaag  atgcgaaaaa  ccataagcaa  aatgcgtaga  aactacgcgg
251 tccgaattac  cgcgcctcct  cgggcggcaa  cgcttcatta  taacagattg
301 ccccttaaaa  aatcagaccc  tgcttttgtg  cgggagttct  aaatttga
```

g518.pep
1 MTFSAAKLNI SALMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR
51 RAASPRATVF RLHQAVRFHK MPKTISKMR R NYAVRITPPP RAATLHYNRL
101 PLKKSDFAFV AESEI*

```
m518.seq
1  ATGACGTTTT CGGCGGCAAA GCTCAACATT TCGGCACGGA TGTGTGTCT
51  TTCGGCAGGA ATGACCGTTT TACTTTCCGC TTTTCTACTG CTCCGACCGG
101 AAGGCAGCAT CTTATTCAAC CATTTTTCAT GCATAAATAT TCTGACCCGG
151 AGAGCGGCAT CTCACACGGC AACCGTGTTT AGACGGCATC AGGCGCGGTT
201 TGCAAGATGC CGTACCATAA ACAAAGGCGT TAGAAACTAC GCGCTCCGAA
251 TCACGCCGCC CTCGCG.GCG GCAACGCGTC ATTATAACAG ATTGCCCTCC
301 GCGGCAGGCT TAGTGCGGCG GGAGCGCCGC CGTTGCGCAG TAATATTGTC
351 TAACGGGAGG AAAAAATCAG ACCCTGCTTT TGTGGCAGAG TCTGAAATTT
401 GA
```

m518.pep

1	MTFSAAKLNI	SARMLCLSAG	MTVLLSAFLI	LRPEGSILFN	HFSSINILTR
51	RAASPQATVF	RRHQARFARC	RTINKRRRNY	AVRITPPSXA	ATRHYNRLPS
101	AAGLVRRERR	RCAVILSNGR	KKSDPAFVAE	SEI*	

Homology with a predicted ORF from *N. gonorrhoeae*

```
m518/g518
```

```
m518.pep      MTFSAAKLNISARMLCLSAGMTVLLSAFLLLRRPEGSILFNHFFSINILTTRRAASFPQATVF  
               |||||              |||||              |||||              |||||  
g518           MTFSAAKLNISALMCLCSAGMTVLLSAFLLLRRPEGSILFNHFFSINILTTRRAASPRATVF  
               10          20          30          40          50          60
```

```
m518.pep      RRHQ-A-RFARC-RTINKRRRNYAVRITPPSXAAATHRYNRLPSAAGLVRERRRCVILSN  
               |   |   | :    : ||:| |||||       ||   |||||  
g518           RLHQAVRFHKMPKTISKMRNRNYAVRITPPFRAATLHYNRLPL-----  
               70          80          90          100
```

```
m518.pep      GRKKSDPAFVAESEI  
               |||||  
g518           --KKSDPAFVAESEI  
               110
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1445>:

```
a518.seq
1  ATGACGTTTT CGGCGGCAAA GCTCAACATT TCGGCACGGA TGTGTGTCT
51  TTCGGCAGGA ATGACCGTTT TACTTTCCGC TTTTCTACTG CTCCGACCGG
101 AAGGCAGCAT CTTATTCAAC CATTTTTCAT GCATAAATAT TCTAACCCGA
151 AGAGCGGCAT CTCCACGGGC AACCGTGTTC AGACGGCATC AGGCGGTACG
201 ATTCCGCAAG ATGCCGACCA TAAACAAAAG GCGTAGAAAC TACGCCGTCC
251 GAATCAGGCC GTCCTCG.CG GCGGCAACGC GTCATTATAA CAGATTGCCC
301 TCC.....
351 .....AAAAAAT CAGACCCTGC TTTGTGGCA GAGTCTGAAA
401 TTGTA
```

This corresponds to the amino acid sequence <SEQ ID 1446; ORF 518.a>:

```
a518.pep
1  MTFSAAKLNI SARMLCLSG MTVLLSAFL LRPESILFN HFFSINILTR
51  RAASPRATVF RRHQAVRFRK MPTINKRRRN YAVRITPSSX AATRHYNRLP
101 S..... .KKSDPAFVA ESEI*
```

m518/a518 79.9% identity in 134 aa overlap

	10	20	30	40	50	60
m518.pep	MTFSAAKLNISARMLCLSGMTVLLSAFL LRPESILFNHFFSINILTRRAASPOATVF					
a518	MTFSAAKLNISARMLCLSGMTVLLSAFL LRPESILFNHFFSINILTRRAASPRATVF					
	10	20	30	40	50	60
	70	80	90	100	110	119
m518.pep	RRHQA-RFARCTINKRRRNYAVRITPPSXAATRHYNRLPSAAGLVRRERRRCVILSNG					
	:					
a518	RRHQAVRFRKMPTINKRRRNYAVRITPSSXAATRHYNRLPS-----					
	70	80	90	100		
	120	130				
m518.pep	RKKSDPAFVAESEIX					
a518	-KKSDPAFVAESEIX					
		110				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1447>:

```
g519.seq
1  atggaatttt tcattatctt gttggcagcc gtcgccgttt tcggcttcaa
51  atcctttgtc gtcaccccc agcaggaagt ccacgttgtc gaaaggctcg
101 ggcgtttcca tcgcgccttg acggccggtt tgaatatttt gattcccttt
151 atcgaccgcg tcgcctaccg ccattcgctg aaagaaatcc ctttagacgt
201 acccagccag gtctgcatca cgcgcgataa tacgcaattg actgttgacg
251 gcatcatcta tttccaagta accgatccca aactcgcttc atacggttcg
301 agcaactaca ttatggcaat taccagctt gcccaaacga cgctgcgttc
351 cgttatcggg cgtatggagt tggacaaaac gtttgaagaa cgcgacgaaa
401 tcaacagtac cgtcgtctcc gccctcgatg aagccgcgcg ggcttggggg
451 gtgaaagtcc tccgttacga aatcaaggat ttggttcgcg cgcaagaaat
501 ctttcgcgca atgcaggcac aaattaccgc cgaacgcgaa aaacgcgccc
551 gtattgccga atccgaaggc cgtaaaatcg aacaaatcaa ccttgccagt
601 ggtcagcgtg aagccgaaat ccaacaatcc gaaggcgagg ctcaggctgc
651 ggtcaatgcg tccaatgccg agaaaatcgc ccgcatcaac cgcgccaaag
701 gcgaagcgga atccctgcgc cttgttgccg aagccaatgc cgaagccaac
751 cgtcaaattg ccgcccct tcaaacccaa agcggggcg atgcggtcaa
801 tctgaagatt gcgggacaat acgttaccgc gttcaaaaat cttgccaaag
851 aagacaatac gcggattaag cccgccaaag ttgccgaaat cgggaaccct
901 aattttcggc ggcatgaaaa attttcgccga gaagcaaaaa cggccaaata
951 a
```

This corresponds to the amino acid sequence <SEQ ID 1448; ORF 519.ng>:

```
g519.pep
1  MEFFIILLAA VAVFGFKSFV VIPQQEVHV ERLGRFHRAL TAGLNILIPF
51  IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
```

101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
 151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS
 201 GQREAEIQQS EGEAQA AVNA SNAEKIARIN RAKGEAESLR LVAEANAEAN
 251 RQIAAALQTQ SGADAVNLKI AGQYVTAFKN LAKEDNTRIK PAKVAEIGNP
 301 NFRRHEKFSP EAKTAK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1449>:

m519.seq (partial)
 1 ..TCCGTATCG GCGTATGGA GTTGGACAAA ACGTTTGAAG AACGCGACGA
 51 AATCAACAGT ACTGTTGTTG CGGCTTTGGA CGAGGCGGCC GGGgCTTgGG
 101 GTGTGAAGGT TTTGCGTTAT GAGATTAAAG ACTTGTTCC GCCGCAAGAA
 151 ATCCTTCGCT CAATGCAGGC GCAAATTACT GCCGAACGCG AAAAACGCGC
 201 CCGTATCGCC GAATCCGAAG GTCGTAATAAT CGAACAATC AACCTTGCCA
 251 GTGGTCAGCG CGAAGCCGAA ATCCAACAAT CCGAAGGCGA GGCTCAGGCT
 301 GCGGTCAATG CGTCAAATGC CGAGAAAATC GCCCGCATCA ACCGCGCCAA
 351 AGGTGAAGCG GAATCCTTGC GCCTTGTTGC CGAAGCCAAT GCCGAAGCCA
 401 TCCGTCAAAT TGCCGCCGCC CTTCAAACCC AAGGCGGTGC GGATGCGGTC
 451 AATCTGAAGA TTGCGGAACA ATACGTCGCT GCGTTCAACA ATCTTGCCAA
 501 AGAAAGCAAT ACGCTGATTA TGCCCGCCAA TGTTGCCGAC ATCGGCAGCC
 551 TGATTCTGC CCGTATGAAA ATTATCGACA GCAGCAAAAC CGCCAAaTAA

This corresponds to the amino acid sequence <SEQ ID 1450; ORF 519>:

m519.pep (partial)
 1 ..SVIGRMELDK TFEERDEINS TVVAALDEAA GAWGVKVLRY EIKDLVPPQE
 51 ILRSMQAQIT AEREKRARIA ESEGRKIEQI NLASGQREAE IQQSEGEAQA
 101 AVNASNAEKI ARINRAKGEA ESLRLVAEAN AEAIRQIAAA LQTQGGADAV
 151 NLKIAEQYVA AFNNLAKESN TLIMPANVAD IGSLISAGMK IIDSSKTAK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 519 shows 87.5% identity over a 200 aa overlap with a predicted ORF (ORF 519.ng) from *N. gonorrhoeae*:

m519/g519

m519.pep				10	20	30
				SVIGRMELDKTFEERDEINSTVVAALDEAA		
g519	YFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIGRMELDKTFEERDEINSTVVSALDEAA					
	90	100	110	120	130	140
m519.pep		40	50	60	70	80
		GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLASGQREAE				
g519		GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLASGQREAE				
		150	160	170	180	190
m519.pep		100	110	120	130	140
		IQQSEGEAQA AVNASNAEKIARINRAKGEAESLRLVAEANAEAIRQIAAALQTQGGADAV				
g519		IQQSEGEAQA AVNASNAEKIARINRAKGEAESLRLVAEANAEANRQIAAALQTQSGADAV				
		210	220	230	240	250
m519.pep		160	170	180	190	200
		NLKIAEQYVA AFNNLAKESNTLIMPANVADIGSL-ISAGMKIIDSSKTAK				
g519		NLKIAGQYVTAFKNLAKEDNTRIKPAKVAEIGNPNFRRHEKFSP EAKTAK				
		270	280	290	300	310

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1451>:

a519.seq
 1 ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
 51 ATCCTTTGTT GTCATCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
 101 GCGGTTTCCA TCGCGCCCTG ACGGCCGTT TGAATATTTT GATTCCCTTT
 151 ATCGACCGCG TCGCTACCG CCATTCGCTG AAAGAAATCC CTTAGACGT

```

201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTCG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TCGGTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAGCGCG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCATGCG TCAAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCGCCCT TCAAACCCAA GCGGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCCG GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAT TATCGACAGC AGCAAACCG CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1452; ORF 519.a>:

a519.pep

```

1  MEFFIILLAA VVVFGRKSFV VIPQEVHVV ERLGRFHRAL TAGLNILIPF
51  IDRVAYRHSI KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEGRKIEQINLAS
201 GQREAEIQQS EGEAQAQVNA SNAEKIARIN RAKGEAESLR LVAEANAIAI
251 RQIAAALQTO GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

m519/a519 99.5% identity in 199 aa overlap

```

                                     10      20      30
m519.pep                               SVIGRMELDKTFEERDEINSTVVAALDEAA
a519      YFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIGRMELDKTFEERDEINSTVVSALDEAA
           90      100      110      120      130      140

                                     40      50      60      70      80      90
m519.pep      GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLASGQREAE
a519      GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLASGQREAE
           150     160     170     180     190     200

                                     100     110     120     130     140     150
m519.pep      IQQSEGEAQAQVNASNAEKIARINRAKGEAESLRLVAEANAIAIRQIAAALQTOGGADAV
a519      IQQSEGEAQAQVNASNAEKIARINRAKGEAESLRLVAEANAIAIRQIAAALQTOGGADAV
           210     220     230     240     250     260

                                     160     170     180     190     200
m519.pep      NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
a519      NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
           270     280     290     300     310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1453>:

g519-1.seq

```

1  ATGGAATTTT TCATTATCTT GTTGGCAGCC GTCGCCGTTT TCGGCTTCAA
51  ATCCTTTGTC GTCATCCCCC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GGCCTTTCCA TCGCGCCCTG ACGGCCGTTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCTACCG CCATTGCGTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGGATAA TACGCAATTG ACTGTTGACG
251 GCATCATCTA TTTCCAAGTA ACCGATCCCA AACTCGCCTC ATACGGTTCG
301 AGCAACTACA TTATGGCAAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGTAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG GGCTTGGGGT
451 GTGAAAGTCC TCCGTTACGA AATCAAGGAT TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCGCA ATGCAGGCAC AAATTACCGC CGAACGCGAA AAACGCGCCC
551 GTATTGCCGA ATCCGAAGGC CGTAAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAGCGTG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCATGCG TCCAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GCGAAGCGGA ATCCTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCGCCCT TCAAACCCAA GCGGGGCGG ATGCGGTCAA

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801 TCTGAAGATT GCGGAACAAT ACGTAGCCGC GTTCAACAAT CTTGCCAAAG
 851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
 901 ATTTCTGCCG GCATGAAAAT TATCGACAGC AGCAAACCG CCAAATAA

This corresponds to the amino acid sequence <SEQ ID 1454; ORF 519-1.ng>:

g519-1.pep

1 MEFFIILLAA VAVFGFKSFV VIPQEVHV ERLGRFHRAL TAGLNILIPF
 51 IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
 101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
 151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS
 201 GQREAEIQQS EGQAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAEAI
 251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
 301 ISAGMKIIDS SKTAK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1455>:

m519-1.seq

1 ATGGAATTTT TCATTATCTT GTTGGTAGCC GTCGCCGCTTT TCGGTTTCAA
 51 ATCCTTTGTT GTCATCCAC AACAGGAAGT CCACGTTGTC GAAAGGCTGG
 101 GCGGTTTCCA TCGCGCCCTG ACGGCGGTT TGAATATTTT GATTCCCTTT
 151 ATCGACCGCG TCGCTACCG CCATTGCGTG AAAGAAATCC CTTTAGACGT
 201 ACCCAGCCAG GTCTGCATCA CGCGGACAA TACGCAGCTG ACTGTTGACG
 251 GCATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTTCG
 301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
 351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
 401 TCAACAGTAC TGTGTGTCG GCTTTGGACG AGGCGGCCGG GGCTTGGGGT
 451 GTGAAGGTTT TGCGTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
 501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC CGAACGCGAA AAACGCGCCC
 551 GTATCGCCGA ATCCGAAGGT CGTAAAATCG AACAAATCAA CCTTGCCAGT
 601 GGTGAGCGG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
 651 GGTCATGCG TCAAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
 701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
 751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GCGGTGCGG ATGCGGTCAA
 801 TCTGAAGATT GCGGAACAAT ACGTCGCTGC GTTCAACAAT CTTGCCAAAG
 851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
 901 ATTTCTGCCG GTATGAAAAT TATCGACAGC AGCAAACCG CCAAATAA

This corresponds to the amino acid sequence <SEQ ID 1456; ORF 519-1>:

m519-1.

1 MEFFIILLVA VAVFGFKSFV VIPQEVHV ERLGRFHRAL TAGLNILIPF
 51 IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
 101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVA ALDEAAGAWG
 151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
 201 GQREAEIQQS EGQAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAEAI
 251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
 301 ISAGMKIIDS SKTAK*

m519-1/g519-1 99.0% identity in 315 aa overlap

	10	20	30	40	50	60
g519-1.pep	MEFFIILLAAVAVFGFKSFVVIPQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL					
m519-1	MEFFIILLVAVAVFGFKSFVVIPQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL					
	10	20	30	40	50	60
g519-1.pep	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
m519-1	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
	70	80	90	100	110	120
g519-1.pep	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMQAQITAERE					
m519-1	RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE					
	130	140	150	160	170	180
g519-1.pep	KRARIAESEGRKIEQINLASGQREAEIQQSEGEQAQAAVNASNAEKIARINRAKGEAESLR					
m519-1	KRARIAESEGRKIEQINLASGQREAEIQQSEGEQAQAAVNASNAEKIARINRAKGEAESLR					
	190	200	210	220	230	240
g519-1.pep	KRARIAESEGRKIEQINLASGQREAEIQQSEGEQAQAAVNASNAEKIARINRAKGEAESLR					
m519-1	KRARIAESEGRKIEQINLASGQREAEIQQSEGEQAQAAVNASNAEKIARINRAKGEAESLR					

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m519-1      KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
              190      200      210      220      230      240
              250      260      270      280      290      300
g519-1.pep  LVAEANAEEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              |||||
m519-1      LVAEANAEEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              250      260      270      280      290      300
              310
g519-1.pep  ISAGMKIIDSSKTAKX
              |||||
m519-1      ISAGMKIIDSSKTAKX
              310

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1457>:

```

a519-1.seq
1  ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
51  ATCCTTTGTT GTCATCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GCGGTTTCCA TCGCGCCCTG ACGGCCGGTT TGAATATTTT GATTCCCTTT
151 ATCGACCCGG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCTC ATACGGTTCG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TGCGTTATGA GATTAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAAGCGC AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAATGCGC AGAAAATCG CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTGTGTCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCGCCCT TCAAACCAA GGCGGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCCGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAAT TATCGACAGC AGCAAAACCG CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1458; ORF 519-1.a>:

```

a519-1.pep.
1  MEFFIILLAA VVVFQFKSFV VIPQQEVHV ERLGRFHRAL TAGLNILIPF
51  IDRVAIRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEGR KIEQINLAS
201 QQREAEIQQS EGAEQAQAVNA SNAEKIARIN RAKGEAESLR LVAEANAEEAI
251 RQIAAALQQT GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

m519-1/a519-1 99.0% identity in 315 aa overlap

```

              10      20      30      40      50      60
a519-1.pep  MEFFIILLAAVVVFQFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
              |||||
m519-1      MEFFIILLVAVAVFQFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
              10      20      30      40      50      60
              70      80      90      100     110     120
a519-1.pep  KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
              |||||
m519-1      KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
              70      80      90      100     110     120
              130     140     150     160     170     180
a519-1.pep  RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAITAERE
              |||||
m519-1      RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAITAERE
              130     140     150     160     170     180
              190     200     210     220     230     240
a519-1.pep  KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
              |||||

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m519-1      KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
              190      200      210      220      230      240
              250      260      270      280      290      300
a519-1.pep  LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              |||||
m519-1      LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              250      260      270      280      290      300
              310
a519-1.pep  ISAGMKIIDSSKTAKX
              |||||
m519-1      ISAGMKIIDSSKTAKX
              310

```

Expression of ORF 519

The primer described in Table 1 for ORF 519 was used to locate and clone ORF 519. ORF 519 was cloned in pET and pGex vectors and expressed in *E. coli* as above described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 4A shows the results of affinity purification, and Figure 4B shows the expression in *E. coli*. Purified Nis-fusion protein was used to immunize mice whose sera were used for ELISA (positive result), FACS analysis (Figure 4C), western blot (Figure 1E), and a bactericidal assay (Figure 4D). These experiments confirm that 519 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 519 are provided in Figure 8. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 519 and the amino acid sequence encoded thereby as provided herein.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1459>:

```

g520.seq
1  atgcctgctc ttctttcaat acgtcgggca aacgcgctgc ctttttcgcg
51  catttcggaa aggatgaagt tgctggtgcc gttaataatg ccggcgatgg
101 atttaacctt gtttgccgcc aaaccttcgc gcacggcttt gatgattggg
151 ataccgcccg ctactgccgc ttcaaattgg acgatgacgt tttgttttc
201 cgccagcggg aagatttcgt tgccgtattc ggcgagcagt tttttgttgg
251 cggtaacgat gtgtttgccg ttttcaatgg ctttcaacac cgcttctttg
301 gcaatgcccg tgccgccgaa caattcgacc aagacatcga cgtctttacg
351 cgcaaacagt tcgaacggat cttttgacaa gggcgggcga cgggccgatt
401 ttggcgggct ttttcttcgc ttaagtcgca catggcagaa atacggattt
451 cgcgcccaca gcggcgggaa atttctctcg cgtgtccccg caacacggca
501 gccgcaccgc cgccgaccgt acctaacgct aaaagaccga tgtttactgg
551 cttcattgtg tctccttgta agccgactga aatgtaaata ttga

```

This corresponds to the amino acid sequence <SEQ ID 1460; ORF 520.ng>:

```

g520.pep
1  MPALLSIRRA NALPFSRISE RMKLLVPLIM PAMDILIFAA KPSRTALMIG
51  IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCCLP FSMAFNTASL
101 AMPVPPNNST KTSTSLRANS SNGSFDKGG RADFGGLFLR LSRTWQKYGF
151 RAPSGGKFPL RCPATRQPHR RRPYLSLKDR CLLASLCLLV SRLKCKY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1461>:

```

m520.seq
1  ATGCCTGCGC TTCTTTCAGT ACATCG.GCA AACGCGCTGC CTTTTTCGCG
51  CATTTCGGRk AGGATGAAGT TGCTGGTGCC GTTAATAATG CCGGCGATGG
101 ATTTAATCCT GTTTGCCGCC AAACCTTCGC GCAGGGCTTT GATGATTGGG
151 ATACCGCCCG CTACTGCCGC TTCAAATTGG ACGATGACGT TTTGTTTTTC
201 CGCCAGCGGG AAGATTTCGT TGCCGTATTC GGCGAGCAGT TTTTGTGTGG
251 CGGTAACGAT GTGTTTGCCG TTTTCAATGG CTTTCAACAC CGCATCTTTG

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301 GCAATGCCGG TACCGCCGaa CAATTCGACG ACGACATCGA CGTCTTCACG
351 TGCGACCACT TCGAACGGAT CTTTGACAAA GGCTGc .CGG ACGGGCAGGT
401 TTGTCGGGCT TTTTCTTCAC TCAAATCGCA CACGGCAGAA ATACGGATTT
451 CGCGCCCCAA GCGACGGGAA ATTCCTCCG CGTTGTCCCG CAACACGGCA
501 GCCGTACCGC CGCCGACCGT ACCCAAACCT AAAAGACCGA TGTTTACTGG
551 CTTCAATTGTG TCTCCTTGTA AGCCGACTGA AATGTAAATA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1462; ORF 520>:

```

m520.pep
  1 MPALLSVHXA NALPFSRISX RMKLLVPLIM PAMDLILFAA KPSRRALMIG
 51 IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCLP FSMAFNTASL
101 AMPVPPNNST TTSTSSRATS SNGSLTKAXR TGRFVGLFLH SNRTRQKYGF
151 RAPSDGKFPP RCXATRQPYR RRPYPNLKDR CLLASLCLLV SRLKCKY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 520 shows 87.3% identity over a 197 aa overlap with a predicted ORF (ORF 520.ng) from *N. gonorrhoeae*:

```

m520/g520

      10      20      30      40      50      60
m520.pep  MPALLSVHRANALPFSRISXRMKLLVPLIMPAMDLILFAAKPSRRALMIGIPPATAASNW
          |||||::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g520       MPALLSIRANALPFSRISERMKLLVPLIMPAMDLILFAAKPSRTALMIGIPPATAASNW
          10      20      30      40      50      60

      70      80      90     100     110     120
m520.pep  TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATS
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g520       TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTKTSTSLRANS
          70      80      90     100     110     120

      130     140     150     160     170     180
m520.pep  SNGSLTKAARTGRFVGLFLHSNRTRQKYGFRAPSDGKFPPRCXATRQPYRRRPYPNLKDR
          |||||::||| :| |||||::||| ||||| ||||| ||||| ||||| :|||
g520       SNGSFDKGGRRADFGGLFLRLSRTWQKYGFRAPSGGKFPLRCPATRQPHRRRPYLSLKDR
          130     140     150     160     170     180

      190
m520.pep  CLLASLCLLVSRKCKY
          ||||| ||||| ||||| |||||
g520       CLLASLCLLVSRKCKY
          190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1463>:

```

a520.seq
  1 ATGCCTGCGC TTCTTTCAGT ACATCGG.CA AACGCGCTGC CTTTTTCGCG
 51 CATTTCCGAG AGGATGAAGT TGCTGGTGCC GTTAATAATG CCGGCGATGG
101 ATTTAATCCT GTTTGCCGCC AAACCTTCGC GCAGGGCTTT GATGATTGGG
151 ATACCGCCCG CTACTGCCGC TTCAAATTGG ACGATGACGT TTTGTTTTTC
201 CGCCAGCGGG AAGATTTCTG TGCCGTATTC GGCGAGCAGT TTTTGTGTTGG
251 CGGTAACGAT GTGTTTGCCG TTTTCAATGG CTTTCAACAC CGCATCTTTG
301 GCAATGCCGG TACCGCCGAA CAATTCGACG ACGACATCGA CGTCTTCACG
351 TGCGACCACT TCGAACGGAT CTTTGACAAA GGCTG. .CGG ACGGGCAGGT
401 TTGTCGGGCT TTTTCTTCAC TCAAATCGCA CACGGCAGAA ATACGGATTT
451 CGCGCCCCAA GCGACGGGAA ATTCCTCCG CGTTGTCCCG CAACACGGCA
501 GCCGTACCGC CGCCGACCGT ACCCAAACCT AAAAGACCGA TGTTTACTGG
551 CTTCAATTGTG TCTCCTTGTA AGCCGACTGA AATGTAAATA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1464; ORF 520.a>:

```

a520.pep
  1 MPALLSVHRX NALPFSRISE RMKLLVPLIM PAMDLILFAA KPSRRALMIG
 51 IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCLP FSMAFNTASL
101 AMPVPPNNST TTSTSSRATS SNGSLTKAXR TGRFVGLFLH SNRTRQKYGF

```

151 RAPS~~SDG~~KFP~~P~~ RCPAT~~RQ~~PY~~R~~ RRPYP~~N~~LK~~D~~R CLLAS~~L~~CLLV SRLKCKY*

m520/a520 98.0% identity in 197 aa overlap

	10	20	30	40	50	60
m520.p ep	MPALLSVHXANALPFSRISXRMKLLVPLIMPAMD	LILFAAKPSRRALMIGIPPATAASNW				
a520	MPALLSVHRXNALPFSRISERMKLLVPLIMPAMD	LILFAAKPSRRALMIGIPPATAASNW				
	10	20	30	40	50	60
	70	80	90	100	110	120
m520.p ep	TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATS					
a520	TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m520.p ep	SNGSLTKAXRTGRFVGLFLHSNRTRQKYGFRAPSDGKFP	PRCXATRQPYRRRPYPNLKDR				
a520	SNGSLTKAXRTGRFVGLFLHSNRTRQKYGFRAPSDGKFP	PRCPATRQPYRRRPYPNLKDR				
	130	140	150	160	170	180
	190					
m520.p ep	CLLASLCLLVSR	LKCKYX				
a520	CLLASLCLLVSR	LKCKYX				
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1465>:

g520-1.seq

```

1  ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51  TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGC CAGCGGGAAG
151 ATTCGTTGCG CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC TTCTTTGGCA ATGCCCGTGC
251 CGCCgAACAA TTCGACGACG ACATCGACGT CTTTACGCGC GACCAGTtCG
301 AACGGATCTT TGACAAAGGC GCGGACGGG CAGATTGGC GGGCTTTTTC
351 TTCGCTTAAG TCGCACATGG CAGAAATACG GATTTCGCGC CCCAAGCGGC
401 GGGAAATTTT CTCTGCGTTG TCCCGCAACA CGGCAGCCGC ACCGCCGCCG
451 ACCgTACCTA AGCCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1466; ORF 520-1.ng>:

g520-1.p~~ep~~

```

1  MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCSASGK
51  ISLPYSASSE LLAVTMCLPF SMAFNTASLA MPVFPNNSTT TSTSLRATSS
101 NGSLTKAADG QIWRAFSSLK SHMAEIRISR PKRREISSAL SRNTAAAPPP
151 TVPKPKRPMF TGFIVSPCKP TEM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1467>:

m520-1.seq

```

1  ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51  TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGC CAGCGGGAAG
151 ATTCGTTGCG CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC ATCTTTGGCA ATGCCCGTAC
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTACGTCG GACCAGTTTCG
301 AACGGATCTT TGACAAAGGC TCGGACGGG CAGTTTGTG GGGCTTTTTC
351 TTTCACTCAA TCGCACACGG CAGAAATACG GATTTCGCGC CCCAAGCGAC
401 GGGAAATTTT CTCCGCGTTG TCCCGCAACA CGGCAGCCGT ACCGCCGCCG
451 ACCGTACCCA AACCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1468; ORF 520-1>:

m520-1.p~~ep~~

```

1  MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCSASGK
51  ISLPYSASSE LLAVTMCLPF SMAFNTASLA MPVFPNNSTT TSTSSRATSS

```

101 NGSLTKAADG QVCRAFSSLK SHTAEIRISR PKRREISSAL SRNTAAVPPP
151 TVPKPKRPMF TGFIVSPCKP TEM*

g520-1/m520-1 97.1% identity in 173 aa overlap

	10	20	30	40	50	60
g520-1.pep	MKLLVPLIMPAMDILILFAAKPSRRALMIGIPPATAASNWTMTFCFSASGKISLPYSASSF					
m520-1	MKLLVPLIMPAMDILILFAAKPSRRALMIGIPPATAASNWTMTFCFSASGKISLPYSASSF					
	10	20	30	40	50	60
	70	80	90	100	110	120
g520-1.pep	LLAVTMCLPFSMAFNNTASLAMPVPPNNSTTTSTSLRATSSNGSLTKAADGQIWRAFSSLK					
m520-1	LLAVTMCLPFSMAFNNTASLAMPVPPNNSTTTSTSSRATSSNGSLTKAADGQVCRAFSSLK					
	70	80	90	100	110	120
	130	140	150	160	170	
g520-1.pep	SHMAEIRISRPKRREISSALSNTAAAPPPTVPKPKRPMFTGFIIVSPCKPTEMX					
m520-1	SHTAEIRISRPKRREISSALSNTAAVPPPTVPKPKRPMFTGFIIVSPCKPTEMX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1469>:

a520-1.seq

```

1  ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51  TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCCGTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGC CAGCGGGAAG
151 ATTTTCGTGC CGTATTTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC ATCTTTGGCA ATGCCGGTAC
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTACGTCG GACCAGTTCG
301 AACGGATCTT TGACAAAGGC TGCGGACGGG CAGGTTTGTC GGGCTTTTTC
351 TTCCTCAAA TCGCACACGG CAGAAATACG GATTTCGCGC CCAAGCGAC
401 GGGAAATTTT CTCCGCGTTG TCCCGCAACA CGGCAGCCGT ACCGCCGCCG
451 ACCGTACCCA AACCTAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1470; ORF 520-1.a>:

a520-1.pep

```

1  MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCFSASGK
51  ISLPYSASSF LLAVTMCLPF SMAFNNTASLA MPVPPNNSTT TSTSSRATSS
101 NGSLTKAADG QVCRAFSSLK SHTAEIRISR PKRREISSAL SRNTAAVPPP
151 TVPKPKRPMF TGFIVSPCKP TEM*

```

m520-1/a520-1 100.0% identity in 173 aa overlap

	10	20	30	40	50	60
a520-1.pep	MKLLVPLIMPAMDILILFAAKPSRRALMIGIPPATAASNWTMTFCFSASGKISLPYSASSF					
m520-1	MKLLVPLIMPAMDILILFAAKPSRRALMIGIPPATAASNWTMTFCFSASGKISLPYSASSF					
	10	20	30	40	50	60
	70	80	90	100	110	120
a520-1.pep	LLAVTMCLPFSMAFNNTASLAMPVPPNNSTTTSTSSRATSSNGSLTKAADGQVCRAFSSLK					
m520-1	LLAVTMCLPFSMAFNNTASLAMPVPPNNSTTTSTSSRATSSNGSLTKAADGQVCRAFSSLK					
	70	80	90	100	110	120
	130	140	150	160	170	
a520-1.pep	SHTAEIRISRPKRREISSALSNTAAVPPPTVPKPKRPMFTGFIIVSPCKPTEMX					
m520-1	SHTAEIRISRPKRREISSALSNTAAVPPPTVPKPKRPMFTGFIIVSPCKPTEMX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1471>:

g521.seq

```

1  ATGAAATCAA AACTCCCCTT AATCCTAATC AACCTTTCCC TGATTTCAG
51  CCCATTGGGT GCGAATGCGG CCAAAATCTA TACCTGCACA ATCAACGGAG
101 AAACCGTTTA CACCACCAAG CCGTCTAAAA GCTGCCACTC AACCGATTTC

```

q521n.pep

```

1  MKSKLPLILI NLSLISSPLG ANAAKIYTCT INGETVYTTK PSKSCHSTDL
51  PPIGNYSSER YILPQTPEPA PSPSNGGQAV KYKAPVKTVS KPAKSNTPPQ
101 QAPVNNRRS ILEAELSNER KALTEAQKML SQARLAKGGN INHQKINAL*
151 SNVLDROONI QALORELGRM *

```

m521.seq

1 ATGAAATCAA AACTCCTCTT AATCCTAATC AACTTTTCCC TGATTTC AAG
51 CCCATTGGGT GCGAATGCGG CCAAAATCTA sACCTGCACA ATCAACGGAG
101 AAACCGTTTA CACCAsCAAG CCGTCCAAAA GCTGCCACTC AACCGATT TG
151 CCCCCAATCG GCAACTACAG CAGCGAACGC TATATCCCGC CCCAAACGCC
201 CGAACCGGTA TCATACCGT CAAACGGCGG ACwGGTTGTC AAATATAAAG
251 CCCCGGTCAA AACAGTATCC AAGCCGGCAA AATCCArTAC GCCGCCGCCG
301 CAACAAGCAC CCTCAAACAA CAGCAGACGC TCCATTCTCG AAACAGAATT
351 GAGCAACGAA CGCAAAGCAT TGGTTGAAGC CCAAAAAATG TTATCACAAG
401 CACGTCTGGC AAAGGGCGGC AACATCAACC ATCAAGAAAT AAATGCATTA
451 CAAAGCAATG TATTGGACAG GCAGCAAAAT ATTCAAGCCC TGCAAAGGGA
501 ACTGGGGCGT ATGTAA

m521.pep

```

1  MKSKLLLLILI NFSLISSPLG ANAAKIXTCT INGETVYTXK PSKSCHSTD
51  PPIGNYSSER YIPQTPPEV SSPSNGGXV KYKAPVKTVS KPAKSXTPPP
101 QQAPSNNRR SILETELSNE RKALVEAQKM LSQARLAKGG NINHQEINAL
151 QSNVLDROON IOALORELGR M*

```

ORF 521 shows 90.6% identity over a 171 aa overlap with a predicted ORF (ORF 521.ng) from *N. gonorrhoeae*:

m521/q521

	10	20	30	40	50	60
m521.pep	MKSKLLILINFLISSPLGANA	AKIXTCTINGETVYTXKPSKSCHSTDLPPIGNYSSER				
		:		:		
g521	MKSKLPLILINLSLISSPLGANA	AKIYTCTINGETVYTTKPSKSCHSTDLPPIGNYSSER				
	10	20	30	40	50	60
	70	80	90	100	110	120
m521.pep	YIPPQTPEPVSSPSNGGXVVKYKAPVKT	SKPAKSXTPPPQQAPSNNRRSILET	ELSNE			
		:	:			:
g521	YILPQTPEPAPSPSNGGQAVKYKAPVKT	SKPAKSNTPP-QQAPVNNSRRSILEAE	LSNE			
	70	80	90	100	110	
	130	140	150	160	170	
m521.pep	RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLD	RQQNIQALQRELGRMX				
	:	:				
g521	RKALTEAQKMLSQARLAKGGNINHQKINALXSNVLD	RQQNIQALQRELGRMX				
	120	130	140	150	160	170

a521.seq

1 ATGAAATCAA AACTCCCCTT AATCCTAATC AACTTTTCCC TGATTTCAAG

```

51  CCCATTGGGT  GCGAATGCGG  CCAAAATCTA  CACCTGCACA  ATCAACGGAG
101  AAACCGTTTA  CACCACCAAG  CCGTCCAAAA  GCTGCCTCTC  AACCGATTTG
151  CCCCCAATCG  GCAACTACAG  CAGCGAACGC  TATATCCCGC  CCCAAACATC
201  CGAACCGACA  CCATCACCGT  CAAACGGCGG  ACAGGCTGTC  AAATATAAAG
251  CCCCAGTCAA  AACAGTATCC  AAGCCGGCAA  AATCCAATAC  GCCGCCGCCG
301  CAACAAGCAC  CCTCAAACAA  CAGCAGACGC  TCCATTCTCG  AAACAGAATT
351  GAGCAACGAA  CGCAAAGCAT  TGGTTGAAGC  CCAAAAAATG  TTATCACAAG
401  CACGTCTGGC  AAAAGGCGGC  AACATCAACC  ATCAAGAAAT  CAACGCATTG
451  CAAAGCAATG  TATTGGACAG  GCAGCAAAAT  ATCCAAGCAC  TGCAAAGAGA
501  ATTGGGACGT  ATGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1476; ORF 521.a>:

```

a521.pep
1  MKSKLPLILI  NFSLISSPLG  ANAAKIYCT  INGETVYTK  PSKSCLSTD
51  PPIGNYSSE  YIPPQTSEPT  PSPSNGGQAV  KYKAPVKTV  S  KPAKSNTPPP
101  QQAPSNNRR  SILETELSNE  RKALVEAQKM  LSQARLAKG  G  NINHQEINAL
151  QSVLDRQON  IQALQRELGR  M*

```

m521/a521 94.2% identity in 171 aa overlap

	10	20	30	40	50	60
m521.pep	MKSLLLLILINFSLISSPLGANAAKIXTCTINGETVYTXKPSKSCSTDLPPIGNYSSE					
a521	MKSKLPLILINFSLISSPLGANAAKIYCTINGETVYTTKPSKSCSTDLPPIGNYSSE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m521.pep	YIPPQTPEPVSSPSNGGXVVKYKAPVKTVSKPAKSXTPPPQQAPSNNRRSILETELSNE					
a521	YIPPQTSEPTSPSNGGQAVKYKAPVKTVSKPAKSNTPPPPQQAPSNNRRSILETELSNE					
	70	80	90	100	110	120
	130	140	150	160	170	
m521.pep	RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLDROQNIQALQRELGRMX					
a521	RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLDROQNIQALQRELGRMX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1477>:

```

g522.seq
1  atgactgagc  cgaaacacga  aacgccgacg  gaagagcagg  ttgccgcgcg
51  caaaaaagca  aaagccaaaa  tccgcaccat  ccgcatttgg  gcgtgggtca
101  ttttgcggtt  gctcgcttca  accgccctgc  tctcccaatg  cgcgatgtcc
151  aaaccgcagg  caaaacagaa  aattgtcgag  tcttgcataa  aaaatattcc
201  gtttgctgaa  aaatggcaga  acgatttgaa  agcgcgcggc  ttggatgcgg
251  acaatacccg  tctcgccgtc  gactactgca  aatgtatgtg  ggagcagcct
301  ttggacggat  tgagcgagaa  acagatcagc  tccttcggca  aactcgggtg
351  acaagaacag  cttgacctgc  tcggcgggcg  aaacgcgttt  gaaactcgag
401  acaacaatg  tgtcgcggat  ttgaaagccg  attga

```

This corresponds to the amino acid sequence <SEQ ID 1478; ORF 522.ng>:

```

g522.pep
1  MTEPKHETPT  EEQVAARKKA  KAKIRTIRIW  AWVILALLAS  TALLSQCAM
51  KPQAKQKIVE  SCMKNIPFAE  KWQNDLKARG  LDADNTRLAV  DYCKCMWEQP
101  LDGLSEKQIS  SFGKLGAQEQ  LDLLGGANAF  ETRDKQCVAD  LKAD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1479>:

```

m522.seq
1  ATGACTGAGC  CGAAACACGA  AATGCTGACG  AAAGAGCAGG  TTGCCGCGCG
51  CAAAAAAGCA  AAAGCCAAAA  TCCGCACCAT  CCGCATTGG  GCGTGGGTCA
101  TTTTGGCGTT  GCTCGCTTTA  ACCGCCCTGC  TCTCCCAATG  CGCGATGTCC
151  AAACCGCAGG  CAAAACAGAA  AATTGTCGAG  TCTTGCCTGA  AGAATATTCC
201  GTTTGCCGAA  AAATGGCAAA  ACGATTGCG  GGCCCGCGGT  TTAGATTCAA
251  ACAATACCCG  CCTCGCCGTC  GACTACTGCA  AATGTATGTG  GGAGCAGCCT

```

787

301 TTGGACAGAT TGAGCGAGAA ACAGATTAGA TCCTTCGGCA AACTCGGCGC
 351 ACAAGAACAG CTTGACCTGC TCGGCGGCGC AAATGCCTTT GAAGCACGTG
 401 ACAAGCAGTG TGTGCCGAT TTGAAATCAG AATAA

This corresponds to the amino acid sequence <SEQ ID 1480; ORF 522>:

m522.pep

1 MTEPKHEMLT KEQVAARKKA KAKIRTIRIW AWVILALLAL TALLSQCAMS
 51 KPQAKQKIVE SCVKNIPFAE KWQNDLRARG LDSNNTRLAV DYCKCMWEQP
 101 LDRLSEKQIR SFGKLGAQEQ LDLLGGANAF EARDKQCVAD LKSE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 522 shows 91.0% identity over a 144 aa overlap with a predicted ORF (ORF 522.ng) from *N. gonorrhoeae*:

m522/g522

	10	20	30	40	50	60
m522.pep	MTEPKHEMLTKEQVAARKKAKAKIRTIRIWAWVILALLALTALLSQCAMSKPQAKQKIVE					
	:					
g522	MTEPKHETPTTEEQVAARKKAKAKIRTIRIWAWVILALLASTALLSQCAMSKPQAKQKIVE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m522.pep	SCVKNIPFAEKWQNDLRARGLDSDNNTRLAVDYCKCMWEQPLDRLSEKQIRSFGLKGAQEQ					
	: : :					
g522	SCMKNIPFAEKWQNDLKARGLDADNTRLAVDYCKCMWEQPLDGLSEKQISSFGLKGAQEQ					
	70	80	90	100	110	120
	130	140				
m522.pep	LDLLGGANAFEARDKQCVADLKSEX					
	: :					
g522	LDLLGGANAFETRDKQCVADLKAD					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1481>:

a522.seq

1 ATGACTGAGC CGAAACACGA AATGCCGACG GAAGAGCAGG TTGCCGCGCG
 51 CAAAAAAGCA AAAGCCAAAA TCCGCACCAT CCGCATTTGG GCATGGGTCA
 101 TTTTGGCGTT GCTCGCTTCA ACCGCCCTGC TCTCCCAATG CGCGATGTCC
 151 AAACCGCAGG CAAAACAGAA AATTGTCGAG TCTTGCGTGA AGAATATTCC
 201 GTTTGCCGAA AAATGGCAAA ACGATTGCG GGCCCGCGGT TTAGATTCAA
 251 ACAATACCCG CCTTACCGTC GACTACTGCA AATGTATGTG GGAGCAGCCT
 301 TTGGACAGAT TGAGCGAGAA ACAGATTAGT TCCTTCGGCA AACTCGGCGC
 351 ACAAGAACAG CTTGACCTGC TCGGCGGCGC AAATGCCTTT GAAACGCGAG
 401 ACAAGCAGTG TGTGCCGAT TTGAAATCAG AATAA

This corresponds to the amino acid sequence <SEQ ID 1482; ORF 522.a>:

a522.pep

1 MTEPKHEMPT EEQVAARKKA KAKIRTIRIW AWVILALLAS TALLSQCAMS
 51 KPQAKQKIVE SCVKNIPFAE KWQNDLRARG LDSNNTRLTV DYCKCMWEQP
 101 LDRLSEKQIS SFGKLGAQEQ LDLLGGANAF ETRDKQCVAD LKSE*

m522/a522 95.8% identity in 144 aa overlap

	10	20	30	40	50	60
m522.pep	MTEPKHEMLTKEQVAARKKAKAKIRTIRIWAWVILALLALTALLSQCAMSKPQAKQKIVE					
	:					
a522	MTEPKHEMPTTEEQVAARKKAKAKIRTIRIWAWVILALLASTALLSQCAMSKPQAKQKIVE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m522.pep	SCVKNIPFAEKWQNDLRARGLDSDNNTRLAVDYCKCMWEQPLDRLSEKQIRSFGLKGAQEQ					
	:					
a522	SCVKNIPFAEKWQNDLRARGLDSDNNTRLTVDYCKCMWEQPLDRLSEKQISSFGLKGAQEQ					
	70	80	90	100	110	120

g523.seq

1	atgactgtat	ggtttgttgc	cgctgttgcc	gtcttaatca	tccaattatt
51	gacgggaacg	gtttatcttt	tggttgtcag	cgcggctttg	gcgggttcgg
101	gcattgccta	cgggctgact	ggcagcacgc	ctgccgccgt	cttgaccgcc
151	gcactgcttt	ccgcgctggg	catttggttc	gtacatgcca	aaaccgccgt
201	gggaaaagt	gaaacggatt	catatcagga	tttgataacc	ggaaaatatg
251	ccgaaatcct	ccgatacaca	ggcggcaacc	gttcgaagt	ttttatcgc
301	ggtacgcact	ggcaggcgca	aaatacgggg	caggaagtgt	ttgaaccggg
351	aacgcgcgcc	ctcatcgtcc	gcaaagaagg	taaccttctt	atcatcgcaa
401	acccttaa				

g523.ppe

1 MTVWFVAAVA VLIIELLTGT VYLLVSAAL AGSGIAYGLT GSTPAAVLTA
51 ALLSALGIWF VHAKTAVGKV ETDSYQDLDT GKAEILRYT GGNRYEVFYR
101 GTHWQAQNTG QEVFEPGTRA LIVRKEGNLL IIANP*

m523.seq (partial)

1	..GCCGCTCTTAA	TCATCGAATT	ATTGACGGGA	ACG GTTTATC	TTTTGGTTGT
51	nAGCGCGGCT	TTGGCGGGTT	CGGGCATTGC	TTACGGGCTG	ACCGGCAGTA
101	CGCTGCGCG	CGTCTTGACC	GnCGCTCTGC	TTTCCGCGCT	GGGTATTTnG
151	TTCGTACACG	CCAAAACCGC	CGTTAGAAAA	GTTGAAACGG	ATT CATATCA
201	GGATTTGGAT	GCCGGACAAT	ATGTCGAAAT	CCTCCGACAC	ACAGGCGGCA
251	ACCGTTACGA	AGTTTTtTAT	CGCGGTACGc	ACTGGCAGGC	TCAAAATACG
301	GGGCAAGAAG	AGCTTTGAAC	AGGAACTCGC	CGCCTCATTG	TCCGCAAGGA
351	AGGCAACCTT	CTTATTATCA	CACACCCTTAA		

m523.pep (partial)

```

1  ..AVLIIELLTG TVYLLVVSAA LAGSGIAYGL TGSTPAAVLT XALLSALGIX
51  FVHAKTAVRK VETDSYQDLG AGQYVEILRH TGGNRYEVFY RGTWHAQNT
101 GQEELEPGTR ALIVRKEGNL LIITHP*

```

Homology with a predicted ORF from *N. gonorrhoeae*

m523/g523

```

                                10      20      30      40      50
m523.pep      AVLIIELLTGTVYLLVVS AALAGSGIAYGLTGSTPAAVLT XALLSALGIXF
                |||||
g523      MTVWFVA AVLIIELLTGTVYLLVVS AALAGSGIAYGLTGSTPAAVLT AALLSALGIWF
                10      20      30      40      50      60

                                60      70      80      90      100     110
m523.pep      VHAKTAVRKVETDSYQDL DAGQYVEILRHTGGNRYEVFYRGTHWQAQNTGQE ELEPGTRA
                ||||| : : : : |||||
g523      VHAKTAVGKVETDSYQDLDTGKYAEILRYTGGNRYEVFYRGTHWQAQNTGQEV FEPGTRA
                70      80      90      100     110     120

                                120
m523.pep      LIVRKEGNLLIITHP
                ||||| : : |

```


g523 LIVRKEGNLLIIANPX
130

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1487>:

```
a523.seq
1  ATGACTGTAT GGTTTGTGTC CGCTGTTGCC GTCTTAATCA TCGAATTATT
51  GACGGGAACG GTTTATCTTT TGGTTGTCAG CGCGGCTTTG GCGGGTTCGG
101 GCATTGCTTA CGGGCTGACC GGCAGCACGC CTGCCGCCGT CTTGACCGCC
151 GCTCTGCTTT CCGCGCTGGG TATTTGGTTC GTACACGCCA AAACCGCCGT
201 GGGAAAAGTT GAAACGGATT CATATCAGGA TTTGGATGCC GGGCAATATG
251 CCGAAATCCT CCGGCACGCA GCGGCAACC GTTACGAAGT TTTTATCGC
301 GGTACGCACT GGCAGGCTCA AAATACGGGG CAAGAAGAGC TTGAACCAGG
351 AACGCGCGCC CTAATCGTCC GCAAGGAAG CAACCTTCTT ATCATCGCAA
401 AACCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1488; ORF 523.a>:

```
a523.pep
1  MTVWFVAAVA VLIIELLTGT VYLLVVSAA AGSGIAYGLT GSTPAAVLTA
51  ALLSALGIWF VHAKTAVGKV ETDSYQDLDA GQYAEILRHA GGNRYEVFYR
101 GTHWQAQNTG QEELEPGTRA LIVRKEGNLL IIAKP*
```

m523/a523 94.4% identity in 126 aa overlap

```

10      20      30      40      50
m523.pep      AVLIIELLTGTVYLLVVSAAAGSGIAYGLTGSTPAAVLTXALLSALGIXF
               |||||
a523           MTVWFVAAVAVLIIELLTGTVYLLVVSAAAGSGIAYGLTGSTPAAVLTAALLSALGIWF
               10      20      30      40      50      60

60      70      80      90      100     110
m523.pep      VHAKTAVRKVETDSYQDLDAQYVEILRHTGGNRYEVFYRGTHWQAQNTGQEELEPGTRA
               |||||:|||||:|||||
a523           VHAKTAVGKVETDSYQDLDAQYAEILRHAGGNRYEVFYRGTHWQAQNTGQEELEPGTRA
               70      80      90      100     110     120

120
m523.pep      LIVRKEGNLLIITHPX
               |||||:|
a523           LIVRKEGNLLIIAKPX
               130
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1489>:

```
g525.seq
1  atgaagtacg tccggttatt tttcctcggc acggcactcg ccggcactca
51  agcggcggtt gccgaaatgg ttcaaactga aggcggcagc taccgcccgc
101 tttatctgaa aaaagatacc ggcttgatta aagtcaaacc gttcaaactg
151 gataaatatc ccgttaccaa tgccgagttt gccgaatttg tcaacagcca
201 cccccaatgg caaaaaggca ggatcggttc caaacaggca gaacccgctt
251 acctgaagca ttggatgaaa aacggcagcc gcagctatgc gccgaaggcg
301 ggcgaattga aacagccggt taccaatatt tcctggtttg ccgccaacgc
351 ctattgcgcc gcacaaggca aacgcctgcc gaccatcgac gaatgggaat
401 ttgccggact tgcttcgcc acgcagaaaa aacggctcaa acgaaccggg
451 ctacaaccgc actattctcg attggtatgc cgacggcgga cggaaaggcc
501 tgcacgatgt cggcaaagca ccgcccgaac tactggggtg tttatgatat
551 gcacgggctg a
```

This corresponds to the amino acid sequence <SEQ ID 1490; ORF 525.ng>:

```
g525.pep
1  MKYVRLFFLG TALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101 GELKQPVTNI SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKKRLKRTR
151 LQPHYSRLVC RRRTERPARC RQSTARTTGV FMICTG *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1491>:

```
m525.seq
1 ATGAAGTATG TCCGTTATT TTwCCTCGGC GCGGCACTCG cCrrCACTCA
51 ArCGGCGGCT GcCGAAATGG TTCAAATCGA AGGCGGCAGc TACCGCCCCrC
101 TTTATCTGAA AaaAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTtG TCAACAGCCA
201 CCCCCAATGG CAAAAAGGCA GGATCGGTTc CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGTC GCAGCTATGc GCCGAAGgCG
301 GgCGAATTAA AACAACCGGT AACCcATGTT TCCTGGwTTG CGCCCAAcGC
351 CTAtTGCGCC GCACAAGGCA AACCGCTGCC GACCATTtGAC GAATGGGAAT
401 TTGCCGGACT TGCTTCCGCC ACGCAGAAAA A.cGGCTCAA ACGAACCCGG
451 CTACAACCGC ACTATTCTCG ATTGGTATGC CGACGGCGGA CGGAAAGGCC
501 TGCACGATGT CGGCA.AAGG CCGCCCGAAC TACTGGGGCG TTTATGATAT
551 GCACGGGCTG A
```

This corresponds to the amino acid sequence <SEQ ID 1492; ORF 525>:

m525.pep

1	<u>MKYVRLFXLG AALAXTQXAA</u>	AEMVQIEGGS	YRPLYLKKDT	GLIKVKPFKL
51	DKYPVTNAEF AEFVNSHPQW	QKGRIGSKQA	EPAYLKHWMK	NGSRSYAPKA
101	GELKQPVNTV SWXAAAYCA	AQGKRLPTID	EFWEFAGLASA	TQKXRLKRTR
151	LOPHYSRLVC RRRTERPARC	RXKAARTTGA	FMICTG*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 525 shows 94.1% identity over a 186 aa overlap with a predicted ORF (ORF 525.ng) from *N. gonorrhoeae*:

```

m525/g525

      10      20      30      40      50      60
m525.pep  MKYVRLFXLGAALAXTQXAAAEMVQIEGGSYRPLYLKQDTGLIKVKPFLDKYPVTNAEF
          |||||:|||||
g525      MKYVRLFFLGTALAGTQAAAAEMVQIEGGSYRPLYLKQDTGLIKVKPFLDKYPVTNAEF
          |||||:|||||

      70      80      90     100     110     120
m525.pep  AEFVNNSHPQWQKGRIGSKQAEPAYLKHWMKNGSRSYAPKAGELKQPVNTNVSXAAANAYCA
          |||||:|||||
g525      AEFVNNSHPQWQKGRIGSKQAEPAYLKHWMKNGSRSYAPKAGELKQPVNTNISWFAANAYCA
          |||||:|||||

      70      80      90     100     110     120
m525.pep  AEFVNNSHPQWQKGRIGSKQAEPAYLKHWMKNGSRSYAPKAGELKQPVNTNVSXAAANAYCA
          |||||:|||||
g525      AEFVNNSHPQWQKGRIGSKQAEPAYLKHWMKNGSRSYAPKAGELKQPVNTNISWFAANAYCA
          |||||:|||||

     130     140     150     160     170     180
m525.pep  AOGKRLPTIDEWEFAGLASATQKXRLKRTRLQPHYSRLVCRRRTERPARCRXKAARTTGA
          |||||:|||||
g525      AOGKRLPTIDEWEFAGLASATQKKRLKRTRLQPHYSRLVCRRRTERPARCRQSTARTTGV
          |||||:|||||

     130     140     150     160     170     180
m525.pep  FMICTGX
          |||||
g525      FMICTGX
          |||||

```

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 1493>:

```

a525.seq
1  ATGAAGTTTA CCCGTTACT CTTTCTCTGT GCGGCACTCG CCGGCACTCA
51  AGCGGCAGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCTGATTA AAGTCAAACC GTTCAAACCTG
151 GATAAATATC CGGTTACCAA TGCCGAGTTT GCCGAATTTG TCAACAGGCCA
201 CCCCCAATGG CAAAAAGGCA GGATCGGTTT CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCG GCAGCTATGC GCCGAAGGCG
301 GGCGATTTTA AACACCCGGT AACCAATGTT TCCTGGTTCC GCGCCAACGC
351 CTATTGCGCC CACCAAGGCA AACGCCCTGC GACCATTTGAC GAATGGGAAT
401 TTGCCGGACT TGCCTCCGCC ACGCAG.AAA AACGGCTCAA ACGAACCCTG
451 CTACAACCGC ACTATTCTCG ACTGGTATGC GGATGGCGAC CGGAAAGACC
501 TGCACGATGT CGGCAAAAG.G TCGCCCGAAC TACTGGGGCG TTTATGATAT
551 GCACGGTCTG A

```

This corresponds to the amino acid sequence <SEQ ID 1494; ORF 525.a>:

```
a525.pep
1  MKFTRLLFLC AALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101 GDLKQPVTNV SWFAANAYCA AQGKRLPTID EWEFAGLASA TQXKRLKRTR
151 LQPHYSRLVC GWRPERPARC RQXVARTTGA FMICTV*
```

m525/a525 90.8% identity in 185 aa overlap

```

      10      20      30      40      50      60
m525.pep  MKYVRLFXLGAALAXTQXAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF
      ||::||: | |||| | | ||||| ||||| ||||| ||||| ||||| ||||| |||||
a525      MKFTRLLFLCAALAGTQAAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF
      10      20      30      40      50      60

      70      80      90      100     110     120
m525.pep  AEFVNSHPQWQKGRIGSKQAEPAAYLKHWKNGSRSYAPKAGELKQPVTNVSWXANAYCA
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a525      AEFVNSHPQWQKGRIGSKQAEPAAYLKHWKNGSRSYAPKAGDLKQPVTNVSWFAANAYCA
      70      80      90      100     110     120

      130     140     150     160     170     180
m525.pep  AQGKRLPTIDWEFAGLASATQXKRLKRTRLQPHYSRLVCRRTTERPARCRXKAARTTGA
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a525      AQGKRLPTIDWEFAGLASATQXKRLKRTRLQPHYSRLVCGWRPERPARCRQXVARTTGA
      130     140     150     160     170     180

m525.pep  FMICTGX
      |||||
a525      FMICTVX
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1495>:

```
g525-1.seq
1  ATGAAGTACG TCCGGTTATT TTTCTCGGC ACGGCACTCG CCGGCACTCA
51  AGCGGCGGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTTG TCAACAGCCA
201 CCCCCAATGG CAAAAAGGCA GGATCGGTTT CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GCGGAATTGA AACAGCCGGT TACCAATATT TCCTGGTTTG CCGCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATCGAC GAATGGGAAT
401 TTGCCGGACT TGCTTCCGCC ACGCAGAAAA ACGGCTCAAA CGAACC CGGC
451 TACAACCGCA CTATTCTCGA TTGGTATGCC GACGGCGGAC GGAAGGCCCT
501 GCACGATGTC GGCAAGACC GCCGAACTA CTGGGGTGTT TATGATATGC
551 ACGGGCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601 TCCGGCAATG CCAACGCGCA AATGTTTTGC AGCGGCGCAT CTGTCGGGGC
651 GAGCGACTCG TCCAATATG CCGCTTCCT CCGTACGGC ATCCGCACCA
701 GCCTGCAATC CAAATACGTC CTGCACAAC TGGGCTTCCG CTGCGCAAGC
751 CGATAA
```

This corresponds to the amino acid sequence <SEQ ID 1496; ORF 525-1.ng>:

```
g525-1.pep
1  MKYVRLFLG TALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101 GELKQPVTNI SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKNGSNEPG
151 YNRTILDWYA DGGKGLHDV GKDRPNYWG VYDMHGLIEW TEDFNSSL
201 SGNANAQMFC SGASVGASDS SNYAAFLRYG IRTSLQSKYV LHNLGFRCS
251 R*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1497>:

```
m525-1.seq
1  ATGAAGTATG TCCGGTTATT TTTCTCGGC GCGGCACTCG CCGGCACTCA
51  AGCGGCGGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
```

```
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTG TCAACAGCCA
201 CCCCCAATGG CAAAAGGCA GGATCGGTTC CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GGCGAATTAA AACACCGGT AACCAATGTT TCCTGGTTTG CCGCCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401 TTGCCGGACT TGCTTCCGCC ACGCAGAAAA ACGGCTCAA CGAACCCGGC
451 TACAACCGCA CTATTCTCGA TTGGTATGCC GACGGCGGAC GGAAAGGCCT
501 GCACGATGTC GGCAAAGGCC GCCCGAATA CTGGGGCGTT TATGATATGC
551 ACGGGCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601 TCCGGCAATG CCAACGCGCA AATGTTTTC AGCGGCGCGT CTATCGGGTC
651 GAGCGACTCG TCCAACATG CCGCCTTCCT CCGCTACGGC ATCCGTACCA
701 GCCTGCAATC CAAATATGTC TTGCACAAC TGGGCTTCCG TTGCACAAGC
751 CGATAA
```

This corresponds to the amino acid sequence <SEQ ID 1498; ORF 525-1>:

m525-1.pep

```
1 MKYVRLFFLG AALAGTQAAA AEMVQIEGGS YRPLYLKDDT GLIKVKPFKL
51 DKYVPTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101 GELKQPVNTV SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKNGSNEPG
151 YNRTILDWYA DGGKRLHDV GKGRPNYWG YDMHGLIEWE TEDFNSSLLS
201 SGNANAQMFC SGASIGSSDS SNYAAFLRYG IRTSLQSKYV LHNLGFRCTS
251 R*
```

m525-1/g525-1 97.6% identity in 251 aa overlap

```
10 20 30 40 50 60
m525-1.pep MKYVRLFFLG AALAGTQAAA AEMVQIEGGS YRPLYLKDDT GLIKVKPFKL DKYVPTNAEF
|||||
g525-1 MKYVRLFFLG TALAGTQAAA AEMVQIEGGS YRPLYLKDDT GLIKVKPFKL DKYVPTNAEF
10 20 30 40 50 60

70 80 90 100 110 120
m525-1.pep AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA GELKQPVNTV SWFAANAYCA
|||||
g525-1 AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA GELKQPVNTI SWFAANAYCA
70 80 90 100 110 120

130 140 150 160 170 180
m525-1.pep AQGKRLPTID EWEFAGLASA TQKNGSNEPG YNRTILDWYADGGKRLHDV GKGRPNYWG
|||||
g525-1 AQGKRLPTID EWEFAGLASA TQKNGSNEPG YNRTILDWYADGGKRLHDV GKDRPNYWG
130 140 150 160 170 180

190 200 210 220 230 240
m525-1.pep YDMHGLIEWE TEDFNSSLLSSG NANAQMFC SGASIGSSDS SNYAAFLRYG IRTSLQSKYV
|||||
g525-1 YDMHGLIEWE TEDFNSSLLSSG NANAQMFC SGASVGS DSSNYAAFLRYG IRTSLQSKYV
190 200 210 220 230 240

250
m525-1.pep LHNLGFRCTSRX
|||||
g525-1 LHNLGFRCSRX
250
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1499>:

a525-1.seq

```
1 ATGAAGTTA CCCGTTACT CTTTCTCTGT GCGGCACTCG CCGGCACTCA
51 AGCGGCAGCT GCCGAAATGG TTCAAATCGA AGCGGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTG TCAACAGCCA
201 CCCCCAATGG CAAAAGGCA GGATCGGTTC CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GCGCATTTAA AACACCGGT AACCAATGTT TCCTGGTTTC CCGCCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401 TTGCCGGACT TGCTTCCGCC ACGCAGAAAA ACGGCTCAA CGAACCCGGC
451 TACAACCGCA CTATTCTCGA CTGGTATGCG GATGGCGACC GGAAAGACCT
501 GCACGATGTC GGCAAAGGTC GCCCGAATA CTGGGGCGTT TATGATATGC
551 ACGGTCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601 TCCGGCAATG CCAACGCGCA AATGTTTTC AGCGGCGCGT CTATCGGGTC
651 GAGCGACTCG TCCAACATG CCGCCTTCCT CCGCTACGGC ATCCGCACCA
701 GCCTGCAATC CAAATATGTC TTGCACAAC TGGGCTTCCG TTGCACAAGC
751 CGATAA
```

This corresponds to the amino acid sequence <SEQ ID 1500; ORF 525-1.a>:

a525-1.pep

```

1  MKFTRLFLFC AALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK  NGSRSYAPKA
101 GDLKQPVNTV SWFAANAYCA AQGKRLPTID EWEFAGLASA  TQKNGSNEPG
151 YNRTILDWYA DGDRLDLDV  GKGRPNYWG  YDMHGLIEWE TEDFNSSLLS
201 SGNANAQMFC SGASIGSSDS SNYAAFLRYG IRTSLQSKYV LHNLGFRCTS
251 R*

```

m525-1/a525-1 97.2% identity in 251 aa overlap

	10	20	30	40	50	60
m525-1.pep	MKYVRLFFLGAALAGTQAAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF					
a525-1						
	10	20	30	40	50	60
	70	80	90	100	110	120
m525-1.pep	AEFVNSHPQWQKGRIGSKQAEPAYLKHWKNGSRSYAPKAGELKQPVNTVSWFAANAYCA					
a525-1						
	70	80	90	100	110	120
	130	140	150	160	170	180
m525-1.pep	AQGKRLPTID EWEFAGLASATQKNGSNEPGYNRTILDWYADGGRKGLHDVGKGRPNYWG					
a525-1						
	130	140	150	160	170	180
	190	200	210	220	230	240
m525-1.pep	YDMHGLIEWETEDFNSSLLSSGNANAQMFCSGASIGSSDSSNYAAFLRYGIRTSLSQSKYV					
a525-1						
	190	200	210	220	230	240
	250					
m525-1.pep	LHNLGFRCTSRX					
a525-1						
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1501>:

g527.seq

```

1  atggtttttac cagtctcctt ttttcagcct gtccagttgg cggcggtcgc
51  gcttggtcgg tctgccgtcg ggatgggagg aagtgatgcg gctgaattgg
101 tccagctgtt tgcactcttc cctcaatgct gccgttttcg cgtcttcttc
151 atacagaagc cgcgcctcgg gtgccgggag gcgttggttg ttcaaacctt
201 taaccttgat tttatgggga aggggaattga gcgtcaggtc gataatatcg
251 ccgatgtcta tgggttttact gtttttgact ttcgagccgt ttacttgaa
301 cctaccagct tccatattgct tttgcgcaag ggaacggggtc ttgaaaaaac
351 gtgccgcca aagccatttg tccagccgca tggcggaaga atcgtgcttg
401 tctttcatat gattttggtt gaaataattg aatttgtttc gagtttagca
451 taa

```

This corresponds to the amino acid sequence <SEQ ID 1502; ORF 527.ng>:

g527.pep

```

1  MVLVPSFFQP VOLAAVALGR SAVGMGGSDA AELVELFALF PQCCRFRVFF
51  IQKPRLCRA ALVVQTFNLD FMGKGIERQV DNIADVYGFT VDFRAVYLN
101 PTQFDMLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIIEVSSLA
151 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1503>:

m527.seq

```

1  ATGGTTTAC CAGTCTCCTT TTTTCAGCCT GTCCAGTTGG CGGCGGTCGC
51  GCTTGGTGCG TCTGCCGTCG GGATAGGCGG AAGTGATGCG GCTGAATTGG
101 TCGAGCTGTT TCGCTCTTC CCTCAATGTT GCCGTTWTCG CGTCCTCTTC
151 ATACAGAAGC CGCGCTCGG ATGCCGGGCG GCCTTGGTGG TTCAAACCTT

```

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201 TAACCKTGAT TTTATAGGGA AGGG.AATtk AgCkTCaGty GrTwATaTCG
 251 CsGATGTmTA TGGTTTTACT GTTTTTGACC TTCGAGCCGT TTA^{CT}TTGAAC
 301 CCTACCCAGT TCGATGTGCT TTTGCGCAAG GGAACGGGTC TTGAAAAAAC
 351 GTGCCGCCCA AAGCCATTG TCCAGCCGCA TGGCGGAAGA ATCGTGCTTG
 401 TCTTTCATAC GATTTTGT^{TT} GAAATAATTG AATTGT^{TT}TC GAGTTTAGCA
 451 TAA

This corresponds to the amino acid sequence <SEQ ID 1504; ORF 527>:

m527.pep
 1 MVLPVSFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCR^RRVLF
 51 IQKPRXGCRA ALVVQTFN^{XD} FIGKXNXASV XXIADVYGFT VFDLRAVYLN
 101 PTQFDVLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
 151 *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 527 shows 90.0% identity over a 150 aa overlap with a predicted ORF (ORF 527.ng) from *N. gonorrhoeae*:

m527/g527

m527.pep	10	20	30	40	50	60
	MVLPVSFFQPVQLAAVALGRSAVGIGGSDAAELVELFALFPQCCR ^R RVLF IQKPRXGCRA					
g527	10	20	30	40	50	60
	MVLPVSFFQPVQLAAVALGRSAVGMGGSDAAELVELFALFPQCCRFRVFFI ^Q KPRLGCRA					
m527.pep	70	80	90	100	110	120
	ALVVQTFN ^{XD} FIGKXNXASVXXIADVYGFTVFDLRAVYLNPTQFDVLLRKGTGLEKTCRP					
g527	70	80	90	100	110	120
	ALVVQTFNLD ^{FM} GKGI ^{ER} QVDNIADVYGFTVFD ^{FR} AVYLNPTQFDMLLRKGTGLEKTCRP					
m527.pep	130	140	150			
	KPFVQPHGGRIVLVFHTILFEIIEFVSSLA					
g527	130	140	150			
	KPFVQPHGGRIVLVFHTILFEIIEFVSSLA					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1505>:

a527.seq
 1 ATGGTTTTAC CAGTCTCCTT TTTTCAGCCT GTCCAGTTGG CGGCGGTGCG
 51 GCTTGGT^{CG} TCTGCCGTCG GGATAGGCGG AAGTGATGCG GCTGAATTGG
 101 TCGAGCTGTT TGC^GCTCTTC CCTCAATGTT GCCGTTTTCG CGTCTCTTTC
 151 ATACAGAAGC CGCGCCTCGG ATGCCGGGCG GCGTTGGTGG TTCAAACCTT
 201 TAACCTTGAT TTTATAGGGA AGGGAATTGA GCGTCAGGTC GATAATATCG
 251 CCGATGCTA TGGTTTTACT GTTTTTGACC TTCGAGCCGT TTA^{CT}TTGAAC
 301 CCTACCCAGT TCGATGTGCT TTTGCGCAAG GGAACGGGTC TTGAAAAAAC
 351 GTGCCGCCCA AAGCCATTG TCCAGCCGCA TGGCGGAAGA ATCGTGCTTG
 401 TCTTTCATAC GATTTTGT^{TT} GAAATAATTG AATTGT^{TT}TC GAGTTTAGCA
 451 TAA

This corresponds to the amino acid sequence <SEQ ID 1506; ORF 527.a>:

a527.pep
 1 MVLPVSFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCR^RRVLF
 51 IQKPR^LGCRA ALVVQTFNLD FIGKGI^{ER}QV DNIADVYGFT VFDLRAVYLN
 101 PTQFDVLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
 151 *

m527/a527 93.3% identity in 150 aa overlap

m527.pep	10	20	30	40	50	60
	MVLPVSFFQPVQLAAVALGRSAVGIGGSDAAELVELFALFPQCCR ^R RVLF IQKPRXGCRA					
a527	10	20	30	40	50	60
	MVLPVSFFQPVQLAAVALGRSAVGIGGSDAAELVELFALFPQCCRFRVLF IQKPR ^L GCRA					

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	70	80	90	100	110	120
m527.pep	ALVVQTFNXXDFIGKXNXASVXXIADVYGFTVFDLRAVYLNPTQFDVLLRKGTGLEKTCRP					
a527	ALVVQTFNLDFIGKGIERQVDNIADVYGFTVFDLRAVYLNPTQFDVLLRKGTGLEKTCRP					
	70	80	90	100	110	120
	130	140	150			
m527.pep	KPFVQPHGGRIVLVFHTILFEIIEFVSSLAX					
a527	KPFVQPHGGRIVLVFHTILFEIIEFVSSLAX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1507>:

```

g528.seq
1   atggaaattc gggtaataaa atatacggca acggctgcgt tgtttgcatt
51  tacggttgca ggctgccggc tggcgggggt gtatgagtgt ttgtccttgt
101 cccgctggtg taagccgaga aaacctgccg ccatcgattt ttgggatatt
151 ggcggcgaga gtccgctgtc tttagaggac tacgagatac cgctttcaga
201 cggcaatcgt tccgtcaggg caaacgaata tgaatccgcg caaaaatctt
251 acttttatag gaaaataggg aagtttgaag cctgcggggt ggattggcgt
301 acgcgtgacg gcaaaccttt ggttgagagg ttcaaacagg aaggtttcga
351 ctgtttggaa aagcaggggt tgcggcgcaa cggcctgtcc gagcgcgtcc
401 gatggtaa

```

This corresponds to the amino acid sequence <SEQ ID 1508; ORF 528.ng>:

```

g528.pep
1   MEIRVIKYTA TAALFAFTVA GCRLAGWYEC LSLSGWCKPR KPAAIDFWDI
51  GGESPLSLED YEIPLSDGNR SVRANEYESA QKSYFYRKIG KFEACGLDWR
101 TRDGKPLVER FKQEGFDCLE KQGLRRNGLS ERVRW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1509>:

```

m528.seq (partial)
1   ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCAAT
51  TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCCTCA
101 CCGGCTGGTG TAAGCCGAGA AAACCGGCTG CCATCGATT TTTGGGATATT
151 GGCggcgaga GTCCGCCGTC TTTAGGGGAC TACGAGATAC CGCTTTTCAGA
201 CGGCAATAGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAATAGGG AAGTTTGAAG C.TGCGGGCT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG GAGGATTTGA
351 CTGCTTGGAA AAG....

```

This corresponds to the amino acid sequence <SEQ ID 1510; ORF 528>:

```

m528.pep (partial)
1   MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLTGWCKPR KPAAIDFWDI
51  GGESPPSLGD YEIPLSDGNS SVRANEYESA QQSYFYRKIG KFEXCGLDWR
101 TRDGKPLIET FKQGGFDCLE K....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 528 shows 89.3% identity over a 121 aa overlap with a predicted ORF (ORF 528.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m528.pep	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD					
g528	MEIRVIKYTATAALFAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPLSLED					
	10	20	30	40	50	60
	70	80	90	100	110	120
m528.pep	YEIPLSDGNSSVRANEYESAQKSYFYRKIGKFEXCGLDWRTRDGKPLIETFKQGGFDCLE					
g528	YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLVERFKQEGFDCLE					
	70	80	90	100	110	120

```

m528.pep      K
              |
g528          KQGLRRNGLSERVRW

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1511>:

```

a528.seq
1   ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT
51  TACGGTTGCA GGCTGCCGGT TGGCAGGTTG GTATGAGTGT TCGTCCCTGT
101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATTT TTGGGATATT
151 GGC GCGAGA GTCCTCCGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
201 CCGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG CCTGCGGGTT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG AAGGTTTTGA
351 TTGTTTGAAA AAGCAGGGGT TGC GCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1512; ORF 528.a>:

```

a528.pep
1   MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI
51  GGESPPSLED YEIPLSDGNR SVRANEYESA QQSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQEGFDCLK KQGLRRNGLS ERVRW*

```

m528/a528 95.0% identity in 121 aa overlap

```

              10      20      30      40      50      60
m528.pep      MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD
              |||||
a528           MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLED
              10      20      30      40      50      60

              70      80      90      100     110     120
m528.pep      YEIPLSDGNSSVRANEYESAQQSYFYRKIGKFEXCGLDWRTRDGKPLIETFKQGGFDCLE
              |||||
a528           YEIPLSDGNRSVRANEYESAQQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQEGFDCLK
              70      80      90      100     110     120

m528.pep      K
              |
a528          KQGLRRNGLSERVRWX
              130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1513>:

```

g528-1.seq
1   ATGGAAATTC GGGTAATAAA ATATACGGCA ACGGCTGCGT TGTTTGCATT
51  TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCTTGT
101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATTT TTGGGATATT
151 GGC GCGAGA GTCCGCTGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
201 CCGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCG CAAAATCTT
251 ACTTTTATAG GAAAATAGGG AAGTTTGAAG CCTGCGGGTT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GGTGAGAGG TTCAAACAGG AAGGTTTCGA
351 CTGTTTGAA AAGCAGGGGT TGC GCGCAA CGGCCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1514; ORF 528-1.ng>:

```

g528-1.pep
1   MEIRVIKYTA TAALFAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI
51  GGESPLSLED YEIPLSDGNR SVRANEYESA QKSYFYRKIG KFEACGLDWR
101 TRDGKPLVER FKQEGFDCLE KQGLRRNGLS ERVRW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1515>:

```

m528-1.seq
1   ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT

```



```

51 TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCCTCA
101 CCGGCTGGTG TAAGCCGAGA AAACCGGCTG CCATCGATT TTGGGATATT
151 GCGGCGGAGA GTCCGCCGTC TTTAGGGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG CCTGCGGGCT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG GAGGATTGA
351 CTGCTTGGAA AAGCAGGGGT TGCGGCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1516; ORF 528-1>:

m528-1.pep..

```

1 MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLTGWCKPR KPAAIDFWDI
51 GGESPPSLGD YEIPLSDGNR SVRANEYESA QQSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQGGFDCLE KQGLRRNGLS ERVRW*

```

g528-1/m528-1 92.6% identity in 135 aa overlap

```

          10      20      30      40      50      60
g528-1.pep MEIRVIKYTATAALFAFTVAGCRLAGWYECSSLSGWCKPRKPAAIDFWDIGGESPLSLED
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m528-1      MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD
          10      20      30      40      50      60

          70      80      90     100     110     120
g528-1.pep YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLVERFKQEGFDCLE
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m528-1      YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLIETFKQGGFDCLE
          70      80      90     100     110     120

          130
g528-1.pep KQGLRRNGLSERVRWX
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m528-1      KQGLRRNGLSERVRWX
          130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1517>:

a528-1.seq

```

1 ATGGAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCAAT
51 TACGGTTGCA GGCTGCCGGT TGGCAGGTG GTATGAGTGT TCGTCCCTGT
101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATT TTGGGATATT
151 GCGGCGGAGA GTCCCTCCGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG CCTGCGGGTT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG AAGGTTTGA
351 TTGTTTGAAA AAGCAGGGGT TGCGGCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1518; ORF 528-1.a>:

a528-1.pep

```

1 MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI
51 GGESPPSLED YEIPLSDGNR SVRANEYESA QQSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQEGFCLK KQGLRRNGLS ERVRW*

```

a528-1/m528-1 97.0% identity in 135 aa overlap

```

          10      20      30      40      50      60
a528-1.pep MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLSGWCKPRKPAAIDFWDIGGESPPSLED
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m528-1      MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD
          10      20      30      40      50      60

          70      80      90     100     110     120
a528-1.pep YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLIETFKQEGFCLK
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m528-1      YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLIETFKQGGFDCLE
          70      80      90     100     110     120

          130
a528-1.pep KQGLRRNGLSERVRWX
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m528-1      KQGLRRNGLSERVRWX
          130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1519>:

g529.seq (partial)

```

1 atgaccata tcaaaccgt cattgccgct ctgcactca tcgggcttgc
51 cgctgctcc ggcagcaaaa ccgaacagcc caagctcgac taccaaagcc
101 ggtcgaccg cctgatcaaa ctcgaagtcc cgctgattt gaacaacccc
151 gaccaaggca acctctaccg cctgcctgcc gggtcgggag ccgtccgcgc
201 cggggatttg gaaaaacgcc gcacaccgc cgtccaacag ccagcggatg
251 ccggaagtat tgaaaagcgt caaaggcgtc cgcttcgagc ggcgacggca
301 gccaacgcct ggcttgtcgt tgacggcaaa tccccgcgc aaatctccgc
351 cgctttctg.

```

This corresponds to the amino acid sequence <SEQ ID 1520; ORF 529.ng>:

g529.pep (partial)

```

1 MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNNP
51 DQGNLYRLPA GSGAVRAGDL EKRRTPAVQQ PADAGSIEKR QRRPLRAATA
101 ANAWLVVDGK SPAEISAAP..

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1521>:

m529.seq

```

1 ATGACCCATA TCAAACCCGT CATTGCCGCG CTCGCACTCA TCGGGCTTGC
51 CGCCTGCTCC GGCAGCAAAA CCGAACAGCC CAAGCTCGAC TACCAAAGCC
101 GGTGCGACCG CCTGATCAAA CTTGAAGTCC CACCTGATTG GAACAACCCC
151 GACCAAGGCA ACCTCTACCG CCTGCCTGCC GGTTCCGGCG CCGTCCGCGC
201 CAGCGATTG GAAAAACGCC GCACACCCGC CGTCCAACAG CCTGCCGATG
251 CCGAAGTATT GAAAAGCGTC AAAGGTGTCC GCCTCGAGCG CGACGGCAGC
301 CAACGCTGGC TCGTTGTCTGA CGGCAAGTCT CCTGCCGAAA TCTGGCCGCT
351 CCTGAAAGCC TTTTGGCAGG AAAACGGCTT CGACATCAAA TCCGAAGAAC
401 CCGCCATCGG ACAAATGGAA ACCGAGTGGG CGGAAAACCG CGCCAAAATC
451 CCCCAGACA GCTTGCGCCG CCTCTTCGAC AAAGTCGGCT TGGGCGGCAT
501 CTACTCCACC GGCGAGCGCG ACAAATTCAT CGTCCGTATC GAACAGGGCA
551 AAAACGGCGT TTCCGACATC TTCTTCGCCC ACAAAGCCAT GAAAGAAGTG
601 TACGGCGGCA AAGACAAAGA CACGACCGTA TGGCAGCCCT CCCCCTCCGA
651 TCCCAACCTC GAAGCCGCTT TCCTGACGCG CTTATGCAA TATTGGGCG
701 TTGACGACA GCAGGCGGAA AACGCATCGG CAAAAAACC TACCCTTCCC
751 GCCGCCAAGC AAATGGCGCG TATCGAAGGC AAAAGCCTGA TTGTCTTGG
801 CGACTACGGC AGAAACTGGC GGCACACCGT GTCGCCCTC GACCGCATCG
851 GGCTGACCGT CGTCGGTCAA AACACCGAAC GCCACGCCTT CCTGTTCAA
901 AAGCCCCGA ACGAAAGCAA TGCAGTTACC GAACAAAAC CCGGCTGTT
951 CAAACGCTG CTGGGCAAAG GCAAAGCGGA GAAACCTGCC GAACAGCCG
1001 AACTGATTGT CTATGCAGAA CCTGTCGCCA ACGGCTCGCG CATCGTCCTG
1051 CTAACAAAG ACGGCAGCGC ATATGCCGGC AAAGACGCAT CCGCATTATT
1101 GGGCAAATC CATTCCGAAC TGCCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1522; ORF 529>:

m529.pep

```

1 MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNNP
51 DQGNLYRLPA GSGAVRASDL EKRRTPAVQQ PADAENVLSV KGVRLERDGS
101 QRWLVVDGKS PAEIWPLLKA FWQENGFDIK SEEPALIGME TEWAENRAKI
151 PQDSLRLRLFD KVGLGGIYST GERDKFIVRI EQGKNGVSDI FFAHKAMKEV
201 YGGKDKDTTV WQPSPPDPNL EAAFLTRFMQ YLGVDDQQA NASAKKPTLP
251 AANEMARIEG KSLIVFGDYG RNWRTVLAL DRIGLTVVGQ NTERHAFLVQ
301 KAPNESNAVT EQKPLFKRL LGKGKAEKPA EQPELIVYAE PVANGSRIVL
351 LNKDGSAYAG KDASALLGKL HSELRL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 529 shows 83.5% identity over a 115 aa overlap with a predicted ORF (ORF 529.ng) from *N. gonorrhoeae*:

g529/m529

```

10      20      30      40      50      60
g529.pep MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNNPDQGNLYRLPA

```

```

a529.seq
1  ATGACCCATA  TCAAACCCGT  CATTGCCGCG  CTCGCACTCA  TCGGGCTTGC
51  CGCCTGCTCC  GGCAGCAAAA  CCGAACAGCG  CAAGCTCGAG  TACCAAAGCC
101 GGTGCGACCG  CCTGATCAAA  CTCGAAGTCC  CACCTGATTT  GAACAACCCC
151 GACCAAGGCA  ACCTCTACCG  CCTGCCTGCC  GGTTCGGGCG  CCGTCCGCGC
201 CAGCGATTTG  GAAAAACGCC  GCACACCCGC  CGTCCAACAG  CCTGCCGATG
251 CGAAGTATT  GAAAAGCGTC  AAAGGTGTCC  GCCTCGAGCG  CGACGGCAGC
301 CAACGCTGGC  TCGTTGTCTA  CGGCAAGTCT  CATGCCGAAA  TCTGGCCGCT
351 CCTGAAGGCC  TTTTGGCAGG  AAAACGGCTT  CGACATCAAA  TCCGAAGAAC
401 CCGCAATCGG  ACAAATGGAA  ACCGAGTGGG  CGGAAAAACG  TGCCAAATC
451 CCCCAAGACA  GCTTGCGCCG  CCTATTCGAC  ACAGTCGGTT  TGGGCGGCAT
501 CTACTCCACC  GGCGAGCGCG  ACAAATTCAT  CGTCCGTATC  GAACAGGGCA
551 AAAACGGCGT  TTCCGACATC  TTCTTCGCCC  ACAAAGCCAT  GAAAGAAGTG
601 TACGGCGGCA  AAGACAAGA  CACGACCCTA  TGGCAGCCCT  CCCCCTCCGA
651 TCCCAACCTC  GAAGCCGCTT  TCCTGACCG  CTTTATGCAA  TATTTGGGCG
701 TTGACGGACA  GCAGGCGGAA  AACGCATCGG  CAAAAAAACC  TACCCTTCCC
751 GCCGCCACCG  AAATGGCGCG  TATCGAAGGC  AAAAGCCCTG  TTGTCTTTGG
801 CGACTACGGC  AGAAATTCGC  GGCGCACCGC  GCTCGCCCTC  GACCGCATCG
851 GGTGACCGT  CGTCGGTCAA  AACACCGAAC  GCCACGCTTT  CCTGGTTCAA
901 AAAGCCCCGA  ACGAAAGCAA  TGCAGTTACC  GAACAAAAAC  CCGGCCCTGT
951 CAAACGCCTG  CTGGGCAAAG  GCAAAGCGGA  GAAACCTGCC  GAACAGCCGG
1001 AACTGATTGT  CTATGCCGAG  CCTGTCCGCA  ACGGCTCGCG  CATCGTCTTG
1051 CTCACAAAG  ACGGCACGCG  ATATGCCGCG  AAAGACGCAT  CCGCATTATT
1101 GGGCAAACTC  CATTCGGAAC  TGC GTTAA

```

a529.pep

1	<u>MTHIKPVIAA</u>	<u>LALIGLAACS</u>	GSKTEQPKLD	YQSRSHRLIK	LEVPPDLNPN
51	DQGNLYRLPA	GSgAVRASDL	EKRRTPAVQK	PADAEVLKSV	KGVRLERDGS
101	QRWLVDGKS	HAElWPLlKA	FWQENGFDIQ	SEEPAlGOME	TEWAENRAKI
151	PQDSLRLRlFD	TVGLGGYlST	GERDKFlVlRI	EQKNGVSDl	FFAHKAMKEV
201	YGGKDKDlTTV	WQPSpSDPNL	EAAFlTRFMQ	YlGVDGQQAE	NASAKKPTlP
251	AAENMARIEG	KSlVlFGDYG	RNWRRtAlAL	DRlGLTVVGQ	NTERHAFlVQ
301	KAPNESNAVT	EQKPlGLFKRL	LKGKGAEKPA	EQPElIVYAE	PVANGSRlVL
351	LNKDGSAAYG	KDASAlLlGLK	LSHL*		

	10	20	30	40	50	60
m529.pep	MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNPNPDQGNLYRLPA					
a529	MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNPNPDQGNLYRLPA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m529.pep	GSGAVRASDLEKRRTPAVQQPADAEVLKSVKGVRLERDGSQRWLVDGKSPAEIWPLLKA					
a529	GSGAVRASDLEKRRTPAVQQPADAEVLKSVKGVRLERDGSQRWLVDGKSHAEIWPLLKA					
	70	80	90	100	110	120
	130	140	150	160	170	180

800

```

m529.pep      FWQENGFDIKSEEPaIGQMETEWaENRAKIPQDSLRRlFDKVGLGGIYSTGERDKFIVRI
a529          FWQENGFDIKSEEPaIGQMETEWaENRAKIPQDSLRRlFDTVGLGGIYSTGERDKFIVRI
              130      140      150      160      170      180

              190      200      210      220      230      240
m529.pep      EQGKNGVSDIFFaHKAMKEVYGGKDKDttVWQPSpSDPNLEaAFLTRFMQYlGVDGQQAe
a529          EQGKNGVSDIFFaHKAMKEVYGGKDKDttVWQPSpSDPNLEaAFLTRFMQYlGVDGQQAe
              190      200      210      220      230      240

              250      260      270      280      290      300
m529.pep      NASAKKPTLPaANEMARIEGKSLIVFGDYGRNWRRTVLaLDRIGlTVVGQNTeRHaFLVQ
a529          NASAKKPTLPaANEMARIEGKSLIVFGDYGRNWRRTaLaLDRIGlTVVGQNTeRHaFLVQ
              250      260      270      280      290      300

              310      320      330      340      350      360
m529.pep      KAPNESNAVTEQKpGLFKRLLGKGKAEKPAEQPElIVYAEPVANGSRIVLLNKDGsAYAG
a529          KAPNESNAVTEQKpGLFKRLLGKGKAEKPAEQPElIVYAEPVANGSRIVLLNKDGsAYAG
              310      320      330      340      350      360

              370
m529.pep      KDASALLGKLHSELRX
a529          KDASALLGKLHSELRX
              370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1525>:

```

g530.seq
1   atgagtgcga gcgcggaat gacgggtttg atatgggtca tcgtgtcatc
51  ctgtgtgatg gatattaaag tgtttgcatt gttatgccgt ccgaacggtt
101 cagacggcat ggctatatat aaagtgtgcc tgaggctttc agggcggcgc
151 ggacttttgc ctgtccgcct tccgtcagcg gaacgagcgg caggcgacg
201 tgcggtccgc atccgcccac gccgataacc gccatttcg gtgcggcggg
251 actgggttcg cagaacatgg tgcgtaaat cggaatcagc cggtcgttga

```

This corresponds to the amino acid sequence <SEQ ID 1526; ORF 530.ng>:

```

g530.pep
1   MSASAAMTGL IWVIVSSCVm DIKVFVMLCR PNGSDGMAIF KVLRLSGRR
51  GLLPVRLPSA ERAAGARAVER IRPRIPPIS VRRDWVRRTW CRKSESAGR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1527>:

```

m530.seq
1   WTGAGTGCGA GCGCGGCAAT GACGGGTyTG ATATGGGTCA TCGTGTcATC
51  STGTGTGATG GATATTAAAG TGtYTGTTGC GwTATGCCGT CCGAACGGTT
101 CGGACGGCAT GGmTATATTT AAAGTTGTCC TGAGGCTTTC AGGGCGGCGC
151 GGACTkTTGC WTGTCCGTTT yCCGTcAGCG GAACGAGCGG CAGGCGGACG
201 TGGGTTTCGC ATCTGCCCAg GCGGATAACC GCCATTTCG GTGCGGCGGG
251 GCTGGGTTTC CAGAACATGG TGTCGTAAAT CGGAATCAGT CGGTcGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1528; ORF 530>:

```

m530.pep
1   XSASAAMTGL IWVIVSSCVm DIKVXVAXCR PNGSDGMXIF KVLRLSGRR
51  GLLXVRFPsa ERAAGGRAVR ICPGRIPPIS VRRGWVRRTW CRKSESVGR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 530 shows 88.8% identity over a 98 aa overlap with a predicted ORF (ORF 530.ng) from *N. gonorrhoeae*:

```

m530/g530
m530.pep      XSASAAMTGLIWVIVSSCVMDIKVXVAXCRPNGSDGMXIFKVLRLSGRRGLLXVRFPsa 60
              |||

```

801

```

g530      MSASAAMTGLIWVIVSSCVMDIKVFVMLCRPNGSDGMAIFKVVLRLSGRRGLLPVRLPSA 60
           10      20      30      40      50      60
m530.pep  ERAAGGRAVRICPGRIIPPISVRRGWVRRTWCRKSESVGR 99
           |||||:||||| | ||||| ||||| ||||| ||||| |||||
g530      ERAAGRAVRIRPRRIIPPISVRRDWVRRTWCRKSESAGR 99

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1529>:

```

a530.seq
  1  ATGAGTGCGA GCGCGGCAAT GACGGGTTTG ATATGGGTCA TCGTGTCA TC
 51  CTGTGTGATG GATATTAAAG TGTGTGTTGC GTTATGCCGT CCGAACGTTT
101  CGGACGGCAT GGCTATATTT AAAGTTGTCC TGAGGCTTTC AGGCGGCGC
151  GGAATTTTGC CTGTCCGCCT TCCGTCAGCG GAACGAGCGG CAGGCGGACG
201  TGCGGTTCGC ATCTGCCCAG GCGGATACC GCCATTTCG GTGCGCGGG
251  GCTGGGTTCG CAGAACATGG TGTCGTAAAT CGGAATCAGC CGTCTGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1530; ORF 530.a>:

```

a530.pep
  1  MSASAAMTGL IWVIVSSCVMDIKVFVLCR PNGSDGMAIF KVVLRRLSGRR
 51  GLLPVRLPSA ERAAGGRAVR ICPGRIIPPIS VRRGWVRRTW CRKSESAGR*

```

m530/a530 93.9% identity in 98 aa overlap

```

m530.pep  XSASAAMTGLIWVIVSSCVMDIKVXVAXCRPNGSDGMXIFKVVLRLSGRRGLLXVRFPSA 60
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a530      MSASAAMTGLIWVIVSSCVMDIKVFVLCRPNGSDGMAIFKVVLRLSGRRGLLPVRLPSA
           10      20      30      40      50      60

m530.pep  ERAAGGRAVRICPGRIIPPISVRRGWVRRTWCRKSESVGRX
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a530      ERAAGGRAVRICPGRIIPPISVRRGWVRRTWCRKSESAGR
           70      80      90      100

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1531>:

```

g531.seq
  1  ATGACCGCCC TACTCGTCAT CCTCGCCCTC GCCCTGATAG CCGTCGGCAC
 51  GGCAGGCATC GTCTATCCCG CCCTGCCCGG CTGGGCATTG ATGTTTGCCG
101  GAACATGGCT GCTTGCCTAT GCCGGCGGCT ATCAAATCTA CGGCGCAGGC
151  ATCTTGTTGA CGGTCGGACT CATCAGCCTT GGCGGCATAC TGGCGGACTA
201  TATGGCAGGC ATGTTGGGGG TAAATACAC TGGGGCAGGC AAATCGCCG
251  TCCGAGGTGC ATTGGCCGGC AGCATCATCG GCATATTTT CTCCCTTCCC
301  GGAATAATAC TCGGCCCTT TATCGGCGCG GCGGCAGGCG AACTGATCGA
351  TCGGCGCAAT ATGCTTCAGG CAGGTAAAGC GGGCTTGGT ACGCTGTTGG
401  GGCTTGTCGT CGGCACGGCG TTCAAAATCG GCTGCGCCGT ATCCATCTTG
451  TTTATCCTGT TGGTGAAATA CATCGCATAC CTGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1532; ORF 531.ng>:

```

g531.pep
  1  MTALLVILAL ALIAVGTAGI VYPALPGLAL MFAGTWLLAY AGGYQIYGAG
 51  ILWTVGLISL GGILADY MAG MLGVKYTGAG KLAVRGALAG SIIGIFFSLP
101  GLILGPFIGA AAGELIDRRN MLQAGKAGLG TLLGLVVGTA FKIGCAVSIL
151  FILLVKYIAY LF

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1533>:

```

m531.seq
  1  ATGACCGTAC TGACCGTCAT CCTCGCCCTC GCCCTGATAG CCGTCGGCAC
 51  GGCAGGCATC GTTTACCCCG CCCTGCCCGG ATTGGCATTG ATGTTTGCCG
101  GAACATGGCT GCTTGCCTAT GCCGGCGGCT ACCAAATCTA CGGCGCGGGC
151  GTTTTGTTGA CGGTCGGACT CATCAGCCTT GCCGGCATAC TGGCGGACTA
201  TGTGGCAGGC ATATGGGGGA CAAATATAC CGGAGCGGGC AAGCTCGCCG
251  TTCGCGGCGC ATTGGCCGGC AGCATCATCG GCATATTTT CTCCCTTCCC
301  GGAATAATAC TCGGTCCCTT TATCGGCGCG GCGGCAGGCG AACTGATCGA

```

351 ACGGCGCAAT ATGCTTCAGG CAGGTAAAGC GGGCTTGGGT ACGCTGTTGG
 401 GGCTTGTCTG CCGCACGGCG TTCAAAATCG GCTGCGCnGT ATCCATCTTG
 451 TTTATCCTGT TGGTGAAATA CATCGCCTAC CTGTTTAA

This corresponds to the amino acid sequence <SEQ ID 1534; ORF 531>:

m531.pep

1 MTVLTVILAL ALIAVGTAGI VYPALPGLAL MFAGTWLLAY AGGYQIYGAG
 51 VLWTVGLISL AGILADYVAG IWGTYTGAG KLAVRGALAG SIIGIFFSLP
 101 GLILGPFIGA AAGELIERN MLQAGKAGLG TLLGLVVGTA FKIGCAVSIL
 151 FILLVKYIAY LF*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 531 shows 94.4% identity over a 162 aa overlap with a predicted ORF (ORF 531.ng) from *N. gonorrhoeae*:

m531/g531

	10	20	30	40	50	60
m531.pep	MTVLTVILALALIAVGTAGIVYPALPGLALMFAGTWLLAYAGGYQIYGAGVLWTVGLISL					
g531	MTALLVILALALIAVGTAGIVYPALPGLALMFAGTWLLAYAGGYQIYGAGILWTVGLISL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m531.pep	AGILADYVAGIWGTYTGAGKLAVRGALAGSIIGIFFSLPGLILGPFIGAAAGELIERN					
	:	:	:	:	:	:
g531	GGILADYVAGMLGVKTYTGAGKLAVRGALAGSIIGIFFSLPGLILGPFIGAAAGELIDRRN					
	70	80	90	100	110	120
	130	140	150	160		
m531.pep	MLQAGKAGLGTLGLVVGTA FKIGCAVSILFILLVKYIAYLF					
g531	MLQAGKAGLGTLGLVVGTA FKIGCAVSILFILLVKYIAYLF					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1535>:

a531.seq

1 ATGACCGCCT TGCTCGTCAT CCTCGCCCTC GCCCTGATAG CCGCCGGTAC
 51 GGCGGGCATC GTTTACCCCG CCCTGCCCGG ATTGGCATTG ATGTTTGCCG
 101 GAACCTGGCT GCTCGCCTAC TCCGGCGGCT ACCAAATCTA CGGCGCGGGC
 151 GTTTTGTTGA CGGTCCGACT CATCAGCCTT GCCGGCATA TGGCGGACTA
 201 TGTGGCAGGC ATATGGGGGA CAAAATATAC CGGAGCGGGC AAGCTCGCCG
 251 TTCGCGGCGC ATTGGCCGGC AGCATCATCG GCATATTTTT CTCCCTTCCC
 301 GGAATAATAC TCGGTCCCTT TATCGGCGCG CGGCGAGGCG AACTGATCGA
 351 ACGGCGCAAT ATGCTTCAGG CAGGTAAAGC GGGCTTGGGT ACGCTGTTGG
 401 GGCTTATCGT CGGTACGGCG TTCAAAATCG GCTGCGCCGT ATCCATCTTG
 451 TTTATCCTGT TGGTGAAATA CATCGCCTAC CTGTTTAA

This corresponds to the amino acid sequence <SEQ ID 1536; ORF 531.a>:

a531.pep

1 MTALLVILAL ALIAAGTAGI VYPALPGLAL MFAGTWLLAY SGGYQIYGAG
 51 VLWTVGLISL AGILADYVAG IWGTYTGAG KLAVRGALAG SIIGIFFSLP
 101 GLILGPFIGA AAGELIERN MLQAGKAGLG TLLGLVVGTA FKIGCAVSIL
 151 FILLVKYIAY LF*

m531/a531 96.9% identity in 162 aa overlap

	10	20	30	40	50	60
m531.pep	MTVLTVILALALIAVGTAGIVYPALPGLALMFAGTWLLAYAGGYQIYGAGVLWTVGLISL					
a531	MTALLVILALALIAAGTAGIVYPALPGLALMFAGTWLLAYS SGGYQIYGAGVLWTVGLISL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m531.pep	AGILADYVAGIWGTYTGAGKLAVRGALAGSIIGIFFSLPGLILGPFIGAAAGELIERN					

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```

a531      |||||
          AGILADYVAGIWGTKYTGAGKLAVRGALAGSIIGIFFSLPGLILGPFIGAAAGELIERN
          70      80      90      100      110      120

          130      140      150      160
m531.pep  MLQAGKAGLGTLLGLVVGTA FKIGCAVSILFILLVKYIAYLFX
          |||||:|||||
a531      MLQAGKAGLGTLLGLIVGTA FKIGCAVSILFILLVKYIAYLFX
          130      140      150      160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1537>:

g532.seq (partial)

```

1  atggctgaaa caatgaaaaa acagggcgat tcgcctgatt tgggtgtacgg
51  tttagaagac aggcgcgcgt tcggtaatgc gctcttgagc gcggttacct
101 atcttttggc gattttctgt ccgatgatta cgcgcgcgt gattgtgggc
151 ggcgcgctgg aattgccggt ggagatgacg gcgtatctgg tgcgatggc
201 gatggttgcg tcgggtgtcg gcacttattt gcaggtcaac cgcttcgggt
251 cggtcggctc ggggatgctg tccatccagc gttaccgtca tgattgcgct
301 cggcgcgggg atgaaagagg gcggtttgag ...

```

This corresponds to the amino acid sequence <SEQ ID 1538; ORF 532.ng>:

g532.pep (partial)

```

1  MAETMKKQAD SPDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51  GALELPVEMT AYLVSAMVA SGVGTYLQVN RFGSVGSGML SIQRYRHDC
101 RRGDERGRFE ...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1539>:

m532.seq

```

1  ATGAGCGGTC AGTTGGGCAA AGGTGCGGAT GCGCCTGATT TGGTGTACGG
51  TTTGGAAGAC AGGCCGCCGT TCGGTAATGC GCTCTTGAGC GCGGTTACCC
101 ATCTTTTGGC GATTTTGTG CCGATGATTA CGCCCGCGCT GATTGTGGGC
151 GGC GCGCTGG AATTGCCGGT GGAGATGACG GCGTATCTCG TGTCGATGGC
201 GATGTTTGGC TCGGGTGTG GCACTTATTT GCAGGTCAAC CGCTTCGGGC
251 CGGTCGGTTC GGGGATGCTG TCCATCCAGT CCGTGAATTT TTCGTTTCGT
301 ACCGTGATGA TTGCGCTGGG CGCGGGGATG AAAGAGGGCG GTTTGACTAA
351 GGATGCGATG ATTTGACGCG TCTTGGGCGT ATCGTTTGTC GGCGCGTTTT
401 TGGTGTGTTT CTCGGCGTGG CTTCTGCCGT ATTTGAAAAA AGTGATTACG
451 CCGACGGTCA GCGGCGTGGT CGTGATGCTC ATTGGTTTGA GTTTGGTACA
501 CGTCGGCATT ACCGATTTG GCGGCGGCTT CGGCGCGAAG GCGGACGGCA
551 CGTTCGGCTC GATGAAAAAC TTGGGGCTGG CATCGCTGGT GTTGCTGATT
601 GTGTTGGTGT TCAACTGCAT GAAAAACCG CTGTTGCGCA TGAGCGGCAT
651 TGCGGTCGGG CTGATTGCCG GCTATATCGT CGCGCTGTTT TTGGGCAAGG
701 TGGATTTTTC CGCGCTGCAA AACCTGCCGC TGGTTACGCT GCGCGTACCG
751 TTTAAATACG GTTTTGCTTT CCACTGGCAC GCGTTTATTG TGGCGGGCGC
801 GATTTTCTTG TTGAGCGTGT TTGAGGCGGT CGGCGATTTA ACCGCGACGG
851 CAATGGTGTG CGACAGCCG ATTGAAGGCG AGGAATACAC CAAACGCCGT
901 CGCGGCGGCG TGTTGGCTGA CGGCTTGGTG TCGGTGATTG CGACGGCTTT
951 GGGTTCGCTG CCGCTGACGA CGTTTGCGCA AAACAACGGC GTGATTCAGA
1001 TGACCGGCGT GGCTTCGCGC CATGTGGGCA AATATATTGC CGTGATTTTG
1051 GTGCTGTTGG GTCTGTTCCC CGTTGTGGT CGCGCGTTTA CGACGATTCC
1101 GAGTCGGGTG TTGGGCGGCG CGATGGTTT GATGTCGGC TTAATTGCGA
1151 TTGCGGGCGT GCGGATTTTG GTCAGTCACG GCATCCGCG GCGCGAAGCG
1201 GTGATTGCGG CAACGTCGGT CGGTTTGGGC TTGGGTGTG CGTTTGAGCC
1251 GGAAGTGTG AAAAACCTGC CCGTCTTGTT CCAAACTCT ATTTCCGCCG
1301 GCGGCATTAC GGCAGTCTTG CTGAATTTGG TCTGCCCCGA AGATAAAACC
1351 GAGGCGGCGG TCAAGTTTGA TACCGACCAC TTGGAACACT GA

```

This corresponds to the amino acid sequence <SEQ ID 1540; ORF 532>:

m532.pep

```

1  MSGQLGKGAD APDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51  GALELPVEMT AYLVSAMVA SGVGTYLQVN RFGPVGSGML SIQSVNFSV
101 TVMIALGAGM KEGGLTKDAM ISTLLGVSVF GAFLVCFSAW LLPYLKKVIT
151 PTVSGVVVML IGLSLVHVGI TDFGGGFGAK ADGTFGSMEN LGLASLVLLI

```

201 VLVFNCMKNP LLRMSGIAVG LIAGYIVALF LGKVDFSALQ NLPLVTLVPV
 251 FKYGFADFVH AFIVAGAIFL LSVFEAVGDL TATAMVSDQP IEGEEYTKRL
 301 RGGVLADGLV SVIATALGSL PLTTFAQNNG VIQMTGVASR HVGKYIAVIL
 351 VLLGLFPVVG RAFTTIPSPV LGGAMVLMFG LIAIAGVRIL VSHGIRRREA
 401 VIAATSVGLG LGVAFEPEVF KNLPVLFQNS ISAGGITAVL LNLVLPEDKT
 451 EAAVKFDTDH LEH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF532 shows 91.4% identity over a 93 aa overlap with a predicted ORF (ORF 532.ng) from *N. gonorrhoeae*:

g532/m532

	10	20	30	40	50	60
g532 . pep	MAETMKQADSPDLVYGLED RPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT					
	:	:				
m532	MSGQLGKGADAPDLVYGLED RPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT					
	10	20	30	40	50	60
	70	80	90	100	110	
g532 . pep	AYLVSMAMVASGVGTYLQVNRFGSVGSGMLSIQRYRHDCARRGDERGRFEX					
m532	AYLVSMAMVASGVGTYLQVNRFGPVGSGMLSIQSVNFSFVTVMIALGAGMKEGGTLTKDAM					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1541>:

a532 . seq

1	ATGAGCGGTC	AGTTGGGCAA	AGGTGCGGAT	GCGCCTGATT	TGGTGTACGG
51	TTTGGAGGAT	AGGCCGCCGT	TCGGTAATGC	GCTCTTGAGC	GCGGTTACCC
101	ATCTTTTGGC	GATTTTGTG	CCGATGATTA	CGCCCGCGCT	GATTGTGGGC
151	GGCGCGCTGG	AATTGCCGGT	GGAGATGACG	GCGTATCTCG	TGTCGATGGC
201	GATGGTTGCG	TCGGGTGTCG	GCACTTATTT	GCAGGTCAAC	CGCTTCGGGC
251	CGGTCCGGTTC	GGGGATGCTG	TCCATCCAGT	CGGTGAATTT	CTCGTTCGTT
301	ACCGTCATGA	TTGCGCTCGG	CGCGGGGATG	AAAGAGGGCG	GTTTGACTAA
351	GGATGCGATG	ATTTTCGACG	TCTTGGGCGT	ATCGTTTGTC	GC CGCGTTT
401	TGGTGTGTTT	TTCGGCGTGG	CTTCTGCCGT	ATTTGAAAAA	AGTGATTACG
451	CCGACGGTCA	GCGGTGTGGT	GGTGATGCTG	ATCGGCTTGA	GTTTGGTACA
501	CGTCCGTATT	ACCGATTTTC	GCGGCGGCTT	CGGCGCAAAG	GCGGACGGCA
551	CGTTCGGCTC	GATGGA AAAC	TTGGGGCTGG	CATCGCTGGT	GCTGCTGATT
601	GTGCTGGTGT	TCAATTGCAT	GAAAAACCCG	CTGCTGCGGA	TGAGCGGCAT
651	TGCGGTCGGT	CTGATTGCCG	GCTATATCGT	CGCGCTGTTT	TTGGGCAAGG
701	TGGATTTTTC	GGCACTGCAA	AACCTGCCGC	TGGTTACGCT	GCCCGTACCG
751	TTTAAATATG	GTTTTGCTTT	TGACTGGCAC	GCATTTATTG	TGGCGGGTGC
801	GATTTTCTTG	TTGAGCGTGT	TTGAGGCGGT	CGGCGATTTG	ACGCGGACGG
851	CAATGGTGTC	CGACCAGCCG	ATTGAAGGCG	AGGAATACAC	CAAACGCTTG
901	CGCGGCGGCG	TGTTGGCGGA	CGGCTTGGTG	TCGGTGATTG	CGACGGCTTT
951	GGGTTTCGCTG	CCGCTGACGA	CGTTTGACAC	AAACAACGGC	GTGATTACAG
1001	TGACCGGCGT	GGCTTCGCGC	CATGTGGGCA	AATATATTGC	CGTGATTTTG
1051	GTGCTGTTGG	GTCTGTTCCC	CGTTGTGCGA	CGCGCGTTTA	CGACGATTCC
1101	GAGTCCGGTG	TTGGGCGGCG	CGATGGTTTT	GATGTTCCGC	TTGATTGCGA
1151	TTGCGGGCGT	GCGGATTTTG	GTCAGCCACG	GCATCCGCAG	GCGCGAAGCG
1201	GTAATTGCGG	CAACGTCGGT	CGGTTTGGGC	TTGGGTGTCG	CGTTTGAGCC
1251	GGAAGTGTTT	AAAAACCTGC	CCGTCTTGTT	CCAAAACCTCT	ATTTCCGCCG
1301	GCGGCATTAC	GGCAGTCTTG	CTGAATTTGG	TCTTGCCCGA	AGATAAAACC
1351	GAGGCGGCGG	TCAAGTTTGA	TACCGACCAC	TTGGAACACT	GA

This corresponds to the amino acid sequence <SEQ ID 1542; ORF 532.a>:

a532 . pep

1	MSGQLGKGAD	APDLVYGLED	RPPFGNALLS	AVTHLLAIFV	PMITPALIVG
51	GALELPVEMT	AYLVSMAMVA	SGVGTYLQVN	RFPGVSGGML	SIQSVNFSFV


```

101 TVMIALGAGM KEGGLTKDAM ISTLLGVSVFV GAFLVCFSAW LLPYLKKVIT
151 PTVSGVVVML IGLSLVHVGI TDFGGGFGAK ADGTFGSMEN LGLASLVLLI
201 VLVFNCKMNP LLRMSGIAVG LIAGYIVALF LGKVDFSALQ NLPLVTLFPV
251 FKYGFADFWDH AFIVAGAIFL LSVFEAVGDL TATAMVSDQP IEGEEYTKRL
301 RGGVLADGLV SVIATAGSL PLTTFAQNNG VIQMTGVASR HVGKYIAVIL
351 VLLGLFPVVG RAFTTIPSPV LGGAMVLMFG LIAIAGVRIL VSHGIRREA
401 VIAATSVGLG LGVAFEPEVF KNLPVLFQNS ISAGGITAVL LNLVLPEDKT
451 EAAVKFDTDH LEH*

```

m532/a532 100.0% identity in 463 aa overlap

m532.pep	MSGQLGKGADAPDLVYGLED	10	20	30	40	50	60
a532	MSGQLGKGADAPDLVYGLED	10	20	30	40	50	60
m532.pep	AYLVSMAMVASGVGT	70	80	90	100	110	120
a532	AYLVSMAMVASGVGT	70	80	90	100	110	120
m532.pep	ISTLLGVSVFVGAFLVCFSAW	130	140	150	160	170	180
a532	ISTLLGVSVFVGAFLVCFSAW	130	140	150	160	170	180
m532.pep	ADGTFGSMENLGLASLVLL	190	200	210	220	230	240
a532	ADGTFGSMENLGLASLVLL	190	200	210	220	230	240
m532.pep	NLPLVTLFPVPFKYGFADFWDH	250	260	270	280	290	300
a532	NLPLVTLFPVPFKYGFADFWDH	250	260	270	280	290	300
m532.pep	RGGVLADGLVSVIATAGSL	310	320	330	340	350	360
a532	RGGVLADGLVSVIATAGSL	310	320	330	340	350	360
m532.pep	RAFTTIPSPVLGGAMVLMFGL	370	380	390	400	410	420
a532	RAFTTIPSPVLGGAMVLMFGL	370	380	390	400	410	420
m532.pep	KNLPVLFQNSISAGGITAVL	430	440	450	460		
a532	KNLPVLFQNSISAGGITAVL	430	440	450	460		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1543>:

g535.seq

```

1 atgccctttc ccgttttcag acaantattt gcttngtcct tgctacggtt
51 ttttgccgta ggtcggattc tcgaatccga catttccaac agcgggtttt
101 cggaaacgat aaacgcgtca aatgtttttt ttgtcggata cgaatatccg
151 gcctgcattt caaatattaca tcgcttccaa tttcgcaaac ttggtatcca
201 gttctttcac gccctgtttg ccgaagttga tggtcagtcg ggcggattcg
251 cctttgtctg cggcatcgat aatcacgccg gtgccgaatt tggcgtgacg
301 gacgttttgt ccgatgcgga agcctgcgta ggtttgcggc tgtttgaagt

```

806

```

351 catcgatgat tttgtcccgt tgtacggtgg tttggcgcggt gttgccgtag
401 ctgtcgaagg cgggtttttt gacggacagg tagtgcaata cttctggcgg
451 gatttccttcg acgaagcggg atgcgatgcc gaattgggtt tgtccgtgca
501 gcatgcggtt ctgtgccatg gtgatgtaga ggcgtttgcy ggcgcgggtg
551 atggcgacgt acatgaggcg gcgttcttct tccagggccg cgcgctcggc
601 aaggctcatt tgcgtgggga aacgcccctc ttccataccg gtgaggaaga
651 cggcgttgaa ttccaagcct ttggcgcggt ggacgggtcat cagttggacg
701 gcttttttcgc ctgcccctgc ttggttttcg ccggattcga gggcgcggtt
751 gctcaagaag gcgaggatgg ggaagcgagg atcgtctga

```

This corresponds to the amino acid sequence <SEQ ID 1544; ORF 535.ng>:

```

g535.pep
  1 MPFPVFRQXF AXSLRFFAV GRILESDISN SGFSETINAS NVFVGYEYEP
 51 ACISNLHRFQ FRKLGIOFFH ALFAEVDGQS GGFAFVCGID NHAGAEFGVT
101 DVLSDAEACV GLRLFVIDD FVPLYGGLAR VAVAVEGGFF DGQVVQYFWR
151 DFFDEAGCDA ELGLSVQHAL LCHGDVEAFA GAGDGDVHEA AFFFEAAALG
201 KAHFAGETPL FHTGEEDGVE FQAFGGVDGH QLDGFFACPC LVFAGFEGGV
251 AQEGEDGEGG IV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1545>:

```

m535.seq
  1 aTGCCCTTtC CCGTTTTTCAG ACGGCCTTTT GCTTTGTCTT TACTtACGTT
 51 TTTTGCCGTA AGTCAGATTTC TTGTATCCGA CATTTCACAC AGCGGTGTTT
101 CGGAAACAAT AGACGCGTCA AATGTTTTTG TCGGATACGA ATATCCGACC
151 TACATTTCAA ATTTACATCT CTTCCAATTT CGCAAACCTG GTGTCCAAC
201 CTTTCACGCC CTGTTTGCCG AAATTGATGG TCAGTCGGGC GGATTCGCCT
251 TTATCTGCGG CATCGATAAT CACGCCGGTG CCGAATTGG CGTGGCGGAC
301 GTTTTGTCCG ATACGGAAAC CTGCGTAGGT TTGGGGCTGT TTGTAGTCGT
351 CGATGATTTT ATCTTTGGAT GCGGCGGTTT GGCGCGTGTT GCCGTAACTG
401 TCGTAGGCAG GCTTTTTTGAC GGACAGGTAG TGCAATACTT CCGGTGGGAT
451 CTCTTCGACG AAGCGGGAGA CGATGCCGAA TTGGGTTTGT CCGTGCACGA
501 TGCGTTGTTG CGCCATGGTG ATGTAGAGGC GTTTGCGGGC GCGGGTGATG
551 GCGACGTACA TGAGGCGGCG TTCTTCTTCG AGGCCGCCGC GTTCGGCAAG
601 GCTCATTTTC CTGGGGAAGC GGCCTTCTTC CATGCCGGTG AGGAAGACGG
651 CGTTAAATTC CAAGCCTTTG GCGGCGTGGA CGGTCATGAG TTGGACGGCC
701 TTTTCGCCTG CGCCTGCCTG GTTTTCACCG GATTCGAGGG CGGCATTGCT
751 TAGGAAGGCG AGAATGGGGA AGGCGGGGTC GTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1546; ORF 535>:

```

m535.pep
  1 MPFPVFRFPF ALSLLTFFAV SQILVSDISN SGVSETIDAS NVFVGYEYPT
 51 YISNLHLFQF RKLGVQLFHA LFAEIDGQSG GFAFICGIDN HAGAEFGVAD
101 VLSDTETCVG LGLFVVVDDF IFGCGGLARV AVTVVGRFLD GQVVQYFGWD
151 LFDEAGDDAE LGLSVQHALL RHGDVEAFAG AGDGDVHEAA FFFEAAAFGK
201 AHFAGEAAFF HAGEEDGVKF QAFGGVDGHE LDGLFACACL VFTGFEGGIA
251 XEGENGEGBV V*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 535 shows 80.9% identity over a 262 aa overlap with a predicted ORF (ORF 535.ng) from *N. gonorrhoeae*:

```

m535/g535
      10      20      30      40      50      59
m535.pep  MPFPVFRFPFALSLLTFFAVSQILVSDISNSGVSETIDASNVF-VGYEYPTYISNLHLFQ
          |||||: || ||| ||||: || ||||| ||||: |||| | ||||: |||| |
g535      MPFPVFRQXFAXSLRFFAVGRILESDISNSGFSETINASNVFVGYEYPACISNLHRFQ
          10      20      30      40      50      60

      60      70      80      90      100     110     119
m535.pep  FRKLGVLQFHALFAEIDGQSGGFVAFICGIDNHAGAEFGVADVLSDTETCVGLGLFVVDD
          ||||: ||: ||||: ||||| ||||: ||||| ||||: ||||: |||| | ||: ||
g535      FRKLGIOFFHALFAEVDGQSGGFVFCGIDNHAGAEFGVTDVLSDAEACVGLRLFVIDD
          70      80      90      100     110     120

```

	120	130	140	150	160	170	179
m535.pep	FIFGCGGLARVAVTVVGR LF DFDQVVQYFGWDLFDEAGDDAELGLSVQHALLRHGDVEAFA						
	:						
g535	FVPLYGGLARVAVAVEGGFFDQVVQYFWRDFFDEAGCDAELGLSVQHALLCHGDVEAFA						
		130	140	150	160	170	180
m535.pep	180	190	200	210	220	230	239
	GAGDGDVHEAAFFFEAAAFGKAHFAGEAAFFHAGEEDGVKFQAFGGVDGHELDGLFACAC						
g535	GAGDGDVHEAAFFFEAAALGKAHFAGETPLFHTGEEDGVEFQAFGGVDGHQLDGGFFACPC						
		190	200	210	220	230	240
m535.pep	240	250	260				
	LVFTGFEGGIA XE GENGEGGVV						
g535	LVFAGFEGGV AQ EGEDGEGGIV						
		250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1547>:

```

a535.seq (partial)
1   TTCAGACGGC CTTTTGCCTT GTCCTTGCTA CAGTTTTTTTG CCATAGGTCG
51  GATTCTCGAA TCCGACATTT CCAACAGCGG TTTTTCGGAA ACGATAGACG
101 CGTCAAATAT TTTTGTCCGA TACGAGTATC CAGCCTGCAT TTCAAATTTA
151 CATCGCTTCC AATTTCGCAA ACTTGGTGTC CAACTCTTTC ACGCCCTGTT
201 TGCCGAAATT GATGGTCAGT CGGGCGGATT CCCTTTTATC TCGGGCATCG
251 ATAATCACGC CGGTGCCGAA TTTGGCGTGG CGGACGTTTT GTCCGATACG
301 GAAACCTGCG TAGGTTTGGG GCTGTTTGTA GTCGTCGATG ATTTTGTCTT
351 TGGGCGCGGC GGTATTGGCGC GTGTTGCCAT AGCGGTCGTA GGCGGGTTTT
401 TTGACGGACA GGTATGCAAA TACTTCGGTG GGGATTCTCT CGACGAAGCG
451 GGAGACGATG CCGAATTGGG TTTGTCCGGT CAGCATCGCT TGTTCGCCCA
501 TGGTGATGTA GAGGCGTTTG CGGGCGCGGG TGATGGCGAC GTACATCAGG
551 CGGCGTCTCT CTTTCAGGCC GCCGCGTTCG GCAAGGCTCA TTTTCGTGGG
601 GAAGCGGCCT TCTTCCATGC CGGTGAGGAA TACGGCGTTA AATTCCAAGC
651 CTTTGGCGGC GTGCACGGTC ATGAGTTGTA CGGCTTTTTT GCCCGCGCCT
701 GCTTGGTTTT GCCTGAGATC GAGAGCAGCA TTGCTTAGGA AAGCGAGGAT
751 GGGGAAGGCG GGGTCGTCTG A

```

This corresponds to the amino acid sequence <SEQ ID 1548; ORF 535.a>:

a535.pep (partial)

1	FRRPFALSL	QFFAIGRILE	SDISNSGFSE	TIDASNIFVG	YEYPACISNL
51	HRQFQFKLGV	QLFHAFIAEI	DGQSGGFAFI	CGIDNHAGAE	FGVADVLSDT
101	ETCVGLGLFV	VDDFVVFGRG	GLARVAIAV	GGFFDQGVVQ	YEGRDFDFDE
151	GDDAELGLSV	QHALLRHGDV	EAFAGAGDGD	VHQAATFFFEA	AAFGKAHFAG
201	EAAFFHAGEE	YGVKFQAFGG	VHGHELYGFF	ARACLVFAGF	ESSIA*ESED
251	GEGGVV*				

m535/a535 88.7% identity in 256 aa overlap

```

      10      20      30      40      50      60
m535.pep  MPFPVFRPPFALSLLTFFAVSQILVSDISNSGVSETIDASNVFVGYEPTYISNLHLFQF
          |||||::| |||||:|||||: |||||
a535      FRRPFALSLLQFFAIGRILESDISNSGFSETIDASNIFVGYEYPACISNLHRFQF
          10      20      30      40      50

      70      80      90      100     110     120
m535.pep  RKLGVQLFHALFAEIDGQSGGFAFICGIDNHAGAEFGVADVLSDTETCVGLGLFVVVDDF
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a535      RKLGVQLFHALFAEIDGQSGGFAFICGIDNHAGAEFGVADVLSDTETCVGLGLFVVVDDF
          60      70      80      90      100     110

      130     140     150     160     170     180
m535.pep  IFGCGGLARVAVTVGRLFDGQVVQYFGWDLFDEAGDDAELGLSVQHALLRHGDVEAFAG
          :|| |||||::||| :||| ||||| :||| ||||| ||||| ||||| ||||| |||||
a535      VFGRGGLARVAIVVGGFFDGQVVQYFGRDFFDEAGDDAELGLSVQHALLRHGDVEAFAG
          120     130     140     150     160     170

```

	190	200	210	220	230	240
m535.pep	AGDGDVHEAAFFFEAAAFGKAHFAGEAAFFHAGEEDGVKFQAFGGVDGHELDGLFACACL					
a535	AGDGDVHQAAFFFEAAAFGKAHFAGEAAFFHAGEEYGVKFQAFGGVHGHELYGFFARACL					
	180	190	200	210	220	230
	250	260				
m535.pep	VFTGFEGGIIAXEGENGEggVVX					
a535	VFAGFESSIAXESEDGEGGVVX					
	240	250				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1549>:

g537.seq

```

1  atgaaatccc tttttatttg gctgcttcta ttgggctcgg cggcaggcgt
51  tttctaccat acccaaaacc aatccctgcc cgcgggcgaa cttgtctatc
101 cgtccgcacc gcaaatacagg gacggcgggc atgcgctgca ctacctcaac
151 cgcataccga cacaatacgg ttgacacgct ctggcacacg cgccggtttt
201 ggaaaaattcc gcccgcaaggc acgcacgcta tctcacgctc aatcccgaa
251 acggacacgg cgaacacccat cccgacaatc cgactacac cgacaaaag
301 ctgaccgaac gcacacgcct tgccgggtat ctctacaacg gcgtgcatga
351 aaacatcagc acggaagagg aagccgccga atcgccgac agcgacatcc
401 gcacgcagca acgccaagtg gacgctttga tgagcgcaat ctaccaccgc
451 ctttcgctgc ttgaccgcca taccgacgaa gcaggtgcgg catttgtgcg
501 cgaaaaacggc aaaaccgtcc tcgtattcaa tcagggcaac ggcagcttcg
551 agcgcgcctg tgcaaaagga aggcggcagc cggaagcagg acggaaatat
601 taccgcaacg cttgccacaa cgggtgcggc gtttatgctg acgaagccat
651 gcccgtaacg gaattgcttt ataccgccta tccggttggc ggcggcgcg
701 tgccttattt ttacggggaa cgtcccgacc ccgtgccgga atatgaaatc
751 acaggcaatc ctgccagcat tgatttttcc gaggcggcag gcaaaattgc
801 gatgaaaagt ttcaagctgt atcagggtaa aaacgaaatc cgccccgtca
851 ggggttttaac cgccggcaac gaccctaacc gcaggctgac cgcgcaccaa
901 ttcgcccttt tcccgtcaa acctttggaa tacggcacgc tttatacggc
951 ggtattcgac tatgtccgca acggacggca cgcgaggcgg aaatggcagt
1001 ttagaaccgg aaaaaccgat tacccttatt ttgaggtaaa cggcgggcag
1051 aactttgctg ttagaaaagg cgaaaaatat ttcattccact ggcgcggacg
1101 ctggtgtctg gaagcgtgta cccgttatat ctaccggcgg cagttcggca
1151 acagcctgtc cactaccgg caggaagcgg gcggcattgt cttcagcgtc
1201 agcgggaatg cggaagcgg catcaggctt actccggaag acagcccgga
1251 acgcggtgta accctttatt tgcaggattg a

```

This corresponds to the amino acid sequence <SEQ ID 1550; ORF 537.ng>:

g537.pep

```

1  MKSLFIWLLL LGSAAGVFIH TONQSLPAGE LVYPSAPQIR DGGDALHYLN
51  RIRTQIGLHA LAHAPVLENS ARRHARYLTL NPEDGHGEHH PDNPHYTAQK
101 LTERTRLAGY LYNGVHENIS TEEEAESSD SDIRTQQRQV DALMSAIYHR
151 LSLDRHTDE AGAAFVRENG KTVLVFNQGN GSFERACAKG RROPEAGRKY
201 YRNACHNGAA VYADEAMPVT ELLYTAYPVG GGALPYFYGE RPDVPVEYEI
251 TGNPASIDFS EAAGKIAMKS FKLYQGKNEI RPVRVLTAGN DPNGLTAHQ
301 FALFPLKPLE YGTLYTAVFD YVRNGRHAQA KWQFRTRKPD YPYFEVNGGE
351 TLAVRKGEKY FIHWRGRWCL EACTRYTYRR QFGNSLSILR HEAGGIVFSV
401 SGMAGSRIRL TPEDSPERGV TLYLQD *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1551>:

m537.seq (partial)

```

1  ATGAAATCCC TTTTATTTCG GCTGCTCCTG TTGGGTTTCG CGGCAGGCGT
51  TTTCTACCAT ACCCAAACC AATCCCTGCC CGCGGGCGAA CTTGTCTATC
101 CGTCCGCACC GCAAATCAGG GACGGCGGCG ATGCGCTGCA CTACCTCAAC
151 CGCATCCGAG CCCAAATCGG TTTGCACAAG CTGGCACACG CGCCGTTT
201 GGAAGAACTCC GCGCGCAGGC ACGCAAGCTA CTCACGCTC AATCCCGAAG
251 ACGGACACGG CGAACACCAT CCCGACAATC CGCACTACAC CGCACAAAAG

```

301 CTGACCGAAC GCACACGCCT TGCCGGGTAT CTCTACAACG GCGTGCATGA
 351 AAACATCAGC ACGGAAGAAG AAGCCGCCGA ATCGTCCGAC AGCGACATCC
 401 GCACGCAGCA ACGCCAAGTG GACGGATTAA TGAGCGCAAT CTACCACCGC
 451 CTTTCCCTAC TTGACCGCCA TACGGATGAG TCAGGAGCGG CATT...

This corresponds to the amino acid sequence <SEQ ID 1552; ORF 537>:

m537.pep (partial)
 1 MKSLFIRLLL LGSAAGVFYH TQXQSLPAGE LVYPSAPQIR DGGDALHYLN
 51 RIRAQIGLHK LAHAPVLENS ARRHASVLTN NPEDGHGEHH PDNPHYTAQK
 101 LTERTRLAGY LYNGVHENIS TEEEAESSD SDIRTQQRQV DGLMSAIYHR
 151 LSLDRHTDE SGAA...

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 537 shows 95.7% identity over a 164 aa overlap with a predicted ORF (ORF 537.ng) from *N. gonorrhoeae*:

m537/g537

	10	20	30	40	50	60
m537.pep	MKSLFIRLLL LGSAAGVFYHTQXQSLPAGELVYPSAPQIRDGGDALHYLN RIRAQIGLHK					
g537	MKSLFIWLLL LGSAAGVFYHTQXQSLPAGELVYPSAPQIRDGGDALHYLN RIRIQIGLHA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m537.pep	LAHAPVLENSARRHASVLTN NPEDGHGEHH PDNPHYTAQK LTERTRLAGY LYNGVHENIS					
g537	LAHAPVLENSARRHARYLTN NPEDGHGEHH PDNPHYTAQK LTERTRLAGY LYNGVHENIS					
	70	80	90	100	110	120
	130	140	150	160		
m537.pep	TEEEAESSD SDIRTQQRQVDGLMSAIYH RLSLLDRHTDE SGAA					
g537	TEEEAESSD SDIRTQQRQVDALMSAIYH RLSLLDRHTDE AGA AFVRENGKTVLVFNQGN					
	130	140	150	160	170	180
	190	200	210	220	230	240
g537	GSFERACAKGR RQPEAGRKYRNACHNGAAVYADEAMPVTELLYTAYPVGGGALPYFYGE					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1553>:

a537.seq
 1 ATGAAATCCC TTTTATTTCG GCTGCTCCTG TTGGGTTCGG CGGCCGGCGT
 51 TTTCTATCAT ACCCAAAACC AATCCCTGCC CGCGGGCGAA CTTGTCTATC
 101 CGTCCGCACC GCAAATCAGG GACGGCGGCG ATGCGCTGCA CTACCTCAAC
 151 CGCATCCGCG CCCAAATCGG TTTGCACAAG CTGGCACACG CGCCGTTTTT
 201 GGAAATTC GCGCGCAGGC ACGCACGCTA TCTCACGCTC AATCCCGAAG
 251 ACGGACACGG CGAACACCAT CCCGACAATC CGCACTACAC CGCACAAAAG
 301 CTGACCGAAC GCACACGCCT TGCCGGGTAT CTCTACAACG GCGTGCATGA
 351 AAACATCAGC ACGGAAGAGG AAGCCGCCGA ATCGTCCGAC AGCGACATCC
 401 GCACGCAGCA ACGCCAAGTG GACGGATTAA TGAGCGCAAT CTACCACCGC
 451 CTTTCCCTAC TTGACCGCCA TACGGATGAG GCAGGAGCGG CATTGTGTGG
 501 CGAAAACGGT AAAACCGTTC TCGTATTCAA TCAGGGCAAC GGCAGGTTTG
 551 AGCGGCATTG CGCCCAAGGC AGAAATCAGC CGGAAGCAGG ACGGAAATAT
 601 TACCGCAACG CCTGCCATAA CGGTGCGGTC GTGTACACCG ACGAAGCCAT
 651 GCGCGCACAG GAGCTGCTCT ATACAGCCTA TCCGTCGCGC AACGGCGCAC
 701 TGCCTTATTT CCACGGCGAG CGTCCAGACC CCGTGCCGGA ATATGAAATC
 751 ACGGGCAATC CTGCCAGCAT TGATTTTTCG GAGGCGGCAG GCAAAATTAC
 801 GATGAAAAGT TTCAAGCTGT ATCAGGGTAA AAACGAAATC CGCCCGCTCA
 851 GGGTTTTTAA CGCCGGCAAC GACCCCAACG GCAGGCTGAC CGCGTACCAA
 901 TTCGCGCTTT TCCCGCTCAA GCCTTTGGAA TACGGTACGC TTTATACGGC
 951 GGTATTCGAC TATGTCCGCA ACGGACGGCG CGCGCAGGCG AAATGGCAGT
 1001 TTAGAACCAG AAAACCCGAT TACCCTTATT TTGAGGTAAA CGGCGGCGAG
 1051 ACACTTGCGG TTAGAAAAGG CGAAAAATAT TTCATCCACT GGCGCGGACG
 1101 CTGGTGTGTA GAAGCGTGTA CCCGTTATAC CTACCGGCAG CGACCCGGCA

1151 GCCGCCTGTC CATAGGAAGG CACAAGGCGG GCGGCATCGT CTCAGCGTT
 1201 GACGGAATGG CGGGCAGCCG CATCAGCCTT GCACCGGAAG GAGAAACGGA
 1251 ACGAGGCGTA ACCCTTTATT TACAGGATTG A

This corresponds to the amino acid sequence <SEQ ID 1554; ORF 537.a>:

a537.pep
 1 MKSLFIRLLL LGSAAGVFYH TQNQSLPAGE LVYPSAPQIR DGGDALHYLN
 51 RIRAQIGLHK LAHAPVLENS ARRHARYLTL NPEDGHGEHH PDNPHYTAQK
 101 LTERTRLAGY LYNGVHENIS TEEEAESSD SDIRTQQRQV DGLMSAIYHR
 151 LSLLDRHTDE AGAAFVRENG KTVLVFNQGN GRFERHCAQG RNQPEAGRKY
 201 YRNACHNGAV VYTDEAMPAQ ELLYTAYPVG NGALPYFHGE RPDVPPEYEI
 251 TGNPASIDFS EAAGKITMKS FKLYQGKNEI RPVRVLTAGN DPNGRLTAYQ
 301 FALFPLKPLE YGTLYTAVFD YVRNGRRAQA KWQFRTRKPD YPFYEVNGGE
 351 TLAVRKGEKY FIHWRGRWCL EACTRYTYRQ RPGSRLSIGR HKAGGIVFSV
 401 DGMAGSRITL APEGETERGV TLYLQD*

m537/a537 98.2% identity in 164 aa overlap

	10	20	30	40	50	60
m537.pep	MKSLFIRLLLLGSAAGVFYHTQXQSLPAGELVYPSAPQIRDGGDALHYLNIRIRAQIGLHK					
a537	MKSLFIRLLLLGSAAGVFYHTQXQSLPAGELVYPSAPQIRDGGDALHYLNIRIRAQIGLHK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m537.pep	LAHAPVLENSARRHASYLTLNPEDGHGEHHPDNPHYTAQKLTERTRLAGYLYNGVHENIS					
a537	LAHAPVLENSARRHARYLTLNPEDGHGEHHPDNPHYTAQKLTERTRLAGYLYNGVHENIS					
	70	80	90	100	110	120
	130	140	150	160		
m537.pep	TEEEAAESSDSDIRTQQRQVDGLMSAIYHRLSLLDRHTDESGAA					
a537	TEEEAAESSDSDIRTQQRQVDGLMSAIYHRLSLLDRHTDEAGAAFVRENGKTVLVFNQGN					
	130	140	150	160	170	180
a537	GRFERHCAQGRNQPEAGRKYRYRNACHNGAVVYTDEAMPAQELLYTAYPVGNGALPYFHGE					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1555>:

g538.seq
 1 atgtcaggta gaacaggacg gaacagtgc actcaggcgc aaccggaacg
 51 cgtcatgctg gtgggcgtaa tggttgataa agatgatacg ggcagcaatg
 101 ccgcccgtct gaacggtttt cagacggcat tggcggaagc cgtcgagctg
 151 gtcaaagcgg cgggcggcga ttccgtacgc gtggagactg ccaaaccgca
 201 ccgcccgcac actgcgctgt ttgtcggcac gggcaaggcg gcggagctgt
 251 cggaagcagt tgccgcagac ggcattgatt tggtcgtatt caaccacgaa
 301 cttactccca cgcaggaacg caatttgga aaaatcctcc aatgccgcgt
 351 attggacaga gtggggctga ttctggcgat ttctgcccgc cgcgcccgcg
 401 cgcaggaagg caggctgcaa gtcgagttgg cgcaattgag ccatttggcg
 451 ggacgcttga tacgcggtta cggacatttg caaagccagc gcggcggtat
 501 cggcatgaaa gggccgggcg aaaccaaact ggaaaccgac cgccgattaa
 551 ccgcccacat gatcaacgcc ttgaaaaaac agcttgccaa cctcaaaaaa
 601 cagcgcgccc tgcgcgcgaa gtcccgcgag tcgggcagaa tcaaaacgtt
 651 tgcgctggtc ggctatacca atgtcgcaa atccagcctg ttcaaccggc
 701 tgaccaagtc gggcatatat gcgaaagacc agcttttcgc cactctcgac
 751 acgacggcgc ggcggctgta catcagtccc gcatgcagca ttatcctgac
 801 cgataccgtc ggattcgtca gcgatctgcc gcacaaactg atttcgcctt
 851 ttcccgccac cttggaagaa accgtgcaag ccgatgtgct gctgcacgtc
 901 gtcgatgctg ccgcccggaa cagcgggag cagattgaag acgtggaaaa
 951 cgtactgcaa gaaatccatg cccacgatat tccgtgcac aaggtgtaca
 1001 acaaaaccga cctgctgccg tctgaagaac aaaacacggg catatggcgc
 1051 gacgctgcgg gaaaaattgc cgcgctccgc atttccgttg ctgaaaatac

This corresponds to the amino acid sequence <SEQ ID 1556; ORF 538.ng>:

g538.pep

```

1  MSGRTGRNSA TQAQPERVML VGVMLDKDDT GSNAARLNGF QTALAEAVEL
51  VKAAGGDSVR VETAKRDRPH TALFVGTGKA AELSEAVAAD GIDL VVFNHE
101 LTPTQERNLE KILQCRVLDL VGLILAIFAR RARTQEGRLQ VELAQLSHLA
151 GRLIRGYGHL QSQRGGIGMK GPGETKLETD RRLTAHRINA LKKQLANLKK
201 QRALRRKSRE SGRIKTFALV GYTNVGKSSL FNRLTKSGIY AKDQLFATLD
251 TTARRLYISP ACSIIILTDV GFVSDLPKHL ISAFSATLEE TVQADVLLHV
301 VDAAARNSGQ QIEDVENVLQ EIAHDIPCI KVINKTDLPL SEEQNTGIWR
351 DAAGKIAAVR ISVAENTGID ALREAIAEYC AAPNTDETE MP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1557>:

m538.seq

```

1  ATGACAGGCA GAACAGGCGG CAACGGCAGT ACCCAAGCGC AACCCGAACG
51  CGTCATGCTG GTGGGCGTAA TGTTGGACAA AGATGGTACG GGCAGTAGTG
101 CCGCCCGTCT GAACGGTTTT CAGACGGCAT TGGCGGAAGC TGTCGAGCTG
151 GTCAAAGCGG CGGGCGGCGA TTCCGTGCGC GTGGAGACTG CCAAACGCGA
201 CCGTCCGCAC ACCGCGCTGT TTGTCGGCAC GGGCAAGGCG GCGGAGCTGT
251 CAGAAGCAGT TGCCGCAGAC GGCATCGATT TGGTCGTATT CAACCACGAA
301 CTCACGCCCA CGCAGGAACG CAACCTTGAA AAAGAACTsA AATGCCGCGT
351 ATTGGACAGG GTAGGGCTGA TTCTGGCGAT TTTCTGCTCGC CGCGCCCGCA
401 CGCAGGAAGG CAGGCTGCAA GTCGAGTTGG CGCAATTGAG CCATTGTGCG
451 GGACGCTTGA TACGCGGTTA CGGCCATCTG CAGAGCCAGC GCGGCGGTAT
501 CGGCATGAAA GGCCCCGGCG AAACCAAACG GGAACCCGAC CGCCGATTGA
551 TCGCCCATCG GATCAATGCC TTGATAAAAC AGCTTGCCAA CCTCAAAAAA
601 CAGCGCGCCC TCGCCGCGAA GTCnCGCGAA TCGGGCACAA TCAAAACGTT
651 TGCGCTGGTC GGCTATACAA ATGTCGGAAA ATCCAGCCTG TTCAACCGGC
701 TGACAAAGTC GGCATATAT GCAAAGGACA AGCTTAGTCC CGAATGCAGC
751 ATTATCCTGA CCGATACCGT CGGATTTCGTn AGCGATCTGC CGCACAAACT
801 GATTTCCGCC TTTTCgCC.A CGCTGGAAGA AACCGCGCAA GCCGATGTGC
851 TGCTGCACGT CGTCGATGCC GCCGCTCCGA ACAGCGGACA GCAGATTGAA
901 GACGTGGAAA ACGTACTGCA AGAAATCCAT GCCGGCGATA TTCCGTGCAT
951 cAAGGTGTAC AACAAAACCG ACCTGCTGCC GTCTGAAGAA CAAAACACGG
1001 GCATATGGCG CGACGCTGCG GGAAAAATTG CCGCCGTCCG CATTTCCGTT
1051 GCTGAAAATA CCGGTATAGA CGCACTGCGC GAAGCcATTG CCGAGTCTTG
1101 TGCCGCCGCA CCAAACACAG ACGAAACCGA AATGCCATGA

```

This corresponds to the amino acid sequence <SEQ ID 1558; ORF 538>:

m538.pep

```

1  MTGRTGGNGS TQAQPERVML VGVMLDKDGT GSSAARLNGF QTALAEAVEL
51  VKAAGGDSVR VETAKRDRPH TALFVGTGKA AELSEAVAAD GIDL VVFNHE
101 LTPTQERNLE KELKCRVLDL VGLILAIFAR RARTQEGRLQ VELAQLSHLA
151 GRLIRGYGHL QSQRGGIGMK GPGETKLETD RRLIAHRINA LIKQLANLKK
201 QRALRRKSRE SGTIKTFALV GYTNVGKSSL FNRLTKSGIY AKDKLSPECS
251 IILTDTVGFV SDLPKHLISA FSXTLEETAQ ADVLLHVDA AAPNSGQQIE
301 DVENVLQEIH AGDIPCIKVY NKTDLLPSEE QNTGIWRDAA GKIAAVRISV
351 AENTGIDALR EAIAESCAAA PNTDETEMP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 538 shows 92.1% identity over a 392 aa overlap with a predicted ORF (ORF 538.ng) from *N. gonorrhoeae*:

m538/g538

	10	20	30	40	50	60
m538.pep	MTGRTGGNGSTQAQPERVMLVGVMLDKDGTGSSAARLNGFQTALAEAVELVKAAGGDSVR					
g538	MSGRTGRNSATQAQPERVMLVGVMLDKDDTGSNAARLNGFQTALAEAVELVKAAGGDSVR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m538.pep	VETAKRDRPHTALFVGTGKAELSEAVAADGIDL VVFNHELTPTQERNLEKELKCRVLDL					
g538	VETAKRDRPHTALFVGTGKAELSEAVAADGIDL VVFNHELTPTQERNLEKILQCRVLDL					

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	70	80	90	100	110	120
m538.pep	130	140	150	160	170	180
	VGLILAIFARRARTQEGRLQVELAQLSHLA	GRRLIRGYGHLQSQ	RGGIGMKGPGETK	LETD		
g538	VGLILAIFARRARTQEGRLQVELAQLSHLA	GRRLIRGYGHLQSQ	RGGIGMKGPGETK	LETD		
	130	140	150	160	170	180
m538.pep	190	200	210	220	230	240
	RRLIAHRINALIKQLANLKKQ	RALRRKSRESGTIKTF	ALVGYTNVGKSSLFN	RRLTKSGIY		
g538	RRLTAHRINALKKQLANLKKQ	RALRRKSRESGRIKTF	ALVGYTNVGKSSLFN	RRLTKSGIY		
	190	200	210	220	230	240
m538.pep	250	260	270	280		
	AKDKL-----SPECSI	ILTDTVGFVSDLP	HKLISAFSXTLEETA	QADVLLHV		
g538	AKDQLFATLDTTARRLYIS	PACSIILTDTVGFVSDLP	HKLISAFSATLEETV	QADVLLHV		
	250	260	270	280	290	300
m538.pep	290	300	310	320	330	340
	VDAAAPNSGQOIEDVENVLQ	EIHAGDIPCIKVYNKTD	LLPSEEQNTGIWRDAAG	KIAAVR		
g538	VDAAARNSGQOIEDVENVLQ	EIHAGDIPCIKVYNKTD	LLPSEEQNTGIWRDAAG	KIAAVR		
	310	320	330	340	350	360
m538.pep	350	360	370	380		
	ISVAENTGIDALREAIAES	CAAPNTDETEMPX				
g538	ISVAENTGIDALREAIAEY	CAAPNTDETEMPX				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1559>:

```

a538.seq
1  ATGACAGGCA GAACAGGCCG CAACGGCAGT ACCCAAGCGC AACCCGAACG
51  CGTCATGCTG GTGGGCGTAA TGTTGGACAA AGATGGTACG GGCAGCAGTG
101 CCACCCGTCT GAACGGTTTT CAGACGGCAT TGGCGGAAGC TGTCGAGCTG
151 GTCAAAGCGG CGGGCGGCGA TTCCGTGCGC GTGGAGACTG CCAAACGCGA
201 CCGTCCGCAC ACCGCGCTGT TTGTCGGCAC GGGCAAGGCG GCGGAGCTGT
251 CGGAAGCAGT TGCCGCAGAC GGCATCGATT TGGTCGTATT CAACCACGAA
301 CTTACGCCCA CGCAGGAACG CAATTTGGAA AAAATCCTCC AATGCCGCGT
351 ATTGGACAGA GTGGGGCTGA TTCTGGCGAT TTTCGCCCCG CGCGCCCGCA
401 CGCAGGAAGG CAGGCTGCAA GTCGAGTTGG CACAATTGAG CCATTTGCGC
451 GGACGCTTGA TACGCGGTTA CGGCCATCTG CAGAGCCAGC GCGGCGGTAT
501 CGGCATGAAA GGCCCCGGCG AAACCAAACG GGAACCGAC CGCCGATTGA
551 TCGCCCATCG GATCAATGCC TTGAAAAAAC AGCTTGCCAA CCTCAAAAAA
601 CAGCGCGCCC TCGCCGCAA GTCCCGCGAA TCGGGCACA TCAAAACGTT
651 TCGCTGGTGC GGCTATACCA ATGTCGGCAA ATCCAGTCTG TTCAACCGGC
701 TGACCAAGTC GGGCATATAT GCGAAAGACC AGCTTTTCGC CACACTCGAC
751 ACGACGGCGC GGCGGCTGTA CATCAGTCCC GAATGCAGCA TTATCCTGAC
801 CGATACCGTC GGATTCGTCA GCGATCTGCC GCACAAACTG ATTTCCGCCT
851 TTTCGCCCAC GCTGGAAGAA ACCGCGCAAG CCGATGTGCT GCTGCACGTC
901 GTCGATGCCG CCGCTCCGAA CAGCGGACAG CAGATTGAAG ACGTGGAAAA
951 CGTACTGCAA GAAATCCATG CCGGCGATAT TCCGTGCATC AAGGTGTACA
1001 ACAAACCGA CCTGCTGCCG TCTGAAGAAC AAAACACGGG CATATGGCGC
1051 GACGCTGCGG GAAAAATTGC CGCCGTCCGC ATTTCCGTTG CTGAAAATAC
1101 CCGTATAGAC GCACTGCGCG AAGCCATTGC CGAGTATTGT GCCGCCGCAC
1151 CAAACACAGA CGAAACCGAA ATGCCATGA

```

This corresponds to the amino acid sequence <SEQ ID 1560; ORF 538.a>:

```

a538.pep
1  MTGRTGRNGS TQAPPERVML VGVM LDKDGT GSSATRLNGF QTALAEAVEL
51  VKAAGGDSVR VETAKRDRPH TALFVGTGKA AELSEAVAAD GIDL VVFNHE
101 LTPTQERNLE KILQCRVLDR VGLILAIFAR RARTQEGRLQ VELAQLSLA
151 GRLIRGYGHL QSQRGGIGMK GPGETKLETD RRLIAHRINA LKKQLANLKK

```


201 QRALRRKSRE SGTIKTFALV GYTNVGKSSL FNRLTKSGIY AKDQLFATLD
 251 TTARRLYISP ECSIILTDTV GFVSDLPHKL ISAFSATLEE TAQADVLLHV
 301 VDAAAPNSGQ QIEDVENVLQ EIHAGDIPCI KVYNKTDLLP SEEQNTGIWR
 351 DAAGKIAAVR ISVAENTGID ALREAIAEYC AAPNTDETE MP*

m538/a538 94.6% identity in 392 aa overlap

	10	20	30	40	50	60
m538.pep	MTGRTGGNGSTQAQPERVMLVGVM LDKDGTGSSAARLNGFQTALAEAVELVKAAGGDSVR					
	: : : : :					
a538	MTGRTGRNGSTQAQPERVMLVGVM LDKDGTGSSATRLNGFQTALAEAVELVKAAGGDSVR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m538.pep	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDL VVFNHELTPTQERNLEKELKCRVLD R					
	: : : : :					
a538	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDL VVFNHELTPTQERNLEKILQCRVLD R					
	70	80	90	100	110	120
	130	140	150	160	170	180
m538.pep	VGLILAIFARRARTQEGRLQVELAQLSHLAGRLIRGYGHLQSQRGGIGMKGPGETKLETD					
	: : : : :					
a538	VGLILAIFARRARTQEGRLQVELAQLSHLAGRLIRGYGHLQSQRGGIGMKGPGETKLETD					
	130	140	150	160	170	180
	190	200	210	220	230	240
m538.pep	RRLIAHRINALIKQLANLKKQALRRKSRESGTIKTFALVG YTNVGKSSLFNRLTKSGIY					
	: : : : :					
a538	RRLIAHRINALKKQLANLKKQALRRKSRESGTIKTFALVG YTNVGKSSLFNRLTKSGIY					
	190	200	210	220	230	240
	250	260	270	280		
m538.pep	AKDKL-----SPECSIILTDTVGFVSDLPHKLISAFSXTLEETAQADVLLHV					
	: : : : : :					
a538	AKDQLFATLDTTARRLYISPECSIILTDTVGFVSDLPHKLISAFSATLEETAQADVLLHV					
	250	260	270	280	290	300
	290	300	310	320	330	340
m538.pep	VDAAAPNSGQQIEDVENVLQEIHAGDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
	: : : : :					
a538	VDAAAPNSGQQIEDVENVLQEIHAGDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
	310	320	330	340	350	360
	350	360	370	380		
m538.pep	ISVAENTGIDALREAIAESCAAPNTDETEMPX					
	: : : : :					
a538	ISVAENTGIDALREAIAEYCAAPNTDETEMPX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1561>:

g539.seq

```

1  atggaggatc tgcaggaaat cgggttcgat gtcgccgccg taaaggtagg
51  tcggcagcgc gaacatcatc gtctgcatca taccagtcgc ggcaacggca
101 aggcggacga tgtattgttt gcgttctttt tggttggcgg cttcgatttt
151 ttgcgcgtca tagggtgcgg cgggtgtagc tgtctgccgg attttcaaca
201 gaatgtcggg gaggcggatt ttgccgtcgt cccagacgac gcggcagcgg
251 tgcgtgctgt aattgaggtc gatgcggacg atgccgtctg tgcgcaaaag
301 ctgctgttcg atcagccaga cgcaggcggc gcaggtaatg ccgctgagca
351 tcagcactgc ttcgtgcgtg ccattatggg tttccacaaa gtcggatttg
401 acttcgggca ggtcgtacag gcggatttgg tcgaggattt cttggggcgg
451 cagttcgggt ttttcgcgt cggcggtgcg tcgtttgtaa taactgccca
501 agccggaatc gatgatgctt tgtgcgactg cctgacagcc gacgcagcag
551 gtttcgcggg cttcgccttc gtagcggacg gtcagatgca ggttttcggg
601 aacgtccagc ccgcagtggg aacaggtttt tttcatggca tttcggtttc

```

```

651 gtctgtgttt ggtgcggcgg cacaatactc ggcaatggct tcgcgcagtg
701 cgtctatacc ggtatatttca gcaacggaaa tgcggacggc ggcaattttt
751 cccgcagcgt cgcgccatat gcccgtgttt tgttcttcag acggcagcag
801 gtcggttttg ttgtacacct tgatgcacgg aatatcgtgg gcatggattt
851 cttgcagtac gttttccacg tcttcaatct gctgcccgt gttccgggcg
901 gcagcatcga cgacgtgcag cagcacatcg gcttgcacgg tttcttccaa
951 ggtggcggaa aaggcggaaa tcagtttgtg cggcagatcg ctgacgaatc
1001 cgacgggtatc ggtcaggata atgctgcatg cgggactgat gtacagccgc
1051 cgcgccgtcg tgtcgagagt ggcgaaaagc tgggtctttcg catatatgcc
1101 cgacttggtc agccggttga acaggctgga tttgccgaca ttggtatag

```

This corresponds to the amino acid sequence <SEQ ID 1562; ORF 539.ng>:

g539.pep

```

1 MEDLQEIGFD VAAVKVGRQR EHHRLHHTQS GNGKADDVLF AFFLVGGFDF
51 LRVIGCGGVA CLPDFQQNVG EADFAVVPDD AAARAVIEV DADDAVCAQK
101 LLFDQPDAGG AGNAAEHQHC FVRAIMGFHK VGLDFGQVVQ ADLVEDFLGR
151 QFGFFRVGGA SFVITAQAGI DDALCDCLTA DAAGFAVFAF VADGQMVFVG
201 NVQPAVETGF FHGISVSSVF GAAQYSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHMPVF CSSDGSRSVL LYTLMHGISW AWISCSTFST SSICCPFLFA
301 AASTCSSTS ACTVSSKVAE KAEISLCGRS LTNPVSVRI MLHAGLMYSR
351 RAVVSRVAKS WSFAVMPDLV SRLNRLDLPT LV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1563>:

m539.seq (partial)

```

1 ATGGAGGATT TGCAGGAAAT CGGGTTCGAT GTCGCCGCCG TAAAGGTAGG
51 TCGGCAGCGC GAACATCATC GTCTGCATCA TCCCAGCCC GGCAACGGCG
101 AGGCGGACGA TGTATTGTTT GCGTCTTTT TGTTGGCGG CTTCCGATTTT
151 TTGCGCGTCA TAGGGTGC GGTTGTAGCC TATCTGCCTG ATTTTCAACA
201 GAATGTCGGA AAGGCGGATT TTGCCGTCGT CCCAGACGac GCGGCaGcgG
251 TCGGTGCTGT AATTGAGGTC GATGCGGACG ATGCCGTCTG TACGCAAAAG
301 CTGCTGTTCG ATCAGCCAGA CGCAGGCGGC GCAGGTGATG CCGCCGAGCA
351 TTAAAACCGC CTCGCGCGTG CCGCCGTGGG TTTCCACAAA GTCGGA CTGG
401 ACTTCGGGCA GGTCTACAG GCGGATTTGG TCGAGGATTT CTGGGGCGG
451 CaGCTCGGTT TTTTGC GCGT CCGCGGTGCG TTGTTGTAA TAACTGCCCA
501 AGCCCGCGTC AATAATGCTT TGTGCGACCG CCTGACAGCC GGCGCaAgG
551 GTTTCGCGGT CTTCGTTTTT GTAACGGACA GTCAGGTGGA GGTGTTTCGG
601 AACATCCAGA CCGCAGTGGA AACAGGTTTT TTTTCATGGCA TTTCGGTTTT
651 GTCTGTGTTT GGTGCGGCGG CACAAGACTC GGCAATgGCT TCGCGCAGTG
701 CGTCTATACC GGTATTTTCA GCAACGGAAA TCGCGACGGC GGCAATTTTT
751 CCCGCAGCGT CGCGCCATAT GCGCGTGT TTCTTTCAG ACGGCAGCAG
801 GTCGGTTTTG TTGTACACCT TgATGCACGG AATATCGCCG GCATGGATT
851 CTTGCAGTAC GTTTTCCACG TCTTCAATCT GCTGTCCGCT GTTCGGAGCG
901 GCGGCATCGA CGACGTGCAG CAGCACATCG GCTTGC GCGG TTTCTTCCAG
951 CGTGGcG.AA AAGGCGGAAA TCAGTTTgTG CCGCAGATCG CTnACGAATC
1001 CGACGGTATC GGTcAGGATA ATGCTGCATT CGGGAC...

```

This corresponds to the amino acid sequence <SEQ ID 1564; ORF 539>:

m539.pep (partial)

```

1 MEDLQEIGFD VAAVKVGRQR EHHRLHHPQP GNGEADDVLF AFFLVGGFDF
51 LRVIGCGGVA YLPDFQQNVG KADFAVVPDD AAARAVIEV DADDAVCTQK
101 LLFDQPDAGG AGDAAEH*NR LARAAGVGHK VGLDFGQVVQ ADLVEDFLGR
151 QLGLRVGGA LfVITAQARV NNALCDRLTA GAQGFVAVFV VTDSQVEVFG
201 NIQTAVETGF FHGISVSSVF GAAQDSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHMPVF CSSDGSRSVL LYTLMHGISP AWISCSTFST SSICCPFLFA
301 AASTCSSTS ACAVSSSVAX KAEISLCGRS LTNPVSVRI MLHSG....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 539 shows 89% identity over a 345 aa overlap with a predicted ORF (ORF 539.ng) from *N. gonorrhoeae*:

m539/g539

```

          10      20      30      40      50      60
m539.pep  MEDLQEIGFDVAAVKVGRQREHHRLHHPQPGNGEADDVLF AFFLVGGFDFLRVIGCGGVA
          |||
g539      MEDLQEIGFDVAAVKVGRQREHHRLHHTQSGNGKADDVLF AFFLVGGFDFLRVIGCGGVA

```

815

	10	20	30	40	50	60
m539.pep	70	80	90	100	110	120
	YLPDFQQNVGKADFAVVPDDAAAVRAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR					
g539	CLPDFQQNVGEADFAVVPDDAAAVRAVIEVDADDAVCAQKLLFDQPDAGGAGNAAEHQHC					
	70	80	90	100	110	120
m539.pep	130	140	150	160	170	180
	LARAAGVFHKVGLDFGQVQADLVEDFLGRQLGFLRVGGALFVITAQARVNNALCDRLTA					
g539	FVRAIMGVFHKVGLDFGQVQADLVEDFLGRQFGFRVGGASFVITAQAGIDDALCDCLTA					
	130	140	150	160	170	180
m539.pep	190	200	210	220	230	240
	GAQGFVAFVFTDSQVEVFGNIQTAVETGFFHGISVSSVFGAAAQDSAMASRSASIPVFS					
g539	DAAGFAVFAFVADGQMVFQVGNQPAVETGFFHGISVSSVFGAAAQYSAMASRSASIPVFS					
	190	200	210	220	230	240
m539.pep	250	260	270	280	290	300
	ATEMRTAAIFPAASRHPVFCSSDGSRSVLLYTLMHGISPAWISCSTFSTSSICPLFGA					
g539	ATEMRTAAIFPAASRHPVFCSSDGSRSVLLYTLMHGISWAWISCSTFSTSSICPLFRA					
	250	260	270	280	290	300
m539.pep	310	320	330	340		
	AASTTCSSTSACAVSSSVAXKAEISLCGRSLTNPTVSVRIMLHSG					
g539	AASTTCSSTSACTVSSKVAEKAEISLCGRSLTNPTVSVRIMLHAGLMYSRRVAVSRVAKS					
	310	320	330	340	350	360
g539	WSFAYMPDLVSRLNRLDLPTLV					
	370	380				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1565>:

```

a539.seq
1  ATGGAGGATT TGCAGGAAAT CGGGTTCGAT GTCGCCGCCG TAAAGGTAGG
51  TCGGCAGCGC GAACATCATC GTCTGCATCA TCCCCAGCCC GGCAACGGCG
101 AGGCGGACGA TGTATTGTTT GCGTTCCTTT TGGTTGGCGG CTTCGATTTT
151 TTGCGCGTCA TAGGGTGCGG CGGTGTAGCC TATCTGCCTG ATTTTCAACA
201 GAATGTCGGA AAGGCGGATT TTGCCGTCGT CCCAGACGAC GCGGCAGCGG
251 TGCCTGCTGT AATTGAGGTC GATGCGGACG ATGCCGCTGT TACGCAAAAG
301 CTGCTGTTTC ATCAGCCAGA CGCAGGCGGC GCAGGTGATG CCGCCGAGCA
351 TTAACACCGC CTCGCGCGTG CCGCGGTGGG TTTCCACAAA GTCGGA CTGG
401 ACTTCGGGCA GGTCTGTACG GCGGATTGG TCGAGGATTT CTTGGGGCGG
451 CAGCTCGGTT TTTGCGCGT CCGCGGTGCG TTGTTTGTA TAACTGCCCA
501 AGCCCGCGTC AATAATGCTT TGTGCGACTG CCTGACAACC GCGCGAGCAG
551 GTTTCGCGGT CTTCGTTTTT GTAACGGACG GTCAGATGCA GGTTTTCGGG
601 AACGTCCAGC CCGCAGTGGA AACAGGTTTT TTTTCATGGCA TTTTCGTTTC
651 GTCTGTGTTT GGTGCGGCGG CACAATACTC GGCAATGGCT TCGCGCAGTG
701 CGTCTATACC GGTATTTTCA GCAACGGAAA TCGCGACGGC GGCAATTTT
751 CCCGCAGCGT CGCGCCATAT GCCCGTGTTT TGTTCTTCAG ACGGCAGCAG
801 GTCGGTTTTG TTGTACACCT TGATGCACGG AATATCGCCG GCATGGATT
851 CTTGCAGTAC GTTTTCCACG TCTCAATCT GCTGTCCGCT GTTCGGAGCG
901 GCGGCATCGA CGACGTGCAG CAGCACATCG GCTTGCGCGG TTTCTTCCAG
951 CGTGGCGGAA AAGGCGGAAA TCAGTTTG TGCGCAGATCG CTGACGAATC
1001 CGACGGTATC GGTGAGGATA ATGCTGCATT CGGGACTGAT GTACAGCCGC
1051 CGCGCCGTCG TGTCGAGTGT GGCGAAAAGC TGGTCTTTCG CATATATGCC
1101 CGACTTGGTC AGCCGGTTGA ACAGACTGGA TTTGCCGACA TTGGTATAG

```

This corresponds to the amino acid sequence <SEQ ID 1566; ORF 539.a>:

```

a539.pep
1  MEDLQEIGFD VAAVKVGRQR EHHRLHHPQP GNGEADDVLF AFFLVGGFDF

```

```

51  LRVIGCGGVA YLPDFQQNVG KADFAVVPDD AAARAVIEV DADDAVCTQK
101 LLFDQPDAGG AGDAAEH*NR LARAAVGFHK VGLDFGQVVQ ADLVEDFLGR
151 QLGFRLVGGG LFVITAQARV NNALCDCLTT GAAGFAVFVF VTDGQMVFVG
201 NVQPAVETGF FHGISVSSVF GAAQYSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHMPVF CSSDGSRSVL LYTLMHGISP AWISCSTFST SSICCPFLGA
301 AASTCSSTS ACAVSSSSVAE KAEISLCGRS LTNPVSVRI MLHSGLMYSR
351 RAVVSSVAKS WSFAYMPDLV SRLNRLDLPT LV*

```

m539/a539 97.1% identity in 345 aa overlap

```

          10      20      30      40      50      60
m539.pep  MEDLQEIGFDVA AVKVGRQREHRLHHPQPGNGEADDVLF AFFLVGGFDFLRVIGCGGVA
          |||
a539      MEDLQEIGFDVA AVKVGRQREHRLHHPQPGNGEADDVLF AFFLVGGFDFLRVIGCGGVA
          10      20      30      40      50      60

          70      80      90     100     110     120
m539.pep  YLPDFQQNVGKADFAVVPDDAAARAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR
          |||
a539      YLPDFQQNVGKADFAVVPDDAAARAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR
          70      80      90     100     110     120

          130     140     150     160     170     180
m539.pep  LARAAVGFHKVGLDFGQVVQADLVEDFLGRQLGFLRVGGALFVITAQARVNNALCDRLTA
          |||
a539      LARAAVGFHKVGLDFGQVVQADLVEDFLGRQLGFLRVGGALFVITAQARVNNALCDCLTT
          130     140     150     160     170     180

          190     200     210     220     230     240
m539.pep  GAQGFVAVFVFTDSQVEVFNGNIQTAVETGFFHGISVSSVFGAAAQDSAMASRSASIPVFS
          |||
a539      GAAGFAVFVFTDQGMQVFGNVQPAVETGFFHGISVSSVFGAAAQYSAMASRSASIPVFS
          190     200     210     220     230     240

          250     260     270     280     290     300
m539.pep  ATEMRTAAIFPAASRHMPVFCSSDGSRSVLLYTLMHGISP AWISCSTFSTSSICCPFLGA
          |||
a539      ATEMRTAAIFPAASRHMPVFCSSDGSRSVLLYTLMHGISP AWISCSTFSTSSICCPFLGA
          250     260     270     280     290     300

          310     320     330     340
m539.pep  AASTCSSTSACAVSSSSVAXKAEISLCGRSLTNPTVSVRIMLHSG
          |||
a539      AASTCSSTSACAVSSSSVAEKAEISLCGRSLTNPTVSVRIMLHSGLMYSRRRAVVSSVAKS
          310     320     330     340     350     360

a539      WSFAYMPDLVSRLNRLDLPTLVX
          370     380

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1567>:

```

g540.seq
1  atgccgccct cccgacgcgg caacgggggtg ttttatcaaa acggcaaaact
51  tgccaatgcg gtttccgctt gccgattgcc aaaccggcaa acctttcccg
101 tgccggtgcc gaaccgatg cgtctgaac cttcagacgg catcggtgtg
151 ttatttgctc actcggacgg gtgcaggttc gtattgtgtc gattcgctgc
201 cgtaatacag cagcccgagt ttgacgggga tgcgtccctg cgatttgccg
251 tgggcgttgg aatcgcgcaa ggaatacgcg cagccgcagt attcctgctg
301 gtagaagttt tcgcgtttgc tgatttcaat catacgcgcg ccgccgccgc
351 ctttgcgcca gttgaagtcc caataggcca catcatcgta aggcgcggcg
401 gcacggtgtc cgcagtcgtt gatttgcgcc atatttttcc agcgtga

```

This corresponds to the amino acid sequence <SEQ ID 1568; ORF 540.ng>:

```

g540.pep
1  MPPSRRNGV FYQNGKLANA VSACRLPNRQ TFPVPVNPMP PSEPSDGIGC

```

51 L FVHSDGCRF V LCRFVAVIQ HAEFDGDASL RFAVGVGIAQ GIRAAAVFLL
 101 VEVFAFADFN HTRAAAFAP VEVPIGHIIV RRGTVSAVV DLRHIFPA *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1569>:

m540.seq (partial)
 1 ..CCGAACCCGA TGCCGTCTGA ACCTTCAGAC GGCATCGGGT GTTTATTTGT
 51 CCACCCGGAT GGGGGCAGGT TCGTATTGTG TCGATTCGTC GCCGTAATAC
 101 AGCACGCCGA GTTTGATGGG GATTCTGCCC TGTGATTTCG GGTGGGCATT
 151 GGAATCCCTC AGGGAATAGG CACAACCGCA ATATTCCTGC TGGTAGAAGT
 201 TTTACGTTT GCTGATTTC AATCATGCGC CGCTGCCGCC GCCTTTGCGC
 251 CAGTTGAAAT CCCAATACAC CACATCATCG TAAGGCGCGG CGGCGCGGTG
 301 TCCGCAGTCG TTGATTTCG CCATATTTT CCAGCGTGA

This corresponds to the amino acid sequence <SEQ ID 1570; ORF 540>:

m540.pep (partial)
 1 ..PNMPSEPSD GIGCLFVHPD GGRFVLCRFV AVIQHAEFDG DSAL*FAVGI
 51 GIPOGIGTTA IFLLEVFTE ADFNHARAAA AFAPVEIPIH HIIVRRGGAV
 101 SAVVDLRHIF PA*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 540 shows 85.7% identity over a 112 aa overlap with a predicted ORF (ORF 540.ng) from *N. gonorrhoeae*:

m540/g540

		10	20	30
m540.pep		PNMPSEPSDGIGCLFVHPDGGRFVLCRFV		
g540	GNGVIFYQNGKLANAVSACRLPNRQTFVPVNPMPSEPSDGIGCLFVHSDGCRFVLCRFV			
	10 20 30 40 50 60			
	40 50 60 70 80 90			
m540.pep	AVIQHAEFDGDSALXFAVGIGIPQIGITTAIFLLVEVTFADFNHARAAAFAFVEIPIH			
	:: :: :: :: :: :: :: ::			
g540	AVIQHAEFDGDASLRFVAVGVGIAQGIRAAAVFLLVEVFAFADFNHTRAAAFAPVEVPIG			
	70 80 90 100 110 120			
	100 110			
m540.pep	HIIVRRGGAVSAVVDLRHIFPAX			
	:			
g540	HIIVRRGGTVSAVVDLRHIFPAX			
	130 140			

L' estremita' N-terminale di meningococco e' assente perche' interviene la fine del contig

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1571>:

a540.seq
 1 ATGCCGTCCT CCCGACGCGG CAACGGGGTG TTTTATCAAA ACGGCAAAC
 51 TGCCAATGCG GTTTCGATT GCAGATTGCC AAACCGGCAA ACCTTCCCG
 101 TGCCGATGCC GAACCGGATG CCGTCTGAAC CTTCAGACGG CATCGGGTGT
 151 TTATTTGTCC ACCCGGATGG GTGCAGGTTT GTATTGTGTC GATTCGTCGC
 201 CGTAATACAG CACGCCGAGT TTGATGGGGA TTCTGCCCTG TGATTGCGCG
 251 TGGGCGTTGG AATCCCTCAG GGAATAGGCA CAACCGCAAT ATTCCTGCTG
 301 GTAGAAAGTT TCACGTTTGC TGATTCAAT CACACGCGCG CTGCCGCCCG
 351 CTTTGCGCCA GTTGAAATCC CAATACACCA CATCATCGTA AGGCGCGCGC
 401 GCGCGGCGGC CGCAGTCGTT AATCTGGTTC ATGTTTTTCC A

This corresponds to the amino acid sequence <SEQ ID 1572; ORF 540.a>:

a540.pep (partial)
 1 MPSSRRNGV FYQNGKLANA VSDCRLPNRQ TFPVPMNPMP PSEPSDGIGC
 51 L FVHSDGCRF V LCRFVAVIQ HAEFDGDASL *FAVGVGIPQ GIGTTAIFLL
 101 VEFTFADFN HTRAAAFAP VEIPIHHIIV RRGGAAGAVV NLVHVF

m540/a540 92.8% identity in 111 aa overlap

```

                                10      20      30
m540.pep                      PNPMPSEPSDGIGCLFVHPDGGRFVLCRFV
                                |||||
a540      GNGVIFYQNGKLANAVSDCRLPNRQTFPVPMPNPMPSEPSDGIGCLFVHPDGGRFVLCRFV
              10      20      30      40      50      60

                                40      50      60      70      80      90
m540.pep      AVIQHAEFDGDSALXFAVGIGIPQGIGTTAIFLLVEVFTFADFNHARAAAFAPVEIPIH
              |||||
a540      AVIQHAEFDGDSALXFAVGIGIPQGIGTTAIFLLVEVFTFADFNHTRAAAFAPVEIPIH
              70      80      90      100     110     120

                                100     110
m540.pep      HIIIVRRGGAVSAVVDLRHIFPAX
              |||||
a540      HIIIVRRGGAAAVVNLVHVFP
              130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1573>:

```

g542.seq
1  atgccgaaat ggtcgcgcat acggcggttg agcgctcctt cgctgatgtt
51 cagcgcggct gtcagccggt tgacttggtg tgcgcgcccg tcgaacgcgg
101 cattcagggg gcggctgaag tcttcagacg gcatagcgtc tgcttcggcc
151 gtttgccccg ccgcccggct gatgccgtct gaaaccgtgt cccacaaatc
201 cgacagcagc cgcaacacgt ccgcctcgcg gcgcaatgtt tcgccccaaat
251 gcccctttgg gacggtttgc aggcaggatg ccgccaagcc gcgcagggtt
301 gggggcaaat cccatattcct gaccggttcg cggttaa

```

This corresponds to the amino acid sequence <SEQ ID 1574; ORF 542.ng>:

```

g542.pep
1  MPKWSRIRRC SVLSLMFSAA VSRLTWCAPP SNAAFRVRLK SSDGIASASA
51  VCPAAGSMPS ETVSHKSDSS RNTSASRRNV SPKCPFGTVC RQDAAKPRRF
101 GGKSHILTGS R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1575>:

```

m542.seq
1  ATGCCGAAAT GGTCGCGCAT ACGGCGTTGC AGCGTCCTTT CACTGATGTT
51  CAGCGCGTCT GTCAGCCGGT TGACTTGGTG TGCGCCGTCG GCAAACGCGG
101 CATTTAGGGT GCGGCTGAAG TCTTCAGACG GCATAGCGTC TGCTTCCGCC
151 GTTTGCCCCG CCGCCGGCCC GATGCCGTCT GAAACCGTGT CCCACAAGTC
201 CGACAGCAGC CGCAACACGT CCGCCTCGCG .CGCAATGTT TCGCCCAAAT
251 GCCCCTTTGG GACGGCTTTC AGGCAGGATG CCGCCAAGCC GCGCAGGTTC
301 GGGGGCAAAT CCCATATCCT GACCGGTTCG CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1576; ORF 542>:

```

m542.pep
1  MPKWSRIRRC SVLSLMFSAS VSRLTWCAPS ANAAFRVRLK SSDGIASASA
51  VCPAAGPMPS ETVSHKSDSS RNTSASRAMF RPNAFLGRNV SPKCPFGTAF
101 RQDAAKPRRF GGKSHILTGS R*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 542 shows 93.7% identity over a 111 aa overlap with a predicted ORF (ORF 542.ng) from *N. gonorrhoeae*:

```

m542/g542

                                10      20      30      40      50      60
m542.pep      MPKWSRIRRC SVLSLMFSAS VSRLTWCAPS ANAAFRVRLK SSDGIASASAVCPAAGPMPS
              |||||
g542      MPKWSRIRRC SVLSLMFSAAVSRLTWCAPPSNAAFRVRLKSSDGIASASAVCPAAGSMPS
              10      20      30      40      50      60

                                70      80      90      100     110
m542.pep      ETVSHKSDSSRNTSASXRNVS PKCPFGTAFRQDAAKPRRF GGKSHILTGSRX

```

```
a542.seq
1  ATGCCGAAAT  GGTGCGGCAT  ACGGCGTTGC  AGCGTCCTTT  CGCTGATGTT
51  CAGCGTGTCT  GCCAGCCGGT  TGACTTGATG  TGCGCCGCCG  CGAAACGCGG
101 CATTCAGGAT  GCGGCTGAAG  TCTTCAGACG  GCATAGCGTC  TGCTTCCGCG
151 GTTGGCCCCG  CCGCCGCCCC  GATGCCGTCT  GAAACCGTGT  CCCACAAGTC
201 CGACAGCAGC  CGCAACACGT  CCGCCTCGCG  GCGCAATGTT  TCGCCCAAAT
251 GCCCCTTTGG  GACGGCTTTC  AGGCAGGATG  CCGCCAAGCC  GCGCAGGTTT
301 GGGGGCAAAT  CCCATATCCT  GACCGGTTTC  CGGTAA
```

a542.pep

1	MPKWSRIRRC	SVLSLMFSVS	ASRLT*CAPP	ANAAFRMLRK	SSDGIASASA
51	VCPAAGPMPS	ETVSHKSDSS	RNTSASRRNV	SEKCPFGTAF	RQDAAKPRRF
101	GGKSHILTGS	R*			

	10	20	30	40	50	60
m542.pep	MPKWSRIRRCSVLSL	MFSASVSRLTWC	APSANAAFRVRLK	SSDGIASASAVCP	AAGPMPS	
a542	MPKWSRIRRCSVLSL	MFSVSASRLTXC	APPANAAFRMRLK	SSDGIASASAVCP	AAGPMPS	
	10	20	30	40	50	60
	70	80	90	100	110	
m542.pep	ETVSHKSDSSRN	TASXRNVSPKCP	FGTAFRQDAAKP	RRFVGKSHIL	TGSRX	
a542	ETVSHKSDSSRN	TASRRNVSPKCP	FGTAFRQDAAKP	RRFVGKSHIL	TGSRX	
	70	80	90	100	110	

```

g543.seq
1  atggtttgtc ggttatttgc cgccgttttt ggctttcaac tcggcaatca
51  gcccgctgat gcctttggct ttgatgattt cgccgaattg gttgcggtac
101 acggtaacca ggcctcgtgc ttcgatggcg acgttgtagg tacgggtattt
151 gccgcgcgtt tggtaggttg taaagtccat attgacgggc ttttgaccgg
201 ggatgcgcac ttccggcacgg acgacgattt ccttgccgcc ctctatgcag
251 atgggattgt ctttgacgtt gacggtcgcg tttttgaatt tcagcatcgt
301 gccggaatag gtgcggatca gcagggtttg aaattctttg gccaacgcct
351 gtttttgcgc gtcggacgcg gtacgccaag ggttgccgac cgccaatgcg
401 gtcatacggt ggaatacgaa atagggaacc gcataggctt cggtctttgg
451 gcgtgcagaa gccgcgtcgc cgctttttag gatgggtcaa aactgtgttg
501 cgttttgccg gatttgtccc atcgcgtcgg ccggggaggc aaatgccatg
551 ccgatgctca aaataccgat gcccaatgcg ctgatgaagg aggatttttt
601 cacgatgtct ttctgaaaa tggatgtgta tgttattctt gcggcttttt
651 ccgcattgcc gccctcagcg tttttctcgg cgaagctggg catgaattta
701 ccgatcaggt tttccagaac cattgcagaa ctggttacgg agatggtgtc
751 gccggcagca aggtttttccg tatcgcgcgc ctgctgcagc ccgatgtact
801 gttcgcccaa aagtcgccga gtcaggattt cgcgcgaaac gtcactgtcg
851 aactgatact tgccgtccaa atcaaggcgc accctgcctt gataggattt
901 cgggtcaagc ccgatagcgc cgacgcgccc gaccaatacg cctgcggatt
951 tgacgggggc attgacctt aaaccgccga tgtcgcggaa atcggcataa
1001 acggcgtaag ttttgcctca ccgcgcgaac gccgcgccg ccgccacgcg
1051 gaaagcgaga aaggcaaccg cgcgcgcgcc gatcaagacg aacagtcgga
1101 cccaaaaattc caatatgttc tttttcatta a

```

g5433.pep
1 MVCRLFAAVF GFQLGNQPVDF AFGFDDFAEL VAVHGNQARA FDGDVVGTVF

```

51  AAALVGGKVH IDGLLTGDAD FGTD DDFLAA LIDDGIVFDV DGRVFEFQHR
101 AGIGADQOGL KFFGQRLFLR VGRGTPRVAD RQCGHTLEIE IGNRIGFGFW
151 ACRSRVAAFE DGQNLGCVLA DLSHCVGRGG KCHADAQNTD AQCADEGGFF
201 HDVFPENGCV CLFCGFFRIA ALSVFLGEAG HEFTDQVFQN HCRTGYGDGV
251 AGSKVFRIAA LLQPDVLFQA KSRSQDLRGN VTAELILAVQ IKAHPRLIGF
301 RVKPSADAP DQYACGFDGG IDLQTADVAE IGINGVSFVR TAERRAARHA
351 ESEKGNRRRA DQDEQSDPKF QYVLH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1581>:

```

m543.seq
1  ATGTTTTGTC GGTTATTTGC CGCCGTTTTT GGCTTTCAAC TCGGCAATCA
51  GTCCGTCAC GCCTTTCGCT TTGATAATTT CGCCGAATTG GTTGCGGTAC
101 ACGGTAACCA GGCTCGCGCC TTCGATGGCG ACGTTGTAGG TACGTATTT
151 ACCGCCGCTT TGGTAGGTGG TGAAGTCCAT GTTGACGGGT TTTTGCCCGG
201 GTACGCCGAC TTCGGCGCGG ACATGATTTT CTTTGCCGCC TTTATTGACG
251 ATGGGATTGT CTTTGACGTT GACGTTGGCG TTTTAAATT TCAGCATCGT
301 GCCGGAATAG GTGCGGATCA GCAGGGTTTG AAATCTTTG GCCAACGCTT
351 GTTTTTGCGC GTCGGACGCG GTGCGCCAAG GGTGCGGAC CGCCAATGCG
401 GTCATACGTT GGAAATCGAA ATAGGGAATC GCATAGGCTT CGGCTTTTTG
451 GCGAGCGGTG TTGGCATCGC CGTTTTTTAA GATGCTCAAT ACTTGAGTGG
501 CGTTTTGACG GATTTGGCTT ACCGCGTCGG CAGGGGCGGC AAATGCCATG
551 CCGATGCTCA AAATACCGAT GCCCAATGCG CTGATGAGGG AGGATTTTTT
601 CATGATTAAG TGTCTAGTT TGAATATGAT GGCATACGTT TATTCGGCGG
651 CTTTTTCCGC ATTGCCGCCG TCGGCATTTT TCTCGGCAA ACTCGTCATG
701 AATTGCGCGA TAAGGTTTTT CAGAACCATT GCAGAACTGG TTACGGAGAT
751 GGTGTCGCCG GCAGCAAGGT TTTCCGTGTC GCCGCCCTGC TGCAGCCCGA
801 TGTA CTGCT GCTC GCCCAAAGT CCCGAAGTCA GGATTGCGC GGAAACGTCTG
851 CTGCTGAACT GATACTTGCC GTCCAAATCG AGGCGCACCC TCGCCTGATA
901 GGATTTCTGG TCAAGTCCGA TAGCGCCGAC GCGCCCGACC AATACGCTG
951 CGGATTTGAC GGGGGCATTG ACCTTCAAAC CGCCGATGTC GCCGAAATCG
1001 GCATAACCG CGTAAGTTTT GTCCGAACCG CCGAACGCCG CACCGCCGGC
1051 CACGCGGAAA GCGAGAAAGG CAACCGCCGC CGCGCCAATC AGGACGAACA
1101 GTCCGACCCA AAATCCAAT ATGTTCTTCT TCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1582; ORF 543>:

```

m543.pep
1  MVCRLFAAVF GFQLGNQSVH AFRFDNFAEL VAVHGNQARA FDGDVVGTVF
51  TAALVGGEVH VDGFPLPGYAD FGADDDFFAA FIDDGIVFDV DVGVFQFQHR
101 AGIGADQOGL KFFGQRLFLR VGRGAPRVAD RQCGHTLEIE IGNRIGFGFL
151 ASGVGIAVFX DAQYLSGVLT DLAYRVGRGG KCHADAQNTD AQCADEGGFF
201 HDXVSXFEYD GIRLFGGFFR IAAVGIFLQK TRHEFADKVF QNHCRGTGYD
251 GVAGSKVFRV AALLQPDVLL AQKSRSQDLR GNVAELILA VQIEAHPRLI
301 GFRVKSDSAD APDQYACGFD GGIDLQTADV AEINGVSF VRTAERRTAG
351 HAESEKGNRR RANQDEQSDP KFQYVLLH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 543 shows 84.2% identity over a 379 aa overlap with a predicted ORF (ORF 543.ng) from *N. gonorrhoeae*:

```

m543/g543
10      20      30      40      50      60
m543.pep MVCRLFAAVFGFQLGNQSVHAFRFDNFAELVAVHGNQARAFDGDVVGTVFTAALVGGEVH
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543      MVCRLFAAVFGFQLGNQPDVAFGFDFFAELVAVHGNQARAFDGDVVGTVFAAALVGGKVH
10      20      30      40      50      60

70      80      90      100     110     120
m543.pep VDGFPLPGYADFGADDDFFAIFIDDGIVFDVDVGVFQFQHRAGIGADQOGLKFFGQRLFLR
:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
g543      IDGLLTGDADFGTD DDFLAA LIDDGIVFDVDGRVFEFQHRAGIGADQOGLKFFGQRLFLR
70      80      90      100     110     120

130     140     150     160     170     180

```


821

```

m543.pep  VVRGAPRVADRQCGHTLEIEIGNRIGFGFLASGVGIAVFXDAQYLSGVLTDLAYRVGRGG
          ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543       VVRGTTPRVADRQCGHTLEIEIGNRIGFGFWACRSRVAAFEDGQNLGCVLADLSHCVGRGG
          130      140      150      160      170      180

          190      200      210      220      230      239
m543.pep  KCHADAQNTDAQCADEGGFFHDXVSXFEYDG-IRLFGGFFRIAAGVIFLGKTRHEFADKV
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543       KCHADAQNTDAQCADEGGFFHDV---FPENGCVCLFCGGFFRIAALSVFLGEAGHEFTDQV
          190      200      210      220      230

          240      250      260      270      280      290      299
m543.pep  FQNHCRITGYGDGVAGSKVFRVAALLQPDVLLAQKRSQDLRGNVAAELILAVQIEAHPRL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543       FQNHCRITGYGDGVAGSKVFRIAALLQPDVLFQKRSQDLRGNVTAELILAVQIKAHPR
          240      250      260      270      280      290

          300      310      320      330      340      350      359
m543.pep  IGFRVKSDSADAPDQYACGFDGGIDLQTDVAEIGINGVSFVRTAERRTAGHAESEKGNR
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543       IGFRVKPDSADAPDQYACGFDGGIDLQTDVAEIGINGVSFVRTAERRAARHAESEKGNR
          300      310      320      330      340      350

          360      370      379
m543.pep  RRANQDEQSDPKFQYVLLHX
          ||||:|||||:|||||:|||||
g543       RRADQDEQSDPKFQYVLFHX
          360      370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1583>:

```

a543.seq
1   ATGGCTTATG GATTACTTGC TGCCGTTTNT AGCCTTCAAC TCGNCAATCA
51  GTCCGTCCAC GCCTTTCGCT TTGATAATTT CGCCGAATTG GTTGCGGTAC
101 ACGGTAACCA GGCTCGCGCC TTCGATGGCG ACGTTGTAGG TACGGTATTT
151 ACCGCCGCTT TGGTAGGTGG TGAAGTCCAT GTTGACGGGT TTTTGCCCGG
201 NNACGCCGAC TTCGGCGCGG ACGATGATTT CTTTGCCGCC TTTATTGACG
251 ATNGGATTGT CTTTGACGTT GACGTTGGCG TTTTAAATT TCAGCATCGT
301 GCCGGAATAG GTGCGGATCA GCAGGGTTTG AAATCTTTG GCCAACGCTT
351 GTTTTTGCGC GTCGGACGCG GTGCGCCAAG GGTGCGCGAC CGCCAATGCG
401 GTCATACGTT GGAAATCGAA ATAGGGAATC GCATAGGCTT CGGCTTTTGT
451 CGGGGCGGTG TTGGCATCAC CGCTTTTAA GATGCTCAAT ACTTGAGTGG
501 CTTTTTGACG GATTTGGTTT ACCGCGTCGG CAGGGGCGGC AAATGCCATG
551 CCGATGCTCA AAATACCGAT GCCCAATGCG CTGATGAAGG AGGATTTTTT
601 CATGATTAAG TGTCTAGTT TGAATATGAT GGCATACGTT TATTCGGCGG
651 CTTTTTCGCG ATTGCCGCGC TCGGCATTTT TCTCGGCAA ACTCGTCATG
701 AATTTGCCGA TAAGGTTTTC CAGAACCATT GCAGAACTGG TTACGGAGAT
751 GGTGTCGCCG GCAGCAAGGT TTTCCGTGTC GCCGCCCTGC TGCAGCCCGA
801 TGTACTGCTC GCCCAAAGT CCCGAAGTCA GGATTTGCGC GGAAACGTCG
851 CTGCTGAAC TACTTGGCC GTCCAAATCG AGGCGCACCC TCGCTGATA
901 GGATTTCCGG TCAAGTCCGA TAGCGCCGAC GCGCCCGACC AATACGCCTG
951 CGGATTTGAC GGGGGCATTG ACCTTCAAC CGCCGATGTC GCCGAAATCG
1001 GCATAAACGG CGTAAGTTT GTCCGAACCG CCGAACGCCG CACCGCCGGC
1051 CACGCGGAAA GCGAGAAAG CAACCGCCGC CGCGCCAATC AGGACGAACA
1101 GTCCGACCCA AAATCCAAT ATGTTCTTTT TCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1584; ORF 543.a>:

```

a543.pep
1   MAYGLLAAXV SLQLXNQSVH AFRFDNFAEL VAVHGNQARA FDGDVVGTVF
51  TAALVGGEVH VDGFLPGXAD FGADDDFFAA FIDDXIVFDV DVGVF*FQHR
101 AGIGADQQGL KFFGQRLFLR VVRGAPRVAD RQCGHTLEIE IGNRIGFGFL
151 AGGVGITAF* DAQYLSGVL TDLYRVGRGG KCHADAQNTD AQCADEGGFF
201 HD*VS*FEYD GIRLFGGFFR IAAVGIFLGK TRHEFADKVF QNHCRITGYGD
251 GVAGSKVFRV AALLQPDVLL AQKRSQDLR GNVAEELILA VQIEAHPRLI
301 GFRVKSDSAD APDQYACGFD GGIDLQTDV AEIGINGVSF VRTAERRTAG

```

351 HAESEKGNRR RANQDEQSDP KFQYVLFH*

m543/a543 96.0% identity in 378 aa overlap

	10	20	30	40	50	60
m543.pep	MVCRLFAAVFGFQLGNQSVHAFRFDNFAELVAVHGNQARAFDGDVVGTVFTAALVGGEVH					
a543	MAYGLLAAVXSLQLXNQSVAHAFRFDNFAELVAVHGNQARAFDGDVVGTVFTAALVGGEVH					
	10	20	30	40	50	60
	70	80	90	100	110	120
m543.pep	VDGFLPGYADFGADDDFFAAFIDDGIVFDVDVGVFQFQHRAGIGADQOGLKFFGQRLFLR					
a543	VDGFLPGXADFGADDDFFAAFIDDXIVFDVDVGVFQFQHRAGIGADQOGLKFFGQRLFLR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m543.pep	VGRGAPRVADRQCGHTLEIEIGNRIGFGFLASGVGIAVFXDAQYLSGVLTDLAYRVGRGG					
a543	VGRGAPRVADRQCGHTLEIEIGNRIGFGFLAGGVGITAFXDAQYLSGVLTDLVYRVGRGG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m543.pep	KCHADAQNTDAQCADEGGFFHDXVSXFEYDGI RLFGGFFRIA AVGIFLGKTRHEFADKVF					
a543	KCHADAQNTDAQCADEGGFFHDXVSXFEYDGI RLFGGFFRIA AVGIFLGKTRHEFADKVF					
	190	200	210	220	230	240
	250	260	270	280	290	300
m543.pep	QNHCRGTGYGDGVAGSKVFRVAALLQPDVLLAQKSRSDLRGNVAAELILAVQIEAHPRLI					
a543	QNHCRGTGYGDGVAGSKVFRVAALLQPDVLLAQKSRSDLRGNVAAELILAVQIEAHPRLI					
	250	260	270	280	290	300
	310	320	330	340	350	360
m543.pep	GFRVKSDSADAPDQYACGFDGGIDLQTDVAEIGINGVSFVRTAERRTAGHAESEKGNRR					
a543	GFRVKSDSADAPDQYACGFDGGIDLQTDVAEIGINGVSFVRTAERRTAGHAESEKGNRR					
	310	320	330	340	350	360
	370	379				
m543.pep	RANQDEQSDPKFQYVLLHX					
a543	RANQDEQSDPKFQYVLFHX					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1585>:

g544.seq

1	atgaaaaaaa	tactcaccgc	cgccgccgctc	gcactgatcg	gcattcctct
51	cgccaccgctc	ctcatccccg	acagtaaaac	cgccgccgcc	ttctccctgc
101	ccgacctgca	cggaaaaacc	gtttccaacg	ccgacctgca	aggcaaagtc
151	accctgatta	atttttggtt	tccctcctgt	ccgggttggtg	tgagcgaaat
201	gccccaaagtc	acaaaaacgg	caaacgacta	caaaaaataaa	gatttccaag
251	tcctcgccgt	tgcccagccc	atcgatccga	tagaaagcgt	ccgccaatac
301	gtcaaagact	acggactgcc	gtttaccgctc	atttatgatg	cggacaaaagc
351	cgtcggacag	gcattcggca	cacagggtta	tccgacttcc	gtccttatcg
401	gcaaaaaagg	cgaaatcctc	aaaacttatg	tcggcgaaac	cgatttcggc
451	aaactctacc	aagaaatcga	taccgcgctg	gcgcaatag	

This corresponds to the amino acid sequence <SEQ ID 1586; ORF 544.ng>:

g544.pep

1	MKKILTA	AAV	ALIGILLATV	LIPDSKTAPA	FSLPDLHGKT	VSNADLQGV
51	TLINFWFPSC	PGCVSEMPKV	TKTANDYKNK	DFQVLAVAQP	IDPIESVRQY	
101	VKDYGLPFTV	IYDADKAVGQ	AFGTQVYPTS	VLIKKGEIL	KTYVGEPDFG	

m544 . seq

1	ATGAwAAAAA	TACTCACCGC	CGCCGTCGTC	GCACTGATCG	GCATCCTCCT
51	TGCCATCGTC	CTCmTCCCCG	ACAGCAAAAC	CGCGCCCGCC	TTCTCCmTGC
101	CCGACCTGCA	CGGAAAAACC	GTTTCCAACG	CCGACCTGCA	AGGCAAAGTA
151	ACCCTGATTA	ATTTTTGGTT	TCCCTCCTGT	CCGGGTTGTG	TGAGCGAwAT
201	GCCCAAAATC	ATTA AAAACGG	CAAATGACTA	TAAAwCAAA	AACTTCCAAG
251	TACTTGCCGT	CGCCCAGCCC	ATCGATCCGA	TAGAAAGCGT	CCGCCAATAT
301	GTCAAAGACT	ACGGTTTGCC	GTTTACCGTC	ATGTATGATG	CGGACAAAGC
351	TGTCGGACAG	GCGTTCGGCA	CACAGGTTTA	TCCGACTTCC	GTCCTTATCG
401	GCAAATAAGG	CGAAATCTTC	AAAACCTACG	TCCGGCAACC	CGATTTCCGG
451	AAACTCTACC	AAGAAATCGA	TACGCGCGTG	GCGCAATAG	

m544 . pep

1	<u>MXKILTA</u> AAVV	<u>ALIGILLA</u> IV	<u>LXPDSKT</u> TAPA	<u>FSXPDLH</u> GKT	<u>VSNADLQ</u> GKV
51	TLINFWF	PSC PGCVS	XMPKI IKTANDY	KXK NFOVLAVA	QPIDIESVRQY
101	VKDYGLP	FTV MYDAD	KAVGQ AFGTQ	VYPTS VLIGK	*GEIF KTYVGE
151	KLYQEID	TRV AQ*			

ORF 544 shows 90.7% identity over a 162 aa overlap with a predicted ORF (ORF 544.ng) from *N. gonorrhoeae*:

m544/g544

	10	20	30	40	50	60
m544.pep	MXKILTA	AAVVALIGILL	AIVLXP	DSKTAPAF	SXPDLHG	KTVSNADLQ
g544	MKKILTA	AAVVALIGILL	ATVLI	PD	SKTAPAF	SLPDLHG
	10	20	30	40	50	60
	70	80	90	100	110	120
m544.pep	PGCVS	XMPKII	KTANDY	KXKNF	QVLAVA	QPIDPIE
g544	PGCVS	EMPKV	TKTANDY	KNKDF	QVLAVA	QPIDPIE
	70	80	90	100	110	120
	130	140	150	160		
m544.pep	AFGTQ	VYPTSV	LIGKX	GEIFK	TYVGEP	DFGKLY
g544	AFGTQ	VYPTSV	LIGK	KEILK	TYVGEP	DFGKLY
	130	140	150	160		

a544.seq

1	ATGAAAAAAA	TACTCACCGC	CGCCGTCGTC	GCACTGATCG	GCATCCTCCT
51	TGCCATCGTC	CTCATCCCCG	ACAGCAAAAC	CGCGCCCGCT	TTCTCCCTGT
101	CCGANCTGCA	CGGAAAAANC	GTTTNC AACG	CCGACCTTGA	AGGCNAAGTT
151	ANCCTGATTA	ANTTTTG GTT	TCCCTCCTGT	CCGGGTGTGA	TGAGCGAAAT
201	GNCCANAATC	ATTA AAAACG	CAATGACTA	TAAAAACAAA	AACTTCCAAG
251	TCCTTGCCGT	CGCCCAGCCC	ATCGATCCGA	TAGAAAGCGT	CCGCCAATAT
301	GTCAAAGACT	ACGTTTGCC	GTTTACCGTC	ATGTATGATG	CGGACAAAGC
351	TGTCGGACAG	GCGTTCGGCA	CACAGGTTTA	TCCGACTTCC	GTCCTTATCG
401	GCAAAAAAGG	CGAAATCCTC	AAA ACTTATG	TCGGCGTAAC	CGATTTCGGC
451	AAACTCTACC	AAGAAATCGA	TACCGCGCTG	GCACAATAG	

a544.pcp

1 MKKILTAADV ALIGILLAIV LIPDSKTAPA FSLSLHGXKX VVNADLQGXV
51 XLIXFWFSPC PGCVSEMXXI IKTANDYKNK NFQVLAVAQP IDPIESVRQY
101 VKDYGLPFTV MYDADKAVGQ AFGTQVYPTS VLIGKKGEIL KTYVGEPDFG

151 KLYQEIDTAL AQ*

m544/a544 88.9% identity in 162 aa overlap

	10	20	30	40	50	60
m544.pep	MXKILTA	AVVALIG	ILLAI	VLXP	DSKTAP	AFSXPDLHGKTVSNADLQ
a544	MKKILTA	AVVALIG	ILLAI	VLIP	DSKTAP	AFSLSXLHGKXVXNADLQ
	10	20	30	40	50	60
	70	80	90	100	110	120
m544.pep	PGCVS	XMPKII	KTANDY	KXKNF	QVLA	VAQPIDPIESVRQYVKDYGLPFTVMYDADKAVGQ
a544	PGCVS	EMXXII	KTANDY	KXKNF	QVLA	VAQPIDPIESVRQYVKDYGLPFTVMYDADKAVGQ
	70	80	90	100	110	120
	130	140	150	160		
m544.pep	AFGTQ	VYPTSV	LIGKXG	EIFKTY	VGEPDF	GKLYQEIDTRVAQX
a544	AFGTQ	VYPTSV	LIGKKG	EILKTY	VGEPDF	GKLYQEIDTALAQX
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1591>:

g547.seq

```

1  atgttcgtag ataacggatt taataaaacg gtagcgagtt ttgccccaaat
51  cgtcgaaact ttcgacgtat tcttccttag gaacgattgc gcctttttta
101 cgcagatgaa acagcgggtgc ggttgggtct gtcggttggg atatctcggt
151 gatataattta caagatgcgg cttcgagatt ccgaaccgct cctttaaaga
201 gcttgggctt ttgatacaga taagtctgtc ggaacgtttt aggactaatg
251 ccgaagtcga gatggatgcc cttacttcc cttactcag aaaatattta
301 aaatttataa tgttacatat agttacaaat attagagttt tttgtgtgtg
351 cgtcaaggaa ttggtgacaa ttttagttaa aaatttgtct ccaaacggaa
401 aaaagcgggt tggtttttgt tggttaa

```

This corresponds to the amino acid sequence <SEQ ID 1592; ORF 547.ng>:

g547.pep

```

1  MFVDNGFNKT VASFAQIVET FDVFFFRNDC AFFTQMKQRC GWVCSLVYLV
51  DIFTRCGFEI PNRSFKELGL LIQISLSERF RTNAEVEMDA HYFPLLRKYL
101 KFIMLHIVTN IRVFCVCVKE LLTILVKNL PNGKKRFVFC C*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1593>:

m547.seq

```

1  ATGTTCTAGT ATAACGGATT TAATAAAACG GTAGCGAGTT TTGCCCCAAAT
51  CGTCGAAACT TTCGACGTAT TCTTCTTTAG GAACGATTGC GCCTTTTSTA
101 CGCAGATGAA ACAGCGGTGC GGTGCGGTCT GTCGTTGGT ATATCTCGTT
151 GATATCTTTC CAAGATGCGG ATTCGAGATT CCGAACCCT CTTTAAAGA
201 GCTTGGGCTT TTGATACAGA TAAGTCTGTC GGAACGTTT AGGACTAATG
251 CCGAAGTCGA GATGGATGCT CATTACTTCC CTTACTCAG AAAATATTTA
301 AAATTTATAA TGTTACATAT ATTTACAAAT ATTAAAGTTT TTTwTTGTGT
351 GTGCGTCAAG GAATTGTTGA CAATTTTAGT TAAAAATTG TCTCCAAACG
401 GAAAAAAGCG GTTGTGTTT TGTGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1594; ORF 547>:

m547.pep

```

1  MFVDNGFNKT VASFAQIVET FDVFFFRNDC AFFTQMKQRC GWVCSLVYLV
51  DIFPRCGFEI PNRSFKELGL LIQISLSERF RTNAEVEMDA HYFPLLRKYL
101 KFIMLHIFTN IKVFCVCVK ELLTILVKNL SPNGKKRFV CC*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 547 shows 97.2% identity over a 142 aa overlap with a predicted ORF (ORF 547.ng) from *N. gonorrhoeae*:

m547/g547

825

	10	20	30	40	50	60
m547.pep	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
g547	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFTRCGFEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m547.pep	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRLKYLKFIMLHIFTNFKVFXCVCK					
g547	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRLKYLKFIMLHIVTNIRVF-CVCK					
	70	80	90	100	110	
	130	140				
m547.pep	ELLTILVKNLSPNGKKRFVFCX					
g547	ELLTILVKNLSPNGKKRFVFCX					
	120	130	140			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1595>:

```
a547.seq
1  ATGTTCTAG  ATAACGGATT  TAATAAAACG  GTAGCGAGTT  TTGCCCAAAT
51  CGTCGAAACT  TTCGACGTAT  TCTTCTTTAG  GAACAATTGC  ACCTTTTTTA
101 CGCAGATGAA  ACAGCGGTGC  GGTGGGTCT  GCTCGTTGGT  ATATCTCGTT
151 GATATCTTTC  CAAGATGCGG  CTTGAGATT  CCGAACCGCT  CCTTTAAAGA
201 GCTTGGGCTT  TTGATACAGA  TAAGTCTGTC  GGAACGTTT  AGGACTAATG
251 CCGAAGTCGA  GATAGATGCT  CATTACTTCC  CCTTACTCAG  AAAATATTTA
301 AAATTTATAA  TGTTACATAT  ATTTACAAAT  ATTAAAGTTT  TTTT.TGTGT
351 GTGCGTCAAG  GAATTGTTGA  CAATTTTAGT  T
```

This corresponds to the amino acid sequence <SEQ ID 1596; ORF 547.a>:

```
a547.pep
1  MFVDNGFNKT  VASFAQIVET  FDVFFFRNNC  TFFTQMKQRC  GWVCSLVYLV
51  DIFPRCGFEI  PNRSFKELGL  LIQISLSERF  RTNAEVEIDA  HYFPLLRLYL
101 KFILHIFTN  IKVFXCVCK  ELLTILV
```

m547/a547 97.6% identity in 127 aa overlap

	10	20	30	40	50	60
m547.pep	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
a547	MFVDNGFNKTVASFAQIVETFDVFFFRNCTFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m547.pep	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRLKYLKFIMLHIFTNFKVFXCVCK					
a547	PNRSFKELGLLIQISLSERFRTNAEVEIDAHYFPLLRLKYLKFIMLHIFTNFKVFXCVCK					
	70	80	90	100	110	120
	130	140				
m547.pep	ELLTILVKNLSPNGKKRFVFCX					
a547	ELLTILV					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1597>:

```
g548.seq
1  atgttttccg  taccgcggtc  ctttttgccg  ggcgttttcc  tacttgccgc
51  gcttgccgcc  tgcaaaccct  aagacaacag  tgcggcgcaa  gccgcttctt
101 caagtgcac  cgcgcgggct  gcggaataat  cggcaaaagg  gcaaaccgca
151 ggtacggata  tgcgtaagga  agacatcggc  ggcgatttca  cactgaccga
201 cggcgaaggc  aagcctttca  gcctgagcga  tttgaaaggc  aaggctcgta
251 ttctgtcttt  cggttttacg  cactgtcccg  atgtctgccc  gacagggtt
```

```

301 ttgacgtaca gcgacacttt gaagcagttg ggcgggcagg ctaaggacgt
351 gaaagtgggtg ttcgtcagca tcgatccgga acgcgacacg cctgaaatca
401 tcggcaagta tgccaaacag ttcaatccgg actttatcgg tctgacggca
451 acgggcggcc aaaacctgcc ggtcatcaag cagcaatacc gcgtggtttc
501 tgccaaaatc aatcaaaaag acgacagcga aaactatttg gtcgaccact
551 cttccgggtgc gtatcttata gataaaaacg gtgaggttgc cattttctcg
601 ccttacggaa gcgagccgga aacgattgct gccgatgtaa ggaccctgct
651 ctga

```

This corresponds to the amino acid sequence <SEQ ID 1598; ORF 548.ng>:

g548.pep

```

1 MFSVPRSFLP GVFVLAALAA CKPQDNSAAQ AASSSASAPA AENAAKPQTR
51 GTDMRKEDIG GDFTLTDGEG KPFSLSDLKG KVVILSFGFT HCPDVCPTGL
101 LTYSDTLKQL GGQAKDVKV FVSIDPERDT PEIIGKYAKQ FNPDFIGLTA
151 TGGQNLPIVK QQYRVVSAKI NQKDDSENYL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1599>:

m548.seq

```

1 ATGTTTTCCG TACCGCGTTC CTTTTGCCG GCGTTTTTCG TACTTGCCGC
51 GCTTGCCGCC TGCAAACCTC AAGACAACAG TCGCGCGCAA GTCGCTTCTT
101 CAAGTGCATC CGCGTCGGCT GCGGAAAATG CGGCAAAGCA AnACACGCGC
151 GGTACGGATA TCGTAAGGA AGACATCGGC GCGGATTTC AAGGTCGTGA
201 CGGCGAAGGC AAGCCTTTCA ACCTGAGCGA TTGAAAAGGC AAGGTCGTGA
251 TTCTGTCTTT CGGCTTTACG CACTGTCCCG ATGTCTGCCG GACAGAGCTT
301 TTGACGTACA GCGACACGTT GAAGCAGTTG GCGGGGCAGG CTAAGGACGT
351 GAAAGTGGTG TTCGTCAGCA TCGATCCGGA ACGCGACACG CCTGAAATCA
401 TCGGCAAGTA TGCCAAACAG TTCAATCCGG ACTTTATCGs TCTGACGGCA
451 ACGGGCGGCC AAAACCTGCC GGTCATCAAG CAGCAATACc GCGTGGTTTC
501 TGCCAAAGTC AATCAAAAmG ACGACAGCGA AAACATTTTG GTCGACCACT
551 CTTCCGGTGC GTATCTCATC GACAAAACG GTGAGGTTGC CATTTTCTCG
601 CCTTACGAA GCGAGCCGGA AACGATTGCT GCCGATGTAA GGACCCTGCT
651 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1600; ORF 548>:

m548.pep

```

1 MFSVPRSFLP GVFVLAALAA CKPQDNSAAQ VASSSASASA AENAAKQXTR
51 GTDMRKEDIG GDFTLTDGEG KPFNLSDLKG KVVILSFGFT HCPDVCPTL
101 LTYSDTLKQL GGQAKDVKV FVSIDPERDT PEIIGKYAKQ FNPDFIXLTA
151 TGGQNLPIVK QQYRVVSAKV NQXDDSENYL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTLL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 548 shows 95.9% identity over a 217 aa overlap with a predicted ORF (ORF 548.ng) from *N. gonorrhoeae*:

m548/g548

	10	20	30	40	50	60
m548.pep	MFSVPRSFLPGVFVLAALAACKPQDNSAAQVASSSASASAAENAAKQXTRGTDMRKEDIG					
	:					
g548	MFSVPRSFLPGVFVLAALAACKPQDNSAAQAASSSASAPAAENAAKPQTRGTDMRKEDIG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m548.pep	GDFTLTDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTLLTYSDTLKQLGGQAKDVKV					
	:					
g548	GDFTLTDGEGKPFSLSDLKGKVVILSFGFTHCPDVCPTGLLTYSDTLKQLGGQAKDVKV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m548.pep	FVSIDPERDTP EIIGKYAKQFNPDFIXLTATGGQNLPIVKQQYRVVSAKVNQXDDSENYL					
	:					
g548	FVSIDPERDTP EIIGKYAKQFNPDFIGLTATGGQNLPIVKQQYRVVSAKINQKDDSENYL					
	130	140	150	160	170	180

827

	190	200	210
m548.pep	VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX		
g548	VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX		
	190	200	210

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1601>:

```
a548.seq
1  ATGTTTTC CG TACCGCGTTC CTTTTTGCCG GCGGTTTTTCG TACTTGCCGC
51  GCTTGCCGCC TGCAAACCTC AAGACAACAG TCGGGCGCAA GTCGCTTCTT
101 CAAGTGCATC CGCGTCGGCT GCGGAAAATG CGGCAAAGCC GCAAACGCGC
151 GGTACGGATA TCGCTAAGGA AGACATCGGC GCGGATTTCA CGCTGACCGA
201 CGGCGAAGGC AAGCCTTTCA ACCTGAGCGA TTTGAAAGGC AAGGTCGTGA
251 TTCTGTCTTT CCGCTTACG CACTGTCCCG ATGTCTGCCG GACAGAGCTT
301 TTGACGTACA GCGACACGTT GAAGCAGTTG GCGGGGCAGG CTAAGGACGT
351 GAAAGTGGTG TTCGTACGCA TCGATCCGGA ACGCGACACG CCTGAAATCA
401 TCGCAAGTA TGCCAAACAG TTCAATCCGG ACTTTATCGG TCTGACGGCA
451 ACGGGCGACC AAAACCTGCC GGTCAATCAAG CAGCAATACC GCGTGGTTTC
501 TGCCAAAGTC AATCAAAAAG ACGACAGCGA AAATATTTG GTCGACCACT
551 CTTCCGGTGC GTATCTCATC GACAAAAACG GTGAGGTTGC CATTTTCTCG
601 CTTACGGAA GCGAGCCGGA AACGATTGCT GCCGATGTAA GGACCCTGCT
651 CTGA
```

This corresponds to the amino acid sequence <SEQ ID 1602; ORF 548.a>:

```
a548.pep
1  MFSVPRSFLP GVFVLAALAA CKPDNSAAQ VASSASASA AENAAKPQTR
51  GTDMRKEDIG GFTLTDEGEG KPFNLSDLKG KVVILSFGFT HCPDVCPTL
101 LTYSDTLKQL GGQAKDVKVV FVSIDPERDT PEIIGKYAKQ FNPDFIGLTA
151 TGDQNLPIVK QQYRVVSAKV NQKDDSENYL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTL*
```

m548/a548 97.7% identity in 217 aa overlap

	10	20	30	40	50	60
m548.pep	MFSVPRSFLPGVFVLAALAAACKPDNSAAQVASSASASAAENAAKQXTRGTDMRKEDIG					
a548	MFSVPRSFLPGVFVLAALAAACKPDNSAAQVASSASASAAENAAKQXTRGTDMRKEDIG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m548.pep	GFTLTDEGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTELLTYSDTLKQLGGQAKDVKVV					
a548	GFTLTDEGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTELLTYSDTLKQLGGQAKDVKVV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m548.pep	FVSIDPERDTPETIIGKYAKQFNPDFIXLTATGGQNLPIVKQQYRVVSAKVNQXDDSENYL					
a548	FVSIDPERDTPETIIGKYAKQFNPDFIGLTATGDQNLPIVKQQYRVVSAKVNQKDDSENYL					
	130	140	150	160	170	180
	190	200	210			
m548.pep	VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX					
a548	VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1603>:

```
g550.seq
1  atgataacgg acaggtttca tctctttcat tttccagtat ctttcattta
51  tcaatctgac aacaaaatgc cgcctgaaaa cagttcagac ggcattttta
101 ccacaaacgg cttacagctt ccattcgccc aacttggcag cgtaagcttc
```

q550.pep

1	MITDRFHLFH	FPVSFIYQSD	NKMPPENSSD	GILTTNGLQL	PFAQLGSVSF
51	QICNRTGCHA	AFHRCFGGSR	SDARQQAGIE	RSRNQVFRAE	FEFLTMSGNH
101	FFGYFFHRQI	CQSIHAGAFH	FFVDGGCADI	QRAPEDEREA	QYVVHLVREV
151	GAAGTDNHVR	TGFFRQRRQD	FRIRVGHGEH	DGFFVHRVQH	FRRQQVCAGE
201	AQEDVFAFNR	IGKYAPAVVF	NGVEFFGFVH	AVFVFAGLVN	HAFGVANGYV
251	FTFQAQIQQL	VQAGNRGGTC	AGAHSRFFD	FTAGITQGVQ	YGGGGNDGRA
301	VLVIMQYKGF	AAFA*			

m550.seq (partial)

1	..GACGGCATCG	GCAAGCACGC	GCTGGCCGTT	GTCTTCAATG	GCGTAGAACT
51	GTTTGGACTC	GTCCATACGG	TCTTTGTCTT	CGCGGGTTTG	GTAAATCACG
101	CCTTTGGAGT	CGCAAACGGT	CACGTTTTCG	CGTTTCAAGC	CCAAATCCAG
151	CAATTGGwTC	AAGCAGGCAA	TCGCGGCCGC	ACCTGCGCCG	GAACACACCA
201	AAGTCGCTTC	TTTCGATTTTA	CGGCCGGTAA	AACGCAkGGC	GTTCAATACG
251	CGCGCGCGCG	TAATGATGGC	CGTCCGTGTC	TGGTCGTCTG	GGAATACGGG
301	GATTTTGCAG	CGTTTGCCTA	A		

m550.pep (partial)

1 ..DGIGKHALAV VFNGVELFGL VHTVFVFAGL VNHAFGVANG HVFAFQAQIQ
51 QLXQAGNRGR TCAGTHQSRF FDFTAGKTXG VQYGGGGNDG RAVLVVVEYG
101 DEAAFA*

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 550 shows ___% identity over a ___ aa overlap with a predicted ORF (ORF 550.ng) from *N. gonorrhoeae*:

m550/g550

		10	20	30	
m550.pep		DGIGKHALAVVFNGVELFGLVHTV F VFAGLVN			
		:: : : :			
g550	DGFFVHRVQHFRRQQVCAGEAQEDVFAFNRI GKYAPAVVFNGVEFFGFVHAVFVFAGLVN				
	190	200	210	220	230 240
	40	50	60	70	80 90
m550.pep	HAFGVANGHVFAFAQIQQLXQAGNRGR TCAGTHQS RFFDFTAGKT XGVQYGGGGNDGRA				
	:: : : : : : :				
g550	HAFGVANGYVFTFOAQIQQLVQAGNRGGTCAGA HQS RFFDFTAGITQG VQYGGGGNDGRA				
	250	260	270	280	290 300
	100				
m550.pep	VLVVVEYGDFAA FAX				
	:::				
g550	VLVIMKYGDFAA FAX				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1607>:

```
a550.seq
1   CTATATCAAT CTGACAGCAA AATGCCGCCT GAAAACAGTT CAGACGGCAT
51  TTTAACCACA AACGGCTTAC AGCTTCCATT CGCTCAGCTT GGCAGCGTAA
101 GCTTCCAAAT CTGCAATCGG ACGGGTTGCC ACGCCGCTTT CCATCGCTGC
151 TTTGGCGGCA GCCGTAGCAA CGCGCGGCAG CAGGCGGGAA TCGAACGGAG
201 TCGGAATCAG GTATTCCGCG CCGAATTCAA ATTTCTTACC GTAAGCGGCA
251 ACCACTTCTT CGGTTACCTC TTCCATCGCC AAATCCGCCA AAGCATACAC
301 GCAGGCGCGT TTCATTTCTT CGTTGATGGT CGTCGCGCCG ACATCCAACG
351 CACCGCGGAA GATGAACGGG AAGACAATA CATTGTTTAC TTGGTTCGGG
401 AAGTCGGAGC GGCCGGTACC GATAACCACG TCCGGACGGG TTTCTTTTCG
451 CAGCGGCGGC AGGATTTCGG GATTCGGGTT GGCCATAGCG AACACGATGG
501 GTTTTTTCGT CATGGTGTTC AGTATTTCAG GCGTCAGCAG GTTCGCGCCG
551 GAGAGGCCCA AGAAGATGTC TTTGCCTTTG ACGGCATCGG CAAGCACGCG
601 CTGGCCGTGG TCTTCAATGG CGTAGAACTG TTTGGACTCG TCCATACGGT
651 CTTTGTCTTC GCGGGTTTGG TAAATCACGC CTTTGGAGTC GCAAACGGTC
701 ACGTTTTTCG GTTTCAAGCC CAAATCCAGC AATTGGTTCA AGCAGGCAAT
751 CGCGGCCGCA CCTGCGCCGG AACACACCAA AGTCGCTTCT TCGATTTTAC
801 GGCCGGTAAA ACGCAGGCGG TTCAATACGG CAGCGGCGGT AATGATGGCC
851 GTGCCGTGCT GGTCGTCGTG GAATACGGGG ATTTTGCAGC GTTTGCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1608; ORF 550.a>:

```
a550.pep
1   LYQSDSKMPP ENSSDGILTA NGLQLPFAQL GSVSFQICNR TGCHAAFHRC
51  FGSSRSNARQ QAGIERSRNQ VFRAEFKFLT VSGNHFFGYL FHRQIRQSIH
101 AGAFHFFVDG RRADIQTAE DEREAYIVH LVREVGAACT DNHVRTGFFR
151 QRRQDFRIRV GHSEHDGFFV HGVQYFRRQQ VRAGEAQEDV FAFDGIGKHA
201 LAVVFNGLVEL FGLVHTVFVF AGLVNHAFGV ANGHVFAFQA QIQQLVQAGN
251 RGRTCAGTHQ SRFFDFTAGK TQGVQYGS GG NDGRAVLVVV EYGDFAAFA*
```

m550/a550 97.2% identity in 106 aa overlap

```

                                     10      20      30
m550.pep                               DGIGKHALAVVFNGVELFGLVHTVFVFAGL
a550      EHDGFFVHGVQYFRRQQVRAGEAQEDVFAFDGIGKHALAVVFNGVELFGLVHTVFVFAGL
              170      180      190      200      210      220

                                     40      50      60      70      80      90
m550.pep      VNHAFGVANGHVFAFQAQIQQLXQAGNRGRTCAGTHQSRFFDFTAGKTQGVQYGGGGNDG
a550      VNHAFGVANGHVFAFQAQIQQLVQAGNRGRTCAGTHQSRFFDFTAGKTQGVQYGS GGNDG
              230      240      250      260      270      280

                                     100
m550.pep      RAVLVVVEYGDFAAFAX
a550      RAVLVVVEYGDFAAFAX
              290      300
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1609>:

```
g552.seq
1   atgaagctga aaaccttggt attgcccttc gccgcactgg cattgtgtgc
51  caacgcattt gccgccccgc ccggcgacgc gtcgttgga cgttggtgctg
101 atacgcagaa tttcgaccgg gatatagaaa aaaatatgat tgaaggcttt
151 aatgccggat ttaaaccgta tgcggacaaa gcccttgccg aaatgccgga
201 agcgaaaaaa gatcaggcgg cagaagcctt taatcgttat cgtgagaatg
251 ttttgaaaga tttgattacg cccgaagtga aacaggctgt ccgcaatacc
301 ttattgaaga atgcccgta aatatacacg caagaagaaa ttgacggcat
351 gattgccttt tacggttcgc ctgtcgggtc gtccgtcggt gccaaaaatc
401 cgcgcttaat caagaaatcg atgagtgaat tagcggtatc ttggactgca
```

451 ttgtcagggg aaatcgcgcg acatcatctg cccgagttta cggaagagtt
501 acggcgcatc atctgcggcg gtatagtggg ttaa

This corresponds to the amino acid sequence <SEQ ID 1610; ORF552.ng>:

g552.pep

1 MKLKTLLLPF AALALCANAF AAPPGDASLA RWLDTQNFDR DIEKNMIEGF
51 NAGFKPYADK ALAEMPEAKK DQAAEFNRY RENVLKDLIT PEVKQAVRNT
101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA
151 LSGKIARHHL PEFTEELRRI ICGGIVD*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1611>:

m552.seq (partial)

1 ..ATTAACTGA AAACCTTGTT ATTGCCCTTC GCCACGCTGG CATTGTGCAC
51 CAATGCTTTT GCCGCCCCGC CCAGCGACGC GTCGTTGGCG CGTTGGCTGG
101 ATACGCAGAA TTTTGACCGG GATATAGAAA AAAATATGAT TGAGGGCTTT
151 AATGCCGGAT TTAAACCGTA TCGGACAAA GCCCTTGCCG AAATGCCGGA
201 AGCGAAAAAA GATCAGGCGG CAGAAGCCTT TAACCGTTAT CGTGAGAATG
251 TTTTGAAAGA TTTGATTACG CCCGAAGTGA AACAGGCTGT CCGCAATACT
301 TTATTGAAGA ATGCCCCGTA GATATACACG CAAGAAGAAA TTGACGGCAT
351 GATTGCCTTT TACGGTTCGC CTGTCCGTCG GTCCGTCGTT GCCAAAAATC
401 CGCGCTTAAT CAAGAAATCG ATGAGTGAAA TAGCGGTATC TTGGACTGCA
451 TTGTCAGGGA AAATCGCGCA ACATCATCTG CCCGAGTTTA CGGAAGAGTT
501 GCGGCGCATC ATCTGCGGCG GTAAAAATCC CGATGCGGGC TGTAAACAAG
551 CCGGACAGGT TGGGAAAAGG CATCAGAAAT AA

This corresponds to the amino acid sequence <SEQ ID 1612; ORF 552>:

m552.pep (partial)

1 ..IKLKTLLLPF ATLALCTNAF AAPPSDASLA RWLDTQNFDR DIEKNMIEGF
51 NAGFKPYADK ALAEMPEAKK DQAAEFNRY RENVLKDLIT PEVKQAVRNT
101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA
151 LSGKIAQHHL PEFTEELRRI ICGKKNPDAG CKQAGQVGKR HQK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 552 shows 97.1% identity over a 174 aa overlap with a predicted ORF (ORF 552.ng) from *N. gonorrhoeae*:

m552/g552

	10	20	30	40	50	60
m552.pep	IKLKTLLLPFATLALCTNAFAAPPSDASLARWLDTQNFDRDIEKNMIEGFNAGFKPYADK					
	: : : : : :					
g552	MKLKTLLLPFAALALCANAFAPPGDASLARWLDTQNFDRDIEKNMIEGFNAGFKPYADK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m552.pep	ALAEMPEAKKDQAAEFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
	: : : : :					
g552	ALAEMPEAKKDQAAEFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m552.pep	YGSPVGQSVVAKNPRLIKKSMEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKKNPDAG					
	: : : : :					
g552	YGSPVGQSVVAKNPRLIKKSMEIAVSWTALSGKIAQHHLPEFTEELRRIICGGIVDX					
	130	140	150	160	170	
	190					
m552.pep	CKQAGQVGKRHQKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1613>:

a552.seq

1 ATTAACTGA AAACCTTGTT ATTGCCCTTC GCCACGCTGG CATTGTGCAC
51 CAATGCTTTT GCCGCCCCGC CCAGCGACGC GTCGTTGGCG CGTTGGCTGG
101 ATACGCAGAA TTTTGACCGG GATATAGAAA AAAATATGAT TGAGGGCTTT
151 AATGCCGGAT TTAAACCGTA TCGGACAAA GCCCTTGCCG AAATGCCGGA

```

201 AGCGAAAAAA GATCAGGCGG CAGAAGCCTT TAACCGTTAT CGTGAGAATG
251 TTTTGAAAGA TTTGATTACG CCCGAAAGTGA AACAGGCTGT CCGCAATACT
301 TTATTGAAGA ATGCCCCGTA GATATACACG CAAGAAGAAA TTGACGGCAT
351 GATTGCCTTT TACGGTTCGC CTGTCGGTCA GTCCGTCGTT GCCAAAAATC
401 CGCGCTTAAT CAAGAAATCG ATGAGTGAAA TAGCGGTATC TTGGACTGCA
451 TTGTCAGGGA AAATCGCGCA ACATCATCTG CCCGAGTTTA CGGAAGAGTT
501 GCGGCGCATC ATCTGCGGCG GTAAAAATCC CGATGCGGGC TGTAAACAAG
551 CCGGACAGGT TGGGAAAAGG CATCAGAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 1614; ORF 552.a>:

```

a552.pep
  1 IKLKTLLLPF ATLALCTNAF AAPPSDASLA RWLDTQNFDR DIEKNMIEGF
 51 NAGFKPYADK ALAEMPEAKK DQAAEAFNRY RENVLKDLIT PEVKQAVRNT
101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA
151 LSGKIAQHHL PEFTEELRRI ICGGKNPDAG CKQAGQVGKR HQK*

```

m552/a552 100.0% identity in 193 aa overlap

```

              10      20      30      40      50      60
m552.pep      IKLKTLLLPFATLALCTNAFAAPPSDASLARWLDTONFDRDIEKNMIEGFNAGFKPYADK
              |||||
a552           IKLKTLLLPFATLALCTNAFAAPPSDASLARWLDTONFDRDIEKNMIEGFNAGFKPYADK
              10      20      30      40      50      60

              70      80      90      100     110     120
m552.pep      ALAEMPEAKKDQAAEAFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF
              |||||
a552           ALAEMPEAKKDQAAEAFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF
              70      80      90      100     110     120

              130     140     150     160     170     180
m552.pep      YGSPVGQSVVAKNPRLIKKS MSEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPDAG
              |||||
a552           YGSPVGQSVVAKNPRLIKKS MSEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPDAG
              130     140     150     160     170     180

              190
m552.pep      CKQAGQVGKRHQKX
              |||||
a552           CKQAGQVGKRHQKX
              190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1615>:

```

m552-1.seq
  1 TTGAATATTA AACTGAAAAC CTTGTTATTG CCCTTCGCCA CGCTGGCATT
 51 GTGCACCAAT GCTTTTGCCG CCCCGCCAG CGACGCGTCG TTGGCGCGTT
101 GGCTGGATAC GCAGAATTTT GACCGGGATA TAGAAAAAAA TATGATTGAG
151 GGCTTTAATG CCGGATTTAA ACCGTATGCG GACAAAGCCC TTGCCGAAAT
201 GCCGGAAGCG AAAAAAGATC AGGCGGCAGA AGCCTTTAAC CGTTATCGTG
251 AGAATGTTTT GAAAGATTG ATTACGCCG AAGTGAAACA GGCTGTCCGC
301 AATACTTTAT TGAAGAATGC CCGTGAGATA TACACGCAAG AAGAAATTGA
351 CGGCATGATT GCCTTTTACG GTTCGCCTGT CGGTCAGTCC GTCGTTGCCA
401 AAAATCCGCG CTTAATCAAG AAATCGATGA GTGAAATAGC GGTATCTTGG
451 ACTGCATTGT CAGGGAAAAT CGCGCAACAT CATCTGCCCG AGTTTACGGA
501 AGAGTTGCGG CGCATCATCT GCGGCGGTAA AAATCCCGAT GCGGGCTGTA
551 AACAAGCCGG ACAGGTTGGG AAAAGGCATC AGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1616; ORF 552-1>:

```

m552-1.pep
  1 LNIKLKTL LL PFATLALCTN AFAAPPSDAS LARWLDTONF DRDIEKNMIE
 51 GFNAGFKPYA DKALAEMPEA KKDQAAEAFN RYRENVKDL ITPEVKQAVR
101 NTLKNAREI YTQEEIDGMI AFYGSVPVQS VVAKNPRLIK KSMSEIAVSW
151 TALSGKIAQH HLPFTEELR RIICGGKNPD AGCKQAGQVG KRHQK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1617>:

a552-1.seq

```

1  TTGAATATTA AACTGAAAAC CTTGTTATTG CCCTTCGCCA CGCTGGCATT
51  GTGCACCAAT GCTTTTGCCG CCCCGCCCAG CGACGCGTCG TTGGCGCGTT
101 GGCTGGATAC GCAGAATTTT GACCGGGATA TAGAAAAAAA TATGATTGAG
151 GGCTTTAATG CCGGATTTAA ACCGTATGCG GACAAAGCCC TTGCCGAAAT
201 GCCGGAAGCG AAAAAAGATC AGGCGGCAGA AGCCTTTAAC CGTTATCGTG
251 AGAATGTTTT GAAAGATTG ATTACGCCG AAGTGAAACA GGCTGTCCGC
301 AATACTTTAT TGAAGAATGC CCGTGAGATA TACACGCAAG AAGAAATTGA
351 CGGCATGATT GCCTTTTACG GTTCGCCTGT CGGTCAGTCC GTCGTTGCCA
401 AAAATCCGCG CTTAATCAAG AAATCGATGA GTGAAATAGC GGTATCTTGG
451 ACTGCATTGT CAGGGAAAAT CGCGCAACAT CATCTGCCG AGTTTACGGA
501 AGAGTTGCGG CGCATCATCT GCGGCGGTAA AAATCCCGAT GCGGGCTGTA
551 AACAAGCCGG ACAGGTTGGG AAAAGGCATC AGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1618; ORF 552-1.a>:

a552-1.pep

```

1  LNIKLKLLLL PFATLALCTN AFAAPPSDAS LARWLDTONF DRDIEKNMIE
51  GFNAGFKPYA DKALAEMPEA KKDQAAEAFN RYRENVLKDL ITPEVKQAVR
101 NTLKKNAREI YTQEEIDGMI AFYGPSVQGS VVAKNPRLIK KSMSEIAVSW
151 TALSGKIAQH HLPEFTEELR RIICGGKNPD AGCKQAGQVG KRHQK*

```

a552-1/m552-1 100.0% identity in 195 aa overlap

	10	20	30	40	50	60
a552-1.pep	LNIKLKLLLLPFATLALCTNAFAAPPSDASLARWLDTONFDRDIEKNMIEGFNAGFKPYA					
m552-1	LNIKLKLLLLPFATLALCTNAFAAPPSDASLARWLDTONFDRDIEKNMIEGFNAGFKPYA					
	10	20	30	40	50	60
	70	80	90	100	110	120
a552-1.pep	DKALAEMPEAKKDQAAEAFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMI					
m552-1	DKALAEMPEAKKDQAAEAFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMI					
	70	80	90	100	110	120
	130	140	150	160	170	180
a552-1.pep	AFYGPSVQGSVVAKNPRLIKKSMSEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPD					
m552-1	AFYGPSVQGSVVAKNPRLIKKSMSEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPD					
	130	140	150	160	170	180
	190					
a552-1.pep	AGCKQAGQVGKRHQKX					
m552-1	AGCKQAGQVGKRHQKX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1619>:

g553.seq

```

1  atggattatc tgcaaaacct gtctttgggc ttgacaaaaa agctgcccg
51  tatactgcaa acagaagtag cggagtgtgg cttggcatgt ctagcggctg
101 tggccggatt ttatggtttc tatacggatt tgcgcgcact gcgttcaaaa
151 tactgtctgt cacttaaggg tgagaatttg gcagatattg ttcgttttgc
201 tgatgatatt gggctgacgg gacgggcgtt gaggctggat ttagacgaat
251 tgggacgatt ggcgctgccc tgtattctac attgggattt gaatcatttt
301 gtggtgctgg aatcggatc ttcggacggg gctgccgtca tggatccggc
351 ttcgggacga cgcaaagtca agacggagga aatatcgcg aagtttacgg
401 gaattgcttt ggaactgtgg ccaaacacgc gtttcgaggc aggggaagaa
451 aagcaggaaa tccgcatact acccatgttg cgcgggattt ctgggctggg
501 gcggaacatt tttcagcttt tggctttggc agcagcaatg gaagtgtttg
551 cttttttaca aaacgtcagc ttcaagatcg gacgtggtga atcgcttgcg
601 ttaatcggac gatcgggctg cggtaaatcg acacttttgg atattttaag
651 cggcaatcta cctcccgaat caggcaaat catgataaat gggcacgaca
701 tttacagctt accgccacct tttattccgc aatttgagtg cgatggtcaa
751 ggcaggacga tgttttatag tggattaaat ttaaaccggg ag

```

This corresponds to the amino acid sequence <SEQ ID 1620; ORF 553.ng>:

g553.pep

m553.seq (partial)

1	ATGGATTATT	TATCAAGACT	GTCCTTTGGA	TTTAACAAAA	AGCTACCTGT
51	CATTCTGCAA	ACAGAAGTTG	CTGAATGTGG	TTTAGCATGC	CTGACATCCA
101	TCTTGTCCCTA	TTATGGCTTT	CACACTGATT	TAAGAACGTT	ACGCCAAAAA
151	TACACCTCTG	CATTAAGGGC	CGCAATCTT	GCAGACATCA	TGAGATTTGG
201	CAATGAATGT	AATTTAACGC	CACGAGCTTT	CGGTTTAGAG	TTAGATGAGC
251	TGTCAAATTT	ACAAC TACCC	TGCATTCTCC	ATTGGAACTT	AAACCATTTT
301	GTTGTACTTT	GTTCCATTTC	CAAAGACAGT	ATCGTCATTA	TGGACCCTGC
351	TGTCGGTATG	CGAAAAATCA	AAATGGACGA	AGTTTCACAA	AAATTCACAG
401	GGATTGCCCT	AGAATTATTC	CCCAATACCC	ATTTTGAAGA	GAAAAAAGAA
451	ACAAAGAAAA	TCAAAATATT	ATCTCTATTA	AGGGGGGGG.T	CAGGCTTAAA
501	ACGCTTTTAA	ATTCAAATGC	TTATATTAGC	TATTCTTTTG	GAAGTCTTTG
551	CATTG...				

m553.pep (partial)

```

1 MDYLSRLSFG FNKKLPVILQ TEVAECGLAC LTSILSYGYF HTDLRTLQK
51 YTLCLKGANL ADIMRFGNEM NLTPRALRL LDELSNLQLP CILHWNLNHF
101 VVLCISKDS IVIMDPAVGM RKIKMDEVSO KFTGIALELF PNTHFEKKE
151 TTKIKILSL RGXSGLKRSI IQMLILAI SL EVFAL...

```

ORF 553 shows 65.5% identity over a 185 aa overlap with a predicted ORF (ORF 553.ng) from *N. gonorrhoeae*:

m553/g553

		10	20	30	40	50	60
g553.pep		MDYLQNLSLGLTKKLPVILQTEVAECGLACLA	AAVAGFYGFYTDLRALRSKYCLSLKG	ENL			
		:	::				
m553		MDYLSRLSFGFNKKLPVILQTEVAECGLAC	LT	SILSYYG	FHTDLR	TLRQKY	TL
		10	20	30	40	50	60
		70	80	90	100	110	120
g553.pep		ADIVRFADDMGLTG	RALRLDLDELG	SLRLPCILH	WDLNHFV	LVESVSSD	GAAVMDPASGR
		::	::	::	::	::	::
m553		ADIMRFGNEMNLTP	RALRLDEL	SLNLQLPCILH	WNLNHFV	VLCSISK	DSIVIMDPAVGM
		70	80	90	100	110	120
		130	140	150	160	170	180
g553.pep		RKVKTEEISRKFTG	IALELWPNT	RFEAGEEKQ	EIRILPMLR	GISGLGRT	LFQLLALAAAM
		::	::	::	::	::	::
m553		RKIKMDEV	SQKFTGIALE	LF	PNT	HFEEKKET	KKIKILSL
		130	140	150	160	170	180
		190	200	210	220	230	240
g553.pep		EVFAFLQNVS	FKIGRGES	LALIGRSG	CGKSTLLD	ILSGNL	PPESGKVMINGHDIYSLPPP
		:					
m553		EVFAL					

a553.seq

1 ATGCCCATC TGCAAAACCT GTCTTTGGGC TTAAAGAAAA AGCTGCCTGT
51 TATCCTGCAA ACAGAAATAT CAGAATGCGG CTTGGCATGT CTGGCGGCTG
101 TGGCGGGATT TCATGTTTC CATACGAATT TACGCGCACT GCGTTCAAAA
151 TAC

a553.pep
1 MPHLQNLSLG LKKKLPVILQ TEISECGLAC LAAVAGFHGF HTNLRALRSK
51 Y

m553/a553 62.7% identity in 51 aa overlap

```

      10          20          30          40          50          60
m553.pep MDYLSRLSFGFNKKLPVILQTEVAECGLACLTSSILSYYGFTDLRTLROKYTLSLKGANL
|::||:::||:|||||||:::||:|||||::: ||:||||:|::|
a553 MPHLQNLSLGLKKKLVPVILQTEISECGLACLAAGVAFHGFHTNLRALRSKY
      10          20          30          40          50

      70          80          90         100         110         120
m553.pep ADIMRFGNEMNLTPRALRLELDELNSNLQLPCILHWNLNHFFVLCSISKDSIVIMDPAVGM

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1625>:

g554.seq.

```
1 atgacagcac ataaaatcct gccgcctctt ctteccatca tcttaggcgt
51 ttctcacgca acggctgcat cgccgcgcc caacagaccg acggtacacg
101 ccgccccac gctccaaaca ccgaaaccc tcacggcggc acacatcggt
151 atcgacctc aaagcaggca gactttatcc gccaaaaaca ccaatacccc
201 tgtcgaaacc gcggcactaa cccaactgat gaccgcatat ttggttttca
251 aaaacatgaa atcgggaaat tccaatctg aagaaaactt aaaaatcccc
301 gaatccgcat gggcttcaga aggaagcaga atgtttgtac gtcccgcgca
351 tacggtcagc accgacaaac tcttaaaagg catgattgcc ctatgcgcaa
401 acgatgccgc cctaaccctt gccgaccggc tgggcaacgg ctcgattgaa
451 aattttgtgc aacaaatgaa caaagaagcc cgacgcttgg gcatgaagaa
501 caccgtattc aaaaaccgga caggcttggg tagagaagga caggtttcca
551 ccgccaagaa cctctccctg ctgtctgaag cattgatgcg cgactttccg
601 gaatattacc cgctgttttc catcaaatcg ttcaagtttg aaacataga
651 aaaaaacaac cgcaatatcc ttttatatag ggacaacaat gtaaacggcc
701 tgaaagccgg gcacacagaa agcggcggct acaaccttgc cgtgtcatac
751 tccgggaacg gcaggcacat ccttgtcatc acataaggtt cggaatcggc
801 ggaaaccgcg gcatcggaca acagcaagct gctgaaccgg gcattcgagg
851 ccttcgatac gcccaaaata tatccgaag gcaaaaccgt tgccccaaatc
901 caaatttccg gaggcagcaa aaaaaccgtc cgcgcaggct tccctaaaga
951 agcctacatc actctgccac ataaagaagc gaaaatggca gaacagattt
1001 tggaaaccat acagccgatt ccgccccgg taaaaaaagg gcagatttta
1051 ggagaaacta aaatcaggga aaacggacat accattgccg aaaaagaaat
1101 cgtcgcatcg gaaaacgtag aaaaaagaag ccggtggcaa aggccttggga
1151 cgcgtctgac aqqcaqtaaa
```

This corresponds to the amino acid sequence <SEQ ID 1626; ORF 554.ng>:

g554.pcp..

1	MTAHKILPVL	LPIILGVSHA	TAASPAPNRP	TVHAAPTLQT	PETLTAAHIV
51	IDLQSRQTL	AKNTNTPVEP	AALTQLMTAY	LVFKNMKSGN	IQSEENLKIP
101	ESAWASEGSR	MFVRPGDVS	TDKLLKGMIA	LCANDAALTL	ADRLNGNSIE
151	NFVQQMNKEA	RRLGMKNTVF	KNPTGLGREG	QVSTAKDLSL	LSEALMRDFP
201	EYYPLFSIK	FKFENIEQNN	RNILLYRDNN	VNGLKAGHTE	SGGYNLAVSY
251	SGNGRHILVI	TLGSESAETR	ASDNKSLNLR	ALQAFDTPKI	YPKGKTVAQI
301	QISGGSKKTV	RAGFLKEAYI	TLPHKEAKMA	EQILETIQPI	PAPVKKGQIL
351	GKIKIRQNGH	TIAEKEIVAL	ENVEKRSRWQ	RLWTRLTGO*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1627>:

m554.seq..

```
1  ATGACAGCAC ATAAATCCT GCCGTCCTG CTTTCCATCA TCTTAGGCGT
51  TTCTCACGCA ACGGCTGCAT CGCCGCGCC CAACAGACCG ACGGTACACG
101 CCGCCCCCAC GTTCCAAACA CCCGAAACCC TCACAGCGGC ACACATCGTT
151 ATCGACCTTC AAGACAAACA GATTTTATCC GCCAAAAACA TCAATACCCC
201 TGTGAAACCG CGGCGACTAA CCCAACTGAT GACCGCATAT CTGGTTTTC
251 AAAACATGAA ATCGGGCAAT ATCCAATCTG AAGAAAACCT AAAAATACCC
```

```

301 GAATCCGCAT GGGCTTCAGA AGGAAGCAGA ATGTTTGTAC GTCCCGGCGA
351 TACGGTCAGC ACCGACAAAC TCTTAAAAGG CATGATTGCA CTATCCGCAA
401 ACGATGCCGC CCTAACCCCTT GCCGGCCGGC TGGGCAACGG CTCGATTGAA
451 AATTTTGTGC AACAAATGAA CAAAGAAGCC CGACGCTTGG GCATGAAGAA
501 CACTGTATTC AAAAACCCGA CAGGCTTGAG TAGAGAAGGA CAGGTTTCCA
551 CCGCCAAAGA CCTCGCCCTG CTGTCTGAAG CATTGATGCG CGACTTTCCG
601 GAATATTACC CGCTGTTTTC CATCAAATCT TTCAAATTCA AAAATATAGA
651 ACAAACAAC CGCAATATCC TTTTATATAG GGACAACAAT GTAAACGGTC
701 TGAAAGCCGG ACACACAGAA AGCGGCGGCT ACAACCTTGC CGTGTCATAC
751 TCCGGCAACG GCAGGCACAT CCTTGTGTC ACATTGGGTT CGGAATCGGC
801 GGAAACACGC GCATCAGACA ACAGCAAGCT GCTGAAGTGG GCATTGCAGG
851 CCTTCGATAC GCCCAAATA TATCCGAAAG GCAAAACCGT TGCCCAAATC
901 CAAATTTCCG GAGGCAGCAA AAAAACCGTC CGCGCAGGCT TCCTCAAAGA
951 AGCCTACATC ACTCTGCCAC ATAAGGAAGC GAAAATGGCA GAACAAATTC
1001 TAGAAACCAT ACAGCCGATT CCCGCCCCAG TAAAAAAGG GCAAAATTTA
1051 GGAAAAATCA AAATCAGACA AAACGGATAC ACCATTGCCG AAAAAGAAAT
1101 CGTCGCACTG GAAAATGTAA AAAAAAGAAG CCGGTGGCAA AGGCTTTGGG
1151 CGTGTCTGAC AGGGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1628; ORF 554>:

m554.pep..

```

1  MTAHKILPVL LSIILGVSHA TAASPAPNRP TVHAAPTFTQ PETLTAAHIV
51  IDLQSKQILS AKNINTPVEP AALTQLMTAY LVFKNMKSGN IQSEENLKIP
101 ESAWASEGSR MFVRPGDTVS TDKLLKGMIA LSANDAALT AGRLNGSIE
151 NFVQQMKEA RRLGMKNTVF KNPTGLSREG QVSTAKDLAL LSEALMRDFP
201 EYYPLFSIKS FKFKNIEQNN RNILLYRDNN VNGLKAGHTE SGGYNLAVSY
251 SGNRHLVI TLGSESAETR ASDNSKLLNW ALQAFDTPKI YPKGKTVAQI
301 QISGGSKKTV RAGFLKEAYI TLPHEAKMA EQILETIQPI PAPVKKGQIL
351 GKI KIRQNGY TIAEKEIVAL ENVKKRSRWQ RLWACLTGQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 554 shows 96.1% identity over a 389 aa overlap with a predicted ORF (ORF 554.ng) from *N. gonorrhoeae*:

m554/g554

	10	20	30	40	50	60
m554 . pep	MTAHKILPVLLSIILGVSHATAASPAPNRP TVHAAPTFTQ PETLTAAHIVIDLQSKQILS					
g554	MTAHKILPVLLPIILGVSHATAASPAPNRP TVHAAPTQLTPETLTAAHIVIDLQSRQTL					
	10	20	30	40	50	60
m554 . pep	AKNINTPVEPAALTQLMTAYLVFKNMKSGNIQSEENLKI PESAWASEGSRMFVRPGDTVS					
g554	AKNTNTPVEPAALTQLMTAYLVFKNMKSGNIQSEENLKI PESAWASEGSRMFVRPGDTVS					
	70	80	90	100	110	120
m554 . pep	AKNINTPVEPAALTQLMTAYLVFKNMKSGNIQSEENLKI PESAWASEGSRMFVRPGDTVS					
g554	AKNTNTPVEPAALTQLMTAYLVFKNMKSGNIQSEENLKI PESAWASEGSRMFVRPGDTVS					
	70	80	90	100	110	120
m554 . pep	TDKLLKGMIALSANDAALTLAGRLNGSIE NFVQQMKEARRLGMKNTVFKNPTGLSREG					
g554	TDKLLKGMIALCANDAALTADRLNGSIE NFVQQMKEARRLGMKNTVFKNPTGLGREG					
	130	140	150	160	170	180
m554 . pep	QVSTAKDLALLSEALMRDFPEYYPLFSIKSFKFKNIEQNNRNILLYRDNNVNGLKAGHTE					
g554	QVSTAKDLSLLSEALMRDFPEYYPLFSIKSFKFENIEQNNRNILLYRDNNVNGLKAGHTE					
	190	200	210	220	230	240
m554 . pep	QVSTAKDLALLSEALMRDFPEYYPLFSIKSFKFKNIEQNNRNILLYRDNNVNGLKAGHTE					
g554	QVSTAKDLSLLSEALMRDFPEYYPLFSIKSFKFENIEQNNRNILLYRDNNVNGLKAGHTE					
	190	200	210	220	230	240
m554 . pep	SGGYNLAVSYSGNRRHILVITLGSESAETR ASDNSKLLNWALQAFDTPKIYPKGKTVAQI					
g554	SGGYNLAVSYSGNRRHILVITLGSESAETR ASDNSKLLNWALQAFDTPKIYPKGKTVAQI					
	250	260	270	280	290	300

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```

g554      SGGYNLAVSYSGNGRHILVITLGSESAETRASDNSKLLNRLQAFDTPKIYPKGKTVAQI
           250      260      270      280      290      300

           310      320      330      340      350      360
m554 . pep QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPI PAPVKKGQILGKIKIRONGY
           |||
g554      QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPI PAPVKKGQILGKIKIRONGH
           310      320      330      340      350      360

           370      380      390
m554 . pep TIAEKEIVALENVKKRSRWQRLWACL TGQX
           |||
g554      TIAEKEIVALENVKKRSRWQRLWTRLTGQX
           370      380      390

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1629>:

```

a554 . seq
1  ATGACAGCAC ATAAAATCCT GCCCGTCCTG CTTTCCATCA TCTTAGGCGT
51  TTCTCAGCA  ACGGCTGCAT CGCCCGCGCC CAACAGACCG ACGGCACACG
101 CCGCCCCAC  GTTCCAAACA CCCGAAACCC TCACAGCGGC ACACATCGTT
151 ATCGACCTTC AAAGCAAACA GATTTTATCC GCCAAAACA  TCAATACCCC
201 TGTCGAACCG GCGGCACTAA CCCAACTGAT GACCGCATAT CTGGTTTTC
251 AAAACATGAA ATCGGGAAT  ATCCGATCTG AAGAAACTT  AAAAATACCC
301 GAATCCGCAT GGGCTTCAGA AGGAAGCAGA ATGTTGTAC  GTCCCGCGA
351 TACGGTCAGC ACCGACAAAC TCTTAAAGG  CATGATTGCA CTATCCGCAA
401 ACGATGCCGC CCTAACCTT  GCCGGCCGGC TGGGCAACGG CTCGATTGAA
451 AATTTTGTGC AACAAATGAA CAAAGAAGCC CGACGCTTGG GCATGAAGAA
501 CACTGTATTC AAAAATCCGA CAGGCTTGAG TAGAGAAGGA CAGGTTTCCA
551 CCGCCAAAGA CCTCGCCCAG CTGTCTGAAG CATTGATGCG CGACTTCCG
601 GAATATTACC CGCTGTTTTT CATCAAATCT TTCAAATTCA AAAATATAGA
651 GCAAAACAAC CGCAATATCC TTTTATATAG GGACAACAAT GTAAACGGTC
701 TGAAAGCCGG ACACACAGAA AGCGGCGGCT ACAACCTTGC CGTGTCATAC
751 TCCGGCAACG GCAGGCACAT CCTTGTCTAT ACATTGGGTT CGGAATCGGC
801 GGAAACACGC GCATCAGACA ACAGCAAGCT GCTGAAGTGG GCATTGCAAG
851 CCTTCGATAC GCCCAAATA  TATCCGAAAG GCAAAACCGT TGCCCAAATC
901 CAAATTTCCG GAGGCAGCAA AAAAACCGTC CGCGCAGGCT TCCTCAAAGA
951 AGCCTACATC ACTCTGCCAC ATAAGGAAGC GAAAATGGCA GAACAAATTC
1001 TAGAAACCAT ACAGCGGATT CCCGCCCCAG TAAAAAAGG GCAAATTTTA
1051 GGAAAAATCA AAATCAGACA AAACGGATAC ACCATTGCCG AAAAAGAAAT
1101 CGTCGCACTG GAAAATGTAA AAAAAAGAAG CCGGTGGCAA AGGCTTTGGG
1151 CGTGTCTGAC AGGGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1630; ORF 554.a>:

```

a554 . pep
1  MTAHKILPVL LSIILGVSHA TAASPAPNRP TAHAAPTFTQ PETLTAAHIV
51  IDLQSKQILS AKNINTPVEP AALTQLMTAY LVFKNMKSNG IRSEENLKIP
101 ESAWASEGSR MFVRPGDVS TDKLLKGMIA LSANDAALTL AGR LGNGSIE
151 NFVQQMKEA  RRLGMKNTVF KNPTGLSREG QVSTAKDLAQ LSEALMRDFP
201 EYYPFISI  KFKNIEQNN RNILLYRDNN VNGLKAGHTE SGGYNLAVSY
251 SNGNRHILVI TLGSESAETR ASDNSKLLNW ALQAFDTPKI  YPKGKTVAQI
301 QISGGSKKTV RAGFLKEAYI TLPHEAKMA EQILETIQPI  PAPVKKGQIL
351 GIKIRQNGY  TIAEKEIVAL ENVKKRSRWQ RLWACL TGQ*

```

m554/a554 99.2% identity in 389 aa overlap

```

           10      20      30      40      50      60
m554 . pep MTAHKILPVLLSIILGVSHATAASPAPNRPTVHAAPTFTQ PETLTAAHIVIDLQSKQILS
           |||
a554      MTAHKILPVLLSIILGVSHATAASPAPNRPTAHAAPTFTQ PETLTAAHIVIDLQSKQILS
           10      20      30      40      50      60

           70      80      90      100     110     120
m554 . pep AKNINTPVEPAALTQLMTAYLVFKNMKSNGNIQSEENLKIPESAWASEGSRMFVRPGDVS
           |||
a554      AKNINTPVEPAALTQLMTAYLVFKNMKSNGNIRSEENLKIPESAWASEGSRMFVRPGDVS

```


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	70	80	90	100	110	120
m554.pep	130	140	150	160	170	180
a554	TDKLLKGMIALSANDAALTLAGRLGNGSIENFVQQMNKEARRLG MKNTVFKNPTGLSREG					
	130	140	150	160	170	180
m554.pep	190	200	210	220	230	240
a554	QVSTAKDLALLSEALMRDFPEYYPLFSIKSFKFKNIEQNNRNILLYRDNNVNLKAGHTE					
	190	200	210	220	230	240
m554.pep	250	260	270	280	290	300
a554	SGGYNLAVSYSGNGRHILVITLGSESAETRASNKLLNWALQAFDTPKIYPKGKTVAQI					
	250	260	270	280	290	300
m554.pep	310	320	330	340	350	360
a554	QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPI PAPVKKGQILGKIKIRQNGY					
	310	320	330	340	350	360
m554.pep	370	380	390			
a554	TIAEKEIVALENVKKRSRWQRLWACL TGQX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1631>:

g556.seq..

```

1  atggacaata agaccaaact gcgcttgggc ggcctgattt tactgaccac
51  cgccgtttta agcctcatta tcgtattgat tgcgattcc tggccgcttg
101 ccatacctgct tgcgcgcgtc atcgtcgccc cgcgtgcggg cggctttggt
151 tggacatccc gccgacagca acgccagttt atcgaaacgtc tgaaaaaatt
201 cgacatcgat cccgaaaaag gcagaatcaa cgaggcaaac ctgcgcgcta
251 tgtaccacag cggcggacaa caccagaaag atgcgattac cctgatctgc
301 ctgtcgcaaa aatgttcggt ggacgaggcg cacgctatgt tcaaaaaacg
351 cccgacacgt caggaaatca atcaaatggc ggcaaaacag tcgcgcgggc
401 agaaacgtcc gcaccgttaa

```

This corresponds to the amino acid sequence <SEQ ID 1632; ORF 556.ng>:

g556.pep.

```

1  MDNKTKLRLG GLILLTTAVL SLIIVLIVDS WPLAILLAIV IVAAAAGGFV
51  WTSRRQORQF IERLKKFDID PEKGRINEAN LRRMYHSGGQ HQKDAITLIC
101 LSQKCSVDEA HAMFKRPTR QEINQMAAKQ SRGQKRPHR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1633>:

m556.seq..

```

1  ATGGACAATA AGACCAAAC T GCGCTTGGGC GGCCTGATTT TACTGACCAC
51  CGCCGTTTTA AGCCTCATT TCGTATTGAT TGTCGATTCC TGGCCGCTTG
101 CCATCCTGCT TGCAGCCGTC ATTGTCGCTG CCGCTGCGGG CGGTTTTGTT
151 TGGACATCCC GCCGACAGCA ACGCCAGTTT ATCGAACGCC TGAaaaaaATT
201 CGACATCGAT CCCGAAAAAG GCAGAATCAA CGAGGCAAAC CTGCGCCGTA
251 TGTACCACAG CGGCGGACAA CACCAGAAAG ATGCGATTAC CCGATCTGTC
301 CTGTGCAAAA AATGTTCGGT GGACGAGGCG CACGCTATGT TCAaaaaaACG
351 CCCGACACGT CAGGAAATCA ATCAAATGGC GGCAaaACAG TCGCGCGGTC
401 AGAAACGTCC GCACCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1634; ORF 556>:

m556.pep..

```

1  MDNKTKLRLG GLILLTTAVL SLIIVLIVDS WPLAILLAIV IVAAAAGGFV
51  WTSRRQORQF IERLKKFDID PEKGRINEAN LRRMYHSGGQ HQKDAITLIC

```

101 LSQKCSVDEA HAMFKKRPTR QEINQMAAKQ SRGQKRPHR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 556 shows 100.0% identity over a 139 aa overlap with a predicted ORF (ORF 556.ng) from *N. gonorrhoeae*:

m556/g556

	10	20	30	40	50	60
m556.pep	MDNKTCLRGLGILLTTAVLSLIIVLIVDSWPLAILLAAVIVAAAAGGFVWTSRRQQRQF					
g556	MDNKTCLRGLGILLTTAVLSLIIVLIVDSWPLAILLAAVIVAAAAGGFVWTSRRQQRQF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m556.pep	IERLKKFDIDPEKGRINEANLRRMYHSGGQHOKDAITLICLSQKCSVDEAHAMFKKRPTR					
g556	IERLKKFDIDPEKGRINEANLRRMYHSGGQHOKDAITLICLSQKCSVDEAHAMFKKRPTR					
	70	80	90	100	110	120
	130	140				
m556.pep	QEINQMAAKQSRGQKRPHRX					
g556	QEINQMAAKQSRGQKRPHRX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1635>:

a556.seq

1	ATGGACAATA	AGACCAAAC	GCGCTTGGGC	GGCCTGATTT	TACTGACCAC
51	CGCCGTTTTA	AGCCTCATT	TCGTATTGAT	TGTCGATTCC	TGGCCGCTTG
101	CCATCCTGCT	TGCCGCCGTC	ATCGTCGCCG	CCGCTGCGGG	CGGCTTTGTT
151	TGGACATCCC	GCCGACAGCA	ACGCCAGTTT	ATCGAACGTC	TGAAAAAATT
201	CGACATCGAT	CCCGAAAAAG	GCAGAAATCAA	CGAGGCAAAC	CTGCGCCGTA
251	TGTACCACAG	CGGCGGACAA	CACCAAAAAG	ATGCGATTAC	CCTGATCTGC
301	CTGTCGCAAA	AATGTTCCGT	GGACGAGGCG	CACGCTATGT	TCAAAAAACG
351	CCCGACACGT	CAGGAAATCA	ATCAAATGGC	GGCAAAACAG	TCGCGCGGTC
401	AGAAACGTCC	GCACCGTTAA			

This corresponds to the amino acid sequence <SEQ ID 1636; ORF 556.a>:

a556.pep

1	MDNKTCLRGLG	GLILLTTAVL	SLIIVLIVDS	WPLAILLAAV	IVAAAAGGFV
51	WTSRRQQRQF	IERLKKFDID	PEKGRINEAN	LRRMYHSGGQ	HOKDAITLIC
101	LSQKCSVDEA	HAMFKKRPTR	QEINQMAAKQ	SRGQKRPHR*	

m556/a556 100.0% identity in 139 aa overlap

	10	20	30	40	50	60
m556.pep	MDNKTCLRGLGILLTTAVLSLIIVLIVDSWPLAILLAAVIVAAAAGGFVWTSRRQQRQF					
a556	MDNKTCLRGLGILLTTAVLSLIIVLIVDSWPLAILLAAVIVAAAAGGFVWTSRRQQRQF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m556.pep	IERLKKFDIDPEKGRINEANLRRMYHSGGQHOKDAITLICLSQKCSVDEAHAMFKKRPTR					
a556	IERLKKFDIDPEKGRINEANLRRMYHSGGQHOKDAITLICLSQKCSVDEAHAMFKKRPTR					
	70	80	90	100	110	120
	130	140				
m556.pep	QEINQMAAKQSRGQKRPHRX					
a556	QEINQMAAKQSRGQKRPHRX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1637>:

g557.seq

```

1  atgaacaaaa tattcettac tgccgcagcc ttggtgctgg gcgcgtgcgg
51  tttccacctg aaaggtgcag acggcatttc tccgccgctg acctaccgga
101 gctggcacat cgaaggcgga caggcattgc aatttccttt ggaaaccgag
151 ctgtatcagg cttcgggcag ggtggacgat gctgccggcg cgcagatgac
201 cctgcgtata gacagcgttt cccaaaacaa ggaaacctat accgttaccc
251 gtgcggcagt catcaacgaa tatcttttga tattgacggt tgaagcgcag
301 gtattgaaac gcggcgagcc ggtcggcaaa ccatgaccg tgcctgccg
351 ccgcattttg gattatgccg acaacgaaat tttgggcaaa caggaagaag
401 aagaaaccct gtggcgga atgcggcagg atgttgccga acagattgtc
451 cgccgcctga cctttctgaa ggcggaatga

```

This corresponds to the amino acid sequence <SEQ ID 1638; ORF 557.ng>:

g557.pep..

```

1  MNKIFLTAAA LVLGACGFHL KGADGISPPL TYRSWHIEGG QALQFPLETA
51  LYQASGRVDD AAGAQMTRLI DSVSONKETY TVTRAAVINE YLLILTVEAQ
101 VLKRGEFVGK PMTVSVRRIL DYADNEILGK QEEEETLWAE MRQDVAEQIV
151 RRLTFLKAE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1639>:

m557.seq..

```

1  ATGAACAAAC TGTTCTTAC TGCCGCAGTG CTGATGCTGG GCGCGTGC GG
51  TTTCCACCTG AAAGGTGCAG ACGGCATTTC TCCGCCGCTG ACCTACCGGA
101 GCTGGCACAT CGAAGGCGGA CAGGCATTGC GGTTCCTTTT GGAAACCGCG
151 CTGTATCAGG CTTCGGGCAG GGTGGACGAT GCTGCCGGCG CGCAGATGAC
201 CCTGCGTATA GACAGCGTTT CCCAAAACAA GGAAACCTAC ACCGTTACCC
251 GTGCGGCAGT CATCAACGAA TATCTTTTGA TATTGACGGT TGAAGCGCAG
301 GTATTGAAAC GCGGCGAGCC GGTCCGTAAA CCGATGACCG TGTCCGTCCG
351 CCGCGTCCTT GCTTATGCCG ACAACGAGAT CTTGGGCAAA CAGGAAGAGG
401 AAGCGGCATT GTGGGCGGAA ATGCGGCAGG ATGCCGCCGA ACAGATTGTC
451 CGCCGCCTGA CCTTTCTGAA GGCGGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1640; ORF 557>:

m557.pep..

```

1  MNKLFLTA AV LMLGACGFHL KGADGISPPL TYRSWHIEGG QALRFPLETA
51  LYQASGRVDD AAGAQMTRLI DSVSONKETY TVTRAAVINE YLLILTVEAQ
101 VLKRGEFVGK PMTVSVRRVL AYADNEILGK QEEEAALWAE MRQDAAEQIV
151 RRLTFLKAE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 557 shows 94.3% identity over a 159 aa overlap with a predicted ORF (ORF 557.ng) from *N. gonorrhoeae*:

m557/g557

	10	20	30	40	50	60
m557.pep	MNKLFLTA AV LMLGACGFHL KGADGISPPL TYRSWHIEGG QALRFPLETA LYQASGRVDD					
	: :					
g557	MNKIFLTAAA LVLGACGFHL KGADGISPPL TYRSWHIEGG QALQFPLETA LYQASGRVDD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m557.pep	AAGAQMTRLIDSVSONKETY TVTRAAVINE YLLILTVEAQ VLKRGEFVGK PMTVSVRRVL					
g557	AAGAQMTRLIDSVSONKETY TVTRAAVINE YLLILTVEAQ VLKRGEFVGK PMTVSVRRIL					
	70	80	90	100	110	120
	130	140	150	160		
m557.pep	AYADNEILGK QEEEAALWAE MRQDAAEQIV RRLTFLKAE X					
	: :					
g557	DYADNEILGK QEEEETLWAE MRQDVAEQIV RRLTFLKAE X					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1641>:

```

a557.seq
  1 ATGAACAAAC TGTTTCTTAC TGCCGCAGTG CTGATGCTGG GCGCGTGCGG
 51 TTTCCACCTG AAAGGTGCAG ACGGCATTTC TCCGCCGCTG ACCTACCGGA
101 GCTGGCACAT CGAAGGCGGA CAGGCATTGC AGTTTCCTTT GGAAACCGCG
151 CTGTATCAGG CTTCGGGTAG GGTGGACGAT GCTGCCGGCG CGCAGATGAC
201 CCTGCGTATA GACAGCGTTT CCCAAACAA GGAAACCTAC ACCGTTACCC
251 GTGCGGCAGT CATCAACGAA TATCTTTTGA TATTGACGGT TGAAGCGCAG
301 GTATTGAAAC GCGGCGAGCC GGTCGGCAAA CCGATGACCG GTCCGTCCG
351 CCGCGTCCTT GCTTATGCCG ACAACGAGAT CTTGGGCAAA CAGGAAGAGG
401 AAGCGGCATT GTGGGCGGAA ATGCGGCAGG ATGCCGCCGA ACAGATTGTC
451 CGCCGCCTGA CCTTTCTGAA GCGCGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1642; ORF 557.a>:

```

a557.pep
  1 MNKLFLTA AV LMLGACGFHL KGADGISPPL TYRSWHIEGG QALQFPLETA
 51 LYQASGRVDD AAGAQM TLRI DSVSQNKETY TVTRAAVINE YLLILTVEAQ
101 VLKRGE PVGK PMTVSVRRVL AYADNEILGK QEEEAALWAE MRQDAAEQIV
151 RRLTFLKAE*

```

m557/a557 99.4% identity in 159 aa overlap

	10	20	30	40	50	60
m557.pep	MNKLFLTA AV LMLGACGFHL KGADGISPPL TYRSWHIEGG QALRFPLETA LYQASGRVDD					
a557	MNKLFLTA AV LMLGACGFHL KGADGISPPL TYRSWHIEGG QALQFPLETA LYQASGRVDD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m557.pep	AAGAQM TLRI DSVSQNKETY TVTRAAVINE YLLILTVEAQ VLKRGE PVGK PMTVSVRRVL					
a557	AAGAQM TLRI DSVSQNKETY TVTRAAVINE YLLILTVEAQ VLKRGE PVGK PMTVSVRRVL					
	70	80	90	100	110	120
	130	140	150	160		
m557.pep	AYADNEILGK QEEEAALWAE MRQDAAEQIV RRLTFLKAE X					
a557	AYADNEILGK QEEEAALWAE MRQDAAEQIV RRLTFLKAE X					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1643>:

```

g558.seq..
  1 ATGGATGCTT GTTTTTTCGT CATTCCCGCA CAGGCGGGAA TTCGGAGATT
 51 CGGGATTGTT TTCAAACGTT CGGGTCGGAT TCTTGCCGGT GCGGGAATGA
101 TGCCCTTATA TACTTTCTCC GAGCTTTATA TGCTTCAACA GGGGACGGCA
151 CATCAAGCAC CGCACTGCGT GTTGCCCGAA CGAGGCTGCC CTCCGATTAG
201 ATTCTATCGC TATAAACAGA CGGGTTTCAA CCGAAAAGGA ATGGGGATAA
251 AGTCCATTTC CGACACCTCT CGGGCGATGC CGTCTGAAAA CCAATCTCCA
301 CTTTCAGACG GCATTGTTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1644; ORF 558.ng>:

```

g558.pep..
  1 MDACFFVIP A QAGIRRF GIV FKRSGRILAG AGMMP LYTFS ELYMLQQGTA
 51 HQAPHCVLPE RGCPIRFYR YKQTGFNRKG MGIKSISDTS RAMPSENQSP
101 LSDGIV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1645>:

```

m558.seq..
  1 ATGAATGCTT GTTTTTTCGT CATTCCACAC CAGGCGGGAA TTCGGAGATT
 51 CGGGATTGTT TTCAAACGTT CGGGTCGGAT TCTTGCCGGT GCAGGAATGA
101 TGCCCTTATA TACTTTCTCC GAGCTTTATA TGTTTCAACA GGGGACGGCA
151 CATCAAGCAC CGCACTGCGT GTTGCCCGAA CGAGACTACC CTCCGATTAG
201 ATTCTATCGC CATAAACAGA CGGGTTTCAA CCGAAAAGGA ATGGGGATAA
251 AGTCCATTTC CGACATCTsT CGGGCGATGC CGTCTGAAAA CCAATCTCCA
301 CTTTCAGACG GCATTGTTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1646; ORF 558>:

m558.pep..

1 MNACFFVIPT QAGIRRFIV FKRSGRILAG AGMMPYTFSELYMFQOQGTAHQAPHCVLPE
 51 HQAPHCVLPE RDYPPIRFYR HKQTGFNRKG MGIKSISDIX RAMPSENQSP
 101 LSDGIV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 558 shows 92.5% identity over a 106 aa overlap with a predicted ORF (ORF 558.ng) from *N. gonorrhoeae*:

m558/g558

	10	20	30	40	50	60
m558.pep	MNACFFVIPTQAGIRRFIVFKRSGRILAGAGMMPYTFSELYMFQOQGT	HAHQAPHCVLPE				
g558	MDACFFVIPAQAGIRRFIVFKRSGRILAGAGMMPYTFSELYMLQOQGT	HAHQAPHCVLPE				
	10	20	30	40	50	60
	70	80	90	100		
m558.pep	RDYPPIRFYRHKQTGFNRKGMGIKSISDIXRAMPSENQSPLSDGIVX					
g558	RGCPPIRFYRYKQTGFNRKGMGIKSISDTSRAMPSENQSPLSDGIVX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1647>:

a558.seq

1	ATGAATGCTT	GTTTTTTCGT	CATTCCCACA	CAGGCGGGAA	TTCGGAGATT
51	CGGGATTGTT	TTCAAACGTT	CGGGTCGGAT	TCTTGCCGGT	GCGGGAATGA
101	TGCCCTTATA	TATAGTGGAT	TAAATTTAAA	TCAGGACAAG	GCGACGAAGC
151	CGCAGACAGT	ACAAATAGTA	CGGCAAGGCG	AGGCAACGCC	GTACTGGTTT
201	AAATTTAATC	CACTATACTT	TCTCCGAGCT	TTATATGTTT	CAACAGAGGA
251	CGGCACATCA	AGCACCACAC	TGCGTGTTGC	CCGAACGAGA	CTGCCCTCCG
301	ATTAGATTCT	ATCGCTATAA	ACAGACGGGT	TTCAACCGAA	AAGGAATGGG
351	AATGAAGTCC	GTTTCCGACA	CCTCTCGGGC	GATGCCGTCT	GAAAACCAAT
401	CTCCACTTTC	AGACGGCATT	GTTTAG		

This corresponds to the amino acid sequence <SEQ ID 1648; ORF 558.a>:

a558.pep

1	MNACFFVIPT	QAGIRRFIV	FKRSGRILAG	AGMMPYIVD	*I*IRTRRRS
51	RRQYK*YGKA	RQRRTGLNLI	HYTFSELYMF	QORTAHQAPH	CVLPERDCPP
101	IRFYRYKQTG	FNKGMGMKS	VSDTSRAMPS	ENQSPLSDGI	V*

m558/a558 70.2% identity in 141 aa overlap

	10	20	30			
m558.pep	MNACFFVIPTQAGIRRFIVFKRSGRILAGAGMMPY	-----				
a558	MNACFFVIPTQAGIRRFIVFKRSGRILAGAGMMPYIVDXIXIRTRRRSR	RRQYKXYGKA				
	10	20	30	40	50	60
	40	50	60	70	80	
m558.pep	-----TFSELYMFQOQGT	HAHQAPHCVLPERDYPPIRFYRHKQTGFNRKGMGIKS				
a558	RQRRTGLNLIHYTFSELYMFQOQGT	HAHQAPHCVLPERDCPPIRFYRYKQTGFNRKGMGMKS				
	70	80	90	100	110	120
	90	100				
m558.pep	ISDIXRAMPSENQSPLSDGIVX					
a558	VSDTSRAMPS	ENQSPLSDGIVX				
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1649>:

g560.seq

1	atgctcatca	tccgcaacct	gatttactgg	ctgatactct	gttccagcct
---	------------	------------	------------	------------	------------

```

51  gattttcttc tttcccttta tgctgctcgc ctgccttttc cgggacgggg
101  cgcacaagat ggcgcggttc tgggtcgga tcctcaactg gtgcgtcaaa
151  cacatcgctc gggtcaaata ccgcatcatc ggcgcggaac acattccgga
201  cggccctccc gtcattctgcg ccaaacacca aagcggtctg gaaacgctcg
251  cgctccaaga gatttttccg ccgcaggttt acgttgccaa gcgcgagttg
301  ttcaaaatcc cttttttcgg ctggggcttg aaactggtca aaaccatagg
351  catagaccgc aacaaccgcc gcgaagccaa cgaacagctc ataaaacagg
401  gtttggcgcg caaaaacgaa ggttattgga ttaccatttt ccccgaggc
451  acgcgccttg cgcccggaaa acgcggcaaa taaaaactcg gcggcgcgcg
501  catggcgaaa atgtttgaga tggacatcgt ccccgctgcc ctcaacagcg
551  gcgaattttg gccgaaaaat tcctttctga aatatccggg ggaaatcacc
601  gtcacatctt gtccgaccat cccgcacgca agcggcagcg aagccgaatt
651  gatggaaaaa tgcgaacacc tcattgaaac gcaacaaccg cttatttccg
701  gcgcaggccc gtttgccgcc gaaatgccgt ctgaaaccgc atga

```

This corresponds to the amino acid sequence <SEQ ID 1650; ORF 560.ng>:

g560.pep..

```

1  MLIIRNLIYW LILCSSLIFL FPFMLLASPF RDGAHKMARV WVGILNWSLK
51  HIVGLKYRII GAEHIPDRPS VICAQHSGW ETLALQEIFP PQVYVAKREL
101 FKIPFFGWGL KLVKTIGIDR NNRREANEQL IKQGLARKNE GYWITIFPEG
151 TRLAPGKR GK YKLGGARMAK MFEMDIVPVA LNSGEFWPKN SFLKYPGEIT
201 VIICPTIPHA SGSEAELEMEK CEHLIETQQP LISGAGPFAA EMPSET*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1651>:

m560.seq

```

1  ATGCTCATCA TCCGCAACCT GATTACTGG CTGATACTCT GTTCCACCCT
51  GATTTTCCTC TTTCCCTTTA TGCTGCTCGC CTCGCCTTTC CGGGACGGGG
101 CGCACAAGAT GGCGCGGGTC TGGGTCGGCA TTCTCAACTG GTCGCTCAAA
151 CACATCGTCG GGCTCAAATA CCGCATCATC GGCGCGGAAA ACATCCCCGA
201 CCGCCCCGCC GTCATCTGCG CCAAACACCA AAGCGGCTGG GAAACGCTCG
251 CCCTTCAGGA CATTTTTCCG CCGCAGGTTT ACGTTGCCAA ACGCGAGTTG
301 TTCAAAATCC CCTTTTTCCG CTGGGGCTTG AAACGTGTCA AAACCATAGG
351 CATAGACCGC AACAACCGCC GCGAAGCCAA CGAGCAGCTC ATAAAACAGG
401 GGTTGGTGCG CAAAAACGAA GGCTATTGGA TTACCATTTT CCCCGAAGGC
451 ACGCGCCTTG CGCCCGGAAA ACGCGGCAAA TACAACTCG GCGGCGCGCG
501 CATGGCGAAA ATGTTTGAGA TGGACATCGT CCCCCTCGCC CTCAACAGCG
551 GCGAATTTTG GCCGAAAAAC TCCTTTCTGA AATATCCGGG GGAAATCACC
601 GTCGTCATCT GTCCGACCAT CCCGCACGCA AGCGGCAGCG AAGCCGAATT
651 GATGGAAAAA TGCGAACATC TCATCGAAAC GCAACAACCG CTTATTTCCG
701 GCGCAGGCCG GTTTGCCGCC AAAATGCCGT CTGAAACCGC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1652; ORF 560>:

m560.pep

```

1  MLIIRNLIYW LILCSTLIFL FPFMLLASPF RDGAHKMARV WVGILNWSLK
51  HIVGLKYRII GAENIPDRPA VICAQHSGW ETLALQDIFP PQVYVAKREL
101 FKIPFFGWGL KLVKTIGIDR NNRREANEQL IKQGLVRKNE GYWITIFPEG
151 TRLAPGKR GK YKLGGARMAK MFEMDIVPVA LNSGEFWPKN SFLKYPGEIT
201 VVICPTIPHA SGSEAELEMEK CEHLIETQQP LISGAGPFAA KMPSETA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 560 shows 97.2% identity over a 246 aa overlap with a predicted ORF (ORF 560.ng) from *N. gonorrhoeae*:

m560/g560

```

          10      20      30      40      50      60
m560.pep  MLIIRNLIYWLILCSTLIFLFPFMLLASPF RDGAHKMARVWVGILNWSLK HIVGLKYRII
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g560       MLIIRNLIYWLILCSSLIFLFPFMLLASPF RDGAHKMARVWVGILNWSLK HIVGLKYRII
          10      20      30      40      50      60

          70      80      90     100     110     120
m560.pep  GAENIPDRPAVICAQHSGWETLALQDIFPPQVYVAKREL FKIPFFGWGLKLVKTIGIDR
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g560       GAEHIPDRPSVICAQHSGWETLALQEIFPPQVYVAKREL FKIPFFGWGLKLVKTIGIDR

```

843

	70	80	90	100	110	120
	130	140	150	160	170	180
m560.pep	NNRREANEQLIKQGLVRKNEGYWITIFPEGTRLAPGKRGKYKLGGARMAKMFEMDIVPVA					
g560	NNRREANEQLIKQGLARKNEGYWITIFPEGTRLAPGKRGKYKLGGARMAKMFEMDIVPVA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m560.pep	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEMEKCEHLIETQQPLISGAGPFAA					
g560	LNSGEFWPKNSFLKYPGEITVIICPTIPHASGSEAELEMEKCEHLIETQQPLISGAGPFAA					
	190	200	210	220	230	240
m560.pep	KMPSETAX					
	:					
g560	EMPSETX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1653>:

a560.seq

1	ATGCTCATCA	TCCGCAACCT	GATTACTGG	CTGATACTCT	GTTCCACCCT
51	GATTTTCCTC	TTTCCCTTTA	TGCTGCTCGC	CTCGCCTTTC	CGAGACGGGG
101	CGCACAAGAT	GGCGCGGGTC	TGGGTCAAAA	TCCTCAACCT	CTCGCTCAAA
151	CACATCGTCG	GGCTCAAATA	CCGCATCATC	GGCGCGGAAA	ACATCCCCGA
201	CCGCCCCGCC	GTCATCTGCG	CCAAACACCA	AAGCGGCTGG	GAAACGCTCG
251	CCCTTCAGGA	CATTTTTCCG	CCGCAGGTTT	ACGTTGCCAA	ACGCGAGTTG
301	TTCAAATCC	CCTTTTTCCG	CTGGGGCTTG	AACTGGTCA	AAACCATAGG
351	CATAGACCGC	AACAACCGCC	GCGAAGCCAA	CGAGCAGCTC	ATAAAACAGG
401	GGTTGGCGCG	CAAAAACGAA	GGCTATTGGA	TTACCATTTT	CCCCGAAGGC
451	ACACGCCTTG	CGCCCGGAAA	ACGCGGCAAA	TACAACTCG	GCGGCGCGCG
501	CATGGCGAAA	ATGTTTGAGA	TGGACATCGT	CCCCGTCGCC	CTCAACAGCG
551	GCGAATTTTG	GCCGAAAAAC	TCCTTTCTGA	AATATCCGGG	GGAAATCACC
601	GTCGTCATCT	GTCCGACCAT	CCGCGACGCA	AGCGGCAGCG	AAGCCGAATT
651	GATGGGAAAA	TGCGAACACC	TCATCGAAAC	GCAGCAGCCG	CTCATTTCCG
701	GCGCAGGCC	GTTTGCCGCC	AAAATGCCGT	CTGAAACCGC	ATGA

This corresponds to the amino acid sequence <SEQ ID 1654; ORF 560.a>:

a560.pep

1	MLIIRNLIYW	LILCSTLIFL	FPFMLLASPF	RDGAHKMARV	WVKILNLSLK
51	HIVGLKYRII	GAENIPDRPA	VICAKHQSGW	ETLALQDIFP	PQVYVAKREL
101	FKIPFFGWGL	KLVTIGIDR	NNRREANEQL	IKQGLARKNE	GYWITIFPEG
151	TRLAPGKRGK	YKLGGARMAK	MFEMDIVPVA	LNSGEFWPKN	SFLKYPGEIT
201	VVICPTIPHA	SGSEAELEMGK	CEHLIETQQP	LISGAGPFAA	KMPSETA*

m560/a560 98.4% identity in 247 aa overlap

	10	20	30	40	50	60
m560.pep	MLIIRNLIYWLILCSTLIFLFPFMLLASPF	RDGAHKMARVWVGILNWSLKHIVGLKYRII				
a560	MLIIRNLIYWLILCSTLIFLFPFMLLASPF	RDGAHKMARVWVKILNLSLKHIVGLKYRII				
	10	20	30	40	50	60
	70	80	90	100	110	120
m560.pep	GAENIPDRPAVICAKHQSGWETLALQDIFPPQVYVAKREL	FKIPFFGWGLKLVTIGIDR				
a560	GAENIPDRPAVICAKHQSGWETLALQDIFPPQVYVAKREL	FKIPFFGWGLKLVTIGIDR				
	70	80	90	100	110	120
	130	140	150	160	170	180
m560.pep	NNRREANEQLIKQGLVRKNEGYWITIFPEGTRLAPGKRGKYKLGGARMAKMFEMDIVPVA					
a560	NNRREANEQLIKQGLARKNEGYWITIFPEGTRLAPGKRGKYKLGGARMAKMFEMDIVPVA					

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	130	140	150	160	170	180
	190	200	210	220	230	240
m560.pep	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEMEKCEHLIETQQPLISGAGPFAA					
a560						
	190	200	210	220	230	240
m560.pep	KMPSETAX					
a560						
	KMPSETAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1655>:

```

m561.seq.
1  ATGATACTGC CAGCCCGTTT TTCAGACGGC ATCAGCCTTT CCCTGCGCCT
51  GAAACTCCTG ACCGGACTGT GGGTCGGGTT GGCGGCATTG TCTGTCGTTT
101 TGACACTGCT GCTCTCTTTG CGTCTGGAAC ACGCGGCCTC CGTCATCGAA
151 GAGGCGGGCA ACTTGAGAAT GCAGGCATAC CGTCTGGCAT ACATGGCGGG
201 TGAAGGCTCG CCCCGTGC GCAGGCATAC TCAGGTTGCC GAATTTGAAA
251 AAAGTTTAAA ACGCATTGCC CAAAGCGATG CCATCCATCC GCTGATTCCT
301 TCGGACACCC CTCTTGCTTA TGATTTGATA CAATCCATGC TGATTATAGA
351 TTGGCAGGCA CACATCCTCC CCCCGCTCCA GTCCTACCGG CGACCGACTC
401 AGGTCGATCT CTACCGCTTT GCCGGAACA TCGAACTGTT TTTGCAGGCA
451 TTGGAATAAT CCAACGAAAA AAACACATGG TGGCTCAGGC GTTTTCAATG
501 GGCAATTATG TTGATGACGC TGGTGTCGTC TGTACTGATG CTGTTTGGC
551 ACCAGATTTC GGTTATCCGG CCGCTGCAGG CGTTAAGGGA AGGTGCGGAA
601 CGCATCGGAC GGAGGTGTTT CGATATTCCG GTTCCCGAAG GCGGTACGCC
651 GGAATTCAAA CAGGTCGGGC GTTGTTCCTA TCAAAATGGG GGCAGGTTGA
701 AAATTTTATA TGATGATTTC GAAGGACAAG TCGCCGAGCA GACACGCAGT
751 CTCGAAAAAC AAAATCAAAA CCTGACCCTG CTGTACCAAA CTACACGGGA
801 CCTGCACCAA TCCTACATAC CGCAACAGGC TGCAGAACAT TTTCTAAACC
851 GTATCCTGCC CGCCGTAGGA GCAGATTCCG GCAGAGTTTG TTTGGACGGC
901 GGATCCGATG TTTATGTTTC CATTTCATCAT GCGGATTGCG GCACAGCAGC
951 TTCGGATTTC GGAAGTACC ATGAGGAAAT CTTCCCATT GAGTACCAGA
1001 ACGAAACATT GGGCAGGCTG TTGCTCAGCT TTCCAAACGG CATTTCCTTT
1051 GATGAAGACG ACCGCATCCT GCTTCAAACA CTAGGCAGGC AATTGGGCGT
1101 ATCGCTTGCC GGCGCAAAAC AGGAGGAAGA AAAACGCCTG CTGTCAGTAT
1151 TGCAAGAACG CAACCTGATT GCGCAAGGAT TACATGACAG CATCGCACAA
1201 GCATTAACGT TCCTAAACCT ACAGGTACAG ATGCTGGAAC CCGCCTTTGC
1251 CGAAAAACAA CGGGAGGAAG CCGCAGAAAA CATCAGCTTT ATCAAACAG
1301 GCGTGCAGGA ATGTTATGAA GATGTCCGCG AACTGCTGCT CAACTCCGT
1351 ACCAAAATCA GCAATAAAGA ATTTCCCGAA GCGGTTGCCG ACCTATTCGC
1401 CCGCTTTACG CAACAAACCG GGATAACGGT CGAAACCGCC TGGGAAAACG
1451 GTTCGTTTCT GCCGCTCAG GAAGCGCAGC TCCAAATGAT TTTTATCCTG
1501 CAGGAAAGCC TGTCCAACAT CCGCAACAC GCGCGCGCCA CCCATGTAAA
1551 ATTCACCCTT TCCGAACACG GCGGACGCTT TACCATGACC ATCCAAGACA
1601 ACGGACAAGG TTTGACACG GAGAAAATAG GAGAACCAC GGCAGCCAT
1651 GTCGGAATGC ACATCATGCA GGAGCGTGCC AAACGCATCC ATGCCGTTTT
1701 AGAAATCCGT TCCCAAGCTC AACAGGGAAC CACCGTCTCA TTGACGGTTG
1751 CATCTGAAGA AAGCTTGAAA TGA

```

This corresponds to the amino acid sequence <SEQ ID 1656; ORF 561>:

```

m561.pep
1  MILPARFSDG ISLSRLKLL TGLWVGLAAL SVVLTLTLLSL RLENAASVIE
51  EAGNLRMQAY RLAYMAGEGS PRAQIDNQVA EFEKSLKRIA QSDAIHPLIP
101 SDTPLAYDLI QSMILIOWQA HILPPLQSYR RPTQVDLYRF AGNIELFLQA
151 LENANEKNTW WLRRFQWAIM LMTLVSSVLM LFHWQIWWIR PLQALREGAE
201 RIGRRCFDIP VPEGGTPEFK QVGRCFNQMG GRLKILYDDL EGQVAEQTRS
251 LEKQONQNLTL LYQTRDLHQ SYIPQQAEEH FLNRILPAVG ADSGRVCLDG
301 GSDVYVSIHH ADCGTAASDL GKYHEEIFPI EYQNETLGR LLSFPNGISL
351 DEDDRILLQT LGRQLGVSLA GAKQEEKRL LAVLQERNLI AQGLHDSIAQ
401 ALTFLNLQVQ MLETAFENK REEAENISF IKTGVQECYE DVRELLNFR
451 TKISNKEFPE AVADLFARFT QQTGITVETA WENGSLPPO EAQLQMIFIL

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501 QESLSNIRKH ARATHVKFTL SEHGGRTMT IQDNGQGFDT EKIGEPTGSH
 551 VGLHIMQERA KRIHAVLEIR SQAQQTTS LTVASEESLK *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m561/g561 89.7% identity in 223 aa overlap

	10	20	30	40	50	60
m561.pep	MILPARFSDGISLSRLKLLTGLWVGLAALSVVLTLLLSRL	LENAASVIEEAGNLRMQAY				
g561	MILPTRFSDGIPLSRLKLLTGLWVGLAALSVVLTLLLSFRL	ENAASVIEEAGNLRMQAY				
	70	80	90	100	110	120
m561.pep	RLAYMAGEGSPRAQIDNQVAEFKSLKRIAQSDAIHPLIPSDT	PLAYDLIQSMLIIDWQA				
g561	RLAYMAGEGSPRAQIDNQIAEFKSLKRISQSDAIHPLIPSDN	PLAYDLIQSMLIIDWQA				
	130	140	150	160	170	180
m561.pep	HILPPLQSYRRPTQVDLYRFAGNIELFLOALENANEKNTWWL	RRFQWAIMLMTLVSSVLM				
g561	NILPPLQAYRRPTQIELYRFAGNIELFLOALENAGEKNTWWL	RRFQWVIMLMTLVSSVLM				
	190	200	210	220	230	240
m561.pep	LFWHQIWVIRPLQALREGAERIGRRCFDIPVPEGGTPEFKQV	GRCFNQMGGRKILYDDL				
g561	LFWHQIWVIRPLQALREGAERIGRRHFDIPVPEDVRPN	SNRSGGVSTKWRSGX				
	250	260	270	280	290	300
m561.pep	EGQVAEQTRSLEKQONQLTLLYQTTTRDLHQSYIPQAAEH	FLNRLPAVGADSGRVCLDG				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1657>:

a561.seq

1	ATGATACTGC	CAGCCCGTTT	TTCAGACGGC	ATCAGCCTTT	CCCTGCGCCT
51	GAAACTCCTG	ACCGGACTGT	GGGTCGGGTT	GGCGGCATTG	TCTGTCGTTT
101	TGACACTGCT	GCTCTCTTTG	CGTCTGGAAA	ACGCGGCCTC	CGTCATCGAA
151	GAGGCGGGCA	ACTTGAGAA	GCAGGCATAC	CGTCTGGCAT	ACATGGCGGG
201	TGAAGGCTCG	CCCCGTGCGC	AAATTGACAA	TCAGGTTGCC	GAATTTGAAA
251	AAAGTTTAAA	ACGCATTGCC	CAAAGCGATG	CCATCCATCC	GCTGATTCTT
301	TCGGACACCC	CTCTTGCTTA	TGATTTGATA	CAATCCATGC	TGATTATAGA
351	TTGGCAGGCA	CACATCCTCC	CCCCGCTCCA	GTCTACCGG	CGACCGACTC
401	AGGTCGATCT	CTACCGCTTT	GCCGGAAACA	TCGAACTGTT	TTTGCAGGCA
451	TTGGAAAATG	CCAACGAAAA	AAACACATGG	TGGCTCAGGC	GTTTTCATATG
501	GGCAATTATG	TTGATGACGC	TGGTGTCTGC	TGTACTGATG	CTGTTTGTGC
551	ACCAGATTTG	GGTTATCCGG	CCGCTGCAGG	CGTTAAGGGA	AGGTGCGGAA
601	CGCATCGGAC	GGAGGTGTTT	CGATATTCCG	GTTCCCGAAG	GCGGTACGCC
651	GGAAATCAAA	CAGGTCGGGC	GTTGTTTCAA	TCAAATGGGC	GGCAGGTTGA
701	AAATTTTATA	TGATGATTTG	GAAGGACAAG	TCGCCGAGCA	GACACGCAGT
751	CTCGAAAAAC	AAAATCAAAA	CCTGACCTTG	CTGTACCAAA	CTACACGGGA
801	TCTGCACCAA	TCCTACATAC	CGCAACAGGC	TGCAGAACAT	TTTCTAAACC
851	GTATCCTGCC	CGCCGTAGGA	GCAGATTCCG	GCAGAGTTTG	TTTGGACGGC
901	GGATCCGATG	TTTATGTTTC	CATTTCATCAT	GCGGATTGCG	GCACAGCAGC
951	TTCGGATTTG	GGGAAGTACC	ATGAGGAAAT	CTTCCCCATT	GAGTACCAGA
1001	ACGAAACATT	GGGCAGGCTG	TTGCTCAGCT	TTCCAAACGG	CATTTCTCTT
1051	GATGAAGACG	ACCGCATCCT	GCTTCAAACA	CTAGGCAGGC	AATTGGGCGT
1101	ATCGCTTGCC	GGCGCAAAAC	AGGAGGAAGA	AAAACGCCTG	CTTGACAGTAT
1151	TGCAGGAACG	CAACCTGATT	GCGCAAGGAT	TACATGACAG	CATCGCACAA
1201	GCATTAACGT	TCCTAAACCT	ACAGGTACAG	ATGCTGGAAA	CCGCCTTTGC
1251	CGAAAAACAA	CGGGAGGAAG	CCGCAGAAAA	CATCGGCTTC	ATCAAAACAG
1301	GCGTGCAGGA	ATGTTATGAA	GATGTCGCG	AACTGCTGCT	CAACTTCCGT
1351	ACCAAAATCA	GTAATAAAGA	ATTTCCTGAA	GCCGTTGCCG	ACCTATTCTC

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1401 GCGCTTTACG CAACAGACCG GCACGACTGT CGAAACCGCT TGGGAAAACG
1451 GCACGCACCT GCCTACACAG GACGAGCAGC TCCAAATGAT TTTCATCCTG
1501 CAAGAAAGCT TGTCCAACAT CCGAAAACAT GCCCAGGCCA CCCATATCAA
1551 ATTCAGACTG CTCAAACAGG ATGGAAGTTT TACAATGACC ATTCAAGACA
1601 ACGGACAGGG TTTTGACACG GAAAACATTG GAGAACCATC GGGCAGCCAT
1651 GTCGGACTGC ATATCATGCA GGAGCGTGCC AAACGCATCC ATGCCGTTTT
1701 AGAAATCCGT TCCCAAGCTC AACAGGGAAC CACCGTCTCA TTGACGGTTG
1751 CATCTGAAGA AAGCTTGAAA TGA

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This corresponds to the amino acid sequence <SEQ ID 1658; ORF 561.a>:

```

a561.pep
1 MILPARFSDG ISLSRLKLL TGLWVGLAAL SVVLTLLLSL RLENAASVIE
51 EAGNLRMQAY RLAYMAGEGS PRAQIDNQVA EFEKSLKRIA QSDAIHPLIP
101 SDTPLAYDLI QSMILIOWQA HILPPLQSYR RPTQVDLYRF AGNIELFLQA
151 LENANEKNTW WLRRFQWAIM LMTLVSSVLM LFWHQIWVIR PLQALREGAE
201 RIGRRCFDIP VPEGGTPEFK QVGRCFNQMG GRLKILYDDL EGQVAEQTRS
251 LEKQONQNTL LYQTTRDLHQ SYIPQAAEH FLNRILPAVG ADSGRVCLDG
301 GSDVYVSIHH ADCGTAASDL GKYHEEIFPI EYQNETLGRLL SFPNGISL
351 DEDDRILLQT LGRQLGVSLA GAKQEEKRL LAVLQERNLI AQGLHDSIAQ
401 ALTFNLQVQ MLETAFENK REEAENIGF IKTGVQECYE DVRELLNFR
451 TKISNKEFPE AVADLFSRFT QQTGTTVETA WENGTHLPTQ DEQLQMIFIL
501 QESLSNIRKH AHATHIKFRL LKQDGSFTMT IQDNGQGFDT ENIGEPGSGH
551 VGLHIMQERA KRIHAVLEIR SQAQQGTTVS LTVASEESLK *

m561/a561 96.9% identity in 590 aa overlap

10 20 30 40 50 60
m561.pep MILPARFSDGISLSRLKLLTGLWVGLAALS SVVLTLLLSL RLENAASVIEEAGNLRMQAY
a561 MILPARFSDGISLSRLKLLTGLWVGLAALS SVVLTLLLSL RLENAASVIEEAGNLRMQAY
10 20 30 40 50 60

70 80 90 100 110 120
m561.pep RLAYMAGEGSPRAQIDNQVAEFEKSLKRIAQSDAIHPLIPSDTPLAYDLIQSMILIOWQA
a561 RLAYMAGEGSPRAQIDNQVAEFEKSLKRIAQSDAIHPLIPSDTPLAYDLIQSMILIOWQA
70 80 90 100 110 120

130 140 150 160 170 180
m561.pep HILPPLQSYRRPTQVDLYRFAGNIELFLQALENANEKNTWWLRRFQWAIMLMTLVSSVLM
a561 HILPPLQSYRRPTQVDLYRFAGNIELFLQALENANEKNTWWLRRFQWAIMLMTLVSSVLM
130 140 150 160 170 180

190 200 210 220 230 240
m561.pep LFWHQIWVIRPLQALREGAERIGRRCFDIPVPEGGTPEFKQVGRCFNQMG GRLKILYDDL
a561 LFWHQIWVIRPLQALREGAERIGRRCFDIPVPEGGTPEFKQVGRCFNQMG GRLKILYDDL
190 200 210 220 230 240

250 260 270 280 290 300
m561.pep EGQVAEQTRSLEKQONQNTLLYQTTRDLHQSYIPQAAEHFLNRILPAVGADSGRVCLDG
a561 EGQVAEQTRSLEKQONQNTLLYQTTRDLHQSYIPQAAEHFLNRILPAVGADSGRVCLDG
250 260 270 280 290 300

310 320 330 340 350 360
m561.pep GSDVYVSIHHADCGTAASDLGKYHEEIFPIEYQNETLGRLLSFPNGISLDEDDRILLQT
a561 GSDVYVSIHHADCGTAASDLGKYHEEIFPIEYQNETLGRLLSFPNGISLDEDDRILLQT
310 320 330 340 350 360

370 380 390 400 410 420
m561.pep LGRQLGVSLAGAKQEEKRL LAVLQERNLIAQGLHDSIAQALTFLNLQVQMLETAFENK
a561 LGRQLGVSLAGAKQEEKRL LAVLQERNLIAQGLHDSIAQALTFLNLQVQMLETAFENK

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	370	380	390	400	410	420
m561.pep	430	440	450	460	470	480
a561	REEEAENISFIKTGVQECYEDVRELLLNFR	TKISNKEFPEAVADLFARFTQQTGITVETA				
	430	440	450	460	470	480
m561.pep	490	500	510	520	530	540
a561	WENGSLFPPQEAQLQMIFILQESLSNIRKHARATHVKFTLSEHGGRFTMTIQDNGQGFD					
	490	500	510	520	530	540
m561.pep	550	560	570	580	590	
a561	EKIGIPTGSHVGLHIMQERAKRIHAVLEIRSQAQGGTTVSLTVASEESLKK					
	550	560	570	580	590	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1659>:

g562.seq..

```

1   atggcaagcc cgtcgagtct gcctttcaat tcgggcaaga ccaaaccgac
51  ggcttttgcc gcgccggttt tggtcggaat catgttttcc acgccgctgc
101 gggcgcgccg caggtctttg tggcgcacgt cggtaacggt ttggtcgttg
151 gtcagtgcgt ggatggtggt cattgcgcct ttgacgatgc cgacgctttc
201 gctcaacact ttggcaaccg gcgagaggca gttggtggtg caggaagcgt
251 tggaaacgac ggtcatgtcg gcggtcagga cgctgtcgtt cagccgctac
301 acgacggttg catcgacatc gtcgccgccc ggtgcggaat tgaggacttt
351 tttcgcgccg ctttcgaggt ggattttggc tttttctttg ctggtgaacg
401 cgccggtgca ttccatgacc aaatcgacac cgagttcttt ccacggcagt
451 tcggcagggg tgcgggtcga gaagaagggg attttgcgcg cgttgacgat
501 gaggttgccg ccgtcgtggg atacgtcggc ttcaaagcgt ccgtgtacgg
551 tgtcgaattt ggtcagatgg gcgttggttt caaggctgcc gctggcggtg
601 acggcgacga tttggagttg gtcttga

```

This corresponds to the amino acid sequence <SEQ ID 1660; ORF 562.ng>:

g562.pep

```

1   MASPSSLPFN SGTKPTAFA APVLVGIMFS TPLRARRRSL WRTSVTVWSL
51  VSAWMVVIAP LTMPTLSLNT LATGERQLVV QEALETTVMS AVRTLSFTFY
101 TTVASTSSPP GAEMRTFFAP LSRWILAFSL LVNAPVHSMT KSTPSSFHGS
151 SAGLRVEKKG ILSPLTMLRP PSWDTASAKR PCTVSNLVRW ALVSRPLPAL
201 TATIWSWS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1661>:

m562.seq

```

1   ATGGCAAGCC CGTCGAGCCT GCCTTTCAAT TCGGGCAGTA CCAAACCGAC
51  GGCTTTTGCC GCGCCGTTT TGGTCGGAAT CATGTTTCC ACGCCGCTGC
101 GGGCGCGCGC CAGGTCTTTG TGGCGCACGT CGGTAACGGT TTGGTCGTTG
151 GTCAGCGCGT GGATGGTGGT CATCGCGCCT TTGACGATGC CGACGCTTTC
201 GCTCAACACT TTGGCAACCG GCGAGAGGCA GTTGGTGGTG CAGGAAGCGT
251 TGGAAACGAC GGTGATGTCG GCGGTCAGGA CGCTGTCGTT CACGCCGTAC
301 ACGACGGTTG CATCGACATC GTCGCCGCC GGTGCGGAAA TGAGGACTTT
351 TTTCGCGCCG CTTTCGAGGT GGATTTTGGC TTTTCTTTG CTGGTGAACG
401 CGCCGGTGCA TTCCATGACC AAATCGACAC CGAGTTCTTT CCACGGCAGT
451 TCGGCAGGGT TCGGGGTCGA GAAGAAGGGG ATTTTGTGCG CGTTGACGAT
501 GAGGTTGCCG CCGTCGTGGG ATACGTCGGC TTCAAAGCGT CCGTGACCGG
551 TGTCGAATTT GGTGAGATGG GCGTTGGTTT CAAGGCTGCC GCTGGCGTTG
601 ACGGCGACGA GTTGGAGTTG GTCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1662; ORF 562>:

m562.pep

```

1   MASPSSLPFN SGTKPTAFA APVLVGIMFS TPLRARRRSL WRTSVTVWSL
51  VSAWMVVIAP LTMPTLSLNT LATGERQLVV QEALETTVMS AVRTLSFTFY

```

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101 TTVASTSSPP GAEMRTFFAP LSRWILAFSL LVNAPVHSMT KSTPSSFHGS
 151 SAGLRVEKKG ILSPLTMLRP PSWDTASAKR PCTVSNLVRW ALVSRPLPLAL
 201 TATSWSWS*

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m562/g562 99.0% identity in 208 aa overlap

	10	20	30	40	50	60
m562.pep	MASPSSLPFNSGSTKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAMVVIAP					
g562	MASPSSLPFNSGKTKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAMVVIAP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m562.pep	LTMPTLSLNTLATGERQLVVQEALETTVMSAVRTLSFTPYTTVASTSSPPGAEMRTFFAP					
g562	LTMPTLSLNTLATGERQLVVQEALETTVMSAVRTLSFTPYTTVASTSSPPGAEMRTFFAP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m562.pep	LSRWILAFSLLVNAPVHSMTKSTPSSFHGSAGLRVEKKGILSPLTMLRPPSWDTSASKR					
g562	LSRWILAFSLLVNAPVHSMTKSTPSSFHGSAGLRVEKKGILSPLTMLRPPSWDTSASKR					
	130	140	150	160	170	180
	190	200	209			
m562.pep	PCTVSNLVRWALVSRPLALTATSWSWSX					
g562	PCTVSNLVRWALVSRPLALTATIWSWSX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1663>:

a562.seq

1	ATGGCAAGCC	CGTCGAGTTT	GTCTTTCAAT	TCGGGCAGTA	CCAAACCGAC
51	GGCTTTTGCC	GCGCCAGTTT	TGGTCGGAAT	CATGTTTTCC	ACGCCGCTGC
101	GGGCGCGGCG	CAGGTCTTTG	TGGCGCACGT	CGGTAACGGT	TTGGTCGTTG
151	GTCAGCGCGT	GGATGGTGGT	CATCGCGCCT	TTGACGATGC	CGACGCTTTC
201	GCTCAACACT	TTGGCAACCG	GCGAGAGGCA	GTTGGTGGTG	CAGGAAGCGT
251	TGGAAACGAC	GGTCATGTCG	GCGGTCAGGA	TGCTGTGCTT	CACGCCGTAC
301	ACGACGGTTG	CATCGACATC	GTCGCCGCC	GGTGCGGAAA	TGAGGACTTT
351	TTTCGCGCCG	CTTTCCAGAT	GAACCTTGGC	TTTTTCTTTG	CTGGTGAACG
401	CGCCGGTGCA	TTCCATGACC	AAATCGACAC	CGAGTTCTTT	CCACGGCAGT
451	TCGGCAGGGT	TGCGGGTCNA	GAAGAANGGG	ATTTTGTCGC	CGTTGACGAT
501	GAGGTTGCCG	CCGTCGTGGG	ATACGTCGGC	TTCAAAGCGT	CCGTGCACGG
551	TGTCGAATTT	GGTGAGGTGG	GCGTTGGTTT	CAAGGCTGCC	GCTGGCGTTG
601	ACGGCGACGA	TTTGGAGTTG	GTCTTGA		

This corresponds to the amino acid sequence <SEQ ID 1664; ORF 562.a>:

a562.pep

1	MASPSSLSFN	SGSTKPTAFA	APVLVGIMFS	TPLRARRRSL	WRTSVTVWSL
51	VSAWMVVIAP	LTMPTLSLNT	LATGERQLVV	QEALETTVMS	AVRMLSFTPY
101	TTVASTSSPP	GAEMRTFFAP	LSR*TLAFSL	LVNAPVHSMT	KSTPSSFHGS
151	SAGLRVXXKG	ILSPLTMLRP	PSWDTASAKR	PCTVSNLVRW	ALVSRPLPLAL
201	TATIWSWS*				

m562/a562 96.6% identity in 208 aa overlap

	10	20	30	40	50	60
m562.pep	MASPSSLPFNSGSTKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAMVVIAP					
a562	MASPSSLSFN SGSTKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAMVVIAP					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m562.pep	LTMPTLSLNTLATGERQLVVQEALETTVMSAVRTLSTPYTTVASTSSPPGAEMRTFFAP					
a562	LTMPTLSLNTLATGERQLVVQEALETTVMSAVRMLSTPYTTVASTSSPPGAEMRTFFAP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m562.pep	LSRWILAFSLLVNAPVHSMKSTPSSFHGGSSAGLRVEKKGILSPLTMRLEPPSWDTSASKR					
a562	LSRXTLAFSLLVNAPVHSMKSTPSSFHGGSSAGLRVXXKGILSPLTMRLEPPSWDTSASKR					
	130	140	150	160	170	180
	190	200	209			
m562.pep	PCTVSNLVRWALVSRPLALTATSWWSX					
a562	PCTVSNLVRWALVSRPLALTATIWSWSX					
	190	200				

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1665>:

g563.seq

1	ATGAACAAAA	CCCTCTATCG	TGTGATTTTC	AACCGCAAAC	GCGGTGCTGT
51	GGTAGCTGTT	GCCGAAACCA	CCAAGCGCGA	AGGTAAAAGC	TGTGCCGATA
101	GTGGTTCGGG	CAGCGTTTAT	GTGAAATCCG	TTCTTTTCAT	TCCTACTCAT
151	TCCAAAGCCT	TTTGTTTTTC	TGCATTAGGC	TTTTCTTTAT	GTTTGGCTTT
201	GGGTACGGTC	AATATTGCTT	TTGCTGACGG	CATTATTACT	GATAAAGCTG
251	CTCCTAAAAC	CCAACAAGCC	ACGATTCTGC	AAACAGGTAA	CGGCATACCG
301	CAAGTCAATA	TTCAAACCCc	tACTTCGGCa	ggGGTTTCTG	TTAATCAATA
351	TGCCCAGTTT	GATGTGGGTA	ATcgCGGGC	GATTTTAAAC	AACAGTCGCA
401	GCAACACCCA	AACACAGCTA	GGCGGTTGGA	TTCAAGGCAA	TCCTTGCTTG
451	ACAAGGGGCG	AAGCACGTGT	GGTTGTAAAC	CAAATCAACA	GCAGCCATCC
501	TTCACAACCTG	AATGGCTATA	TTGAAGTGGG	TGGACGACGT	GCAGAAGTCG
551	TTATTGCCAA	TCCGGCAGGG	ATTGCAGTCA	ATGGTGGTGG	TTTTATCAAT
601	GCTTCCCGTG	CCACTTTGAC	GACAGGCCAA	CCGCAATATC	AAGCAGGAGA
651	CTTTAGCGGC	TTTAAGATAA	GGCAAGGCAA	TGCTGTAATC	GCCGGACACG
701	GTTCGGATGC	CCGTGATACC	GATTTACAC	GTATTCTTTT	GTATGCCAAC
751	AAAATCACCT	TGATCAGTAC	GGCCGAACAA	GCAGGCATTG	GTAATCAAGG
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6101 cggetTCaga TTTCGCTTCC TCTTTTTCAT ATCCTATAAA CATGTGA

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This corresponds to the amino acid sequence <SEQ ID 1666; ORF 563.ng>:

g563.pep..

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The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1667>:

m563.seq..

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6101 ACATTCAAAT CACCGACGAA GCCGCACAAA TCCGGCTGAC AGGCAAAACA
 6151 GCGGCACAAA CCAAAGCCGA TATTGATACA AACGTAACCA CAGACACCGC
 6201 CGAATGACAT TCGGGCAGCT TGAAGAACAC CTTCAACAAA GAAGCGGTGC
 6251 AAAGTGAACT GGATTTACAA AGAACCGTCA GCCAAGATTT TAGTAAAAAT
 6301 GTTCAACAAG CCAATACCGA GATTAACCAA CATTTAGACA AACTCAAAGC
 6351 AGACAAAGAA GCAGCCGAAA CAGCAGCAGC CGAGGCATTA GCCAATGGCG
 6401 ATATGGAAC TGCCAAACGC AAAGCCCATG AAGCTCAAGA TGCGGCAGCA
 6451 AAAGCAGATA ATTGGCAACA AGGCAAAGTC ATTCTCAACA TGTTAGCCTC
 6501 AGGTTTAGCT GCGCCGACCC AAAGCGGAGC GGGCATCGCT GCGGCTACCG
 6551 CATCGCCAGC CGTATCGTAT GCGATTGGAC AGCACTTTAA AGATTTAGCC
 6601 GGTCAAACG CGAATGGTAA ACTAACCGCC AGTCAAGAAA CCGCACACGT
 6651 TCTTGCCAC GCGGTATTAG GAGCAGCGGT TGCCGCAGTA GGAGACAACA
 6701 ATGCTCTAGC AGGAGCATTG AGTGCGGGCG GGTGGAAGC GGCTGCGCCT
 6751 TACATCAGCA AATGGTTATA CGGCAAAGAA AAAGGAAGCG ACTTAACGGC
 6801 GGAAGAGAAA GAGACTGTAA CAGCGATTAC AAATGTATTG GGTACGGCTA
 6851 CGGGTGCGGC AGTCGGCAAC AGCGCAACAG ATGCAGCGCA AGGCAGCCTG
 6901 AATGCGCAAA GTGCGGTGGA GAATAATGAT ACTGTAGAGC AAGTGAAAT
 6951 TGCTCTTAGG CACCCTAGAA TTGCTATTGC AATTGGATCT GTACATAAAG
 7001 ATCTTGCTC TACATTAGAG CCTAATATTT CAACAATTGC TTCAACTTTT
 7051 CAATTAAATT TATTTCTTAA TAGTGAAATTT GGTGGTGAAG GTGGAGTTGG
 7101 CAATGCATTC AGGCACGTTT TATGGCAAGC AACCATCACA CGAGAATTTG
 7151 GCAAAGATAT TGCTGTTAAA GTAGGAAATA GTCATGAAAG TGGGGAAAAA
 7201 ATTAATTATT CTATAAGACG TAATCTTTCA TTAGATAAAG CAGATGAAAT
 7251 GATTGATCAA CTAAATAACG AAATAGGAAG AGAAATAGCA TTAAATACCA
 7301 ATAGGTTAAA CACAAAAGAG TTAGTTGGAT TAATCTGGA AACTTATAAA
 7351 AATAATGGTT TTTATCAAGC AGAAAGAAAC AGTAATGGAA ATTATGATGT
 7401 TGTAAGAAAA AGATTATCTG AAAAAGATTA CCAGAAATCA AGCAATATAT
 7451 TGATTCACTT AGATAATACT GGTGCCCGAT TTAAATTC A GCAGAGGAGA
 7501 AAACAAATCA GAGCACAAAT TTCAGCCAGA CAATGGAGAA GATAA

This corresponds to the amino acid sequence <SEQ ID 1668; ORF 563>:

m563.pep..

1 MNKTLRYVIF NRKRGAVVAV AETTKREGKS CADSDSGSAH VKSVFPFGTTH
 51 APVCRSNIFS FSLLGFSLCL AVGTANIAFA DGIIADKAAP KTQQATILQT
 101 GNGIPQVNIQ TPTSAGVSVN QYAQFDVGNR GAILNNSRSN TQTQLGGWIQ
 151 GNPWLARGEA RVVQNQINSS HSSQMNGYIE VGGRRAEVVI ANPAGIAVNG
 201 GGFINASRAT LTTGQFPQYQA GDLSGFKIRQ GNVVIAGHGL DARDTDFTRI
 251 LSYHISKIDAP VWGQDVRVVA GQNDVVATGN AHSPILNNA ANTSNNTANN
 301 GTHIPLFAID TGKLGMYAN KITLISTAEQ AGIRNQQLF ASSGNVAIDA
 351 NGRLVNSGTM AAANAKDTDN TAEHKVNIRS QGVENSGTAV SQQGTQIHSQ
 401 SIQNTGTLLS SGEILIHNSG SLKNETSGTI EAARLAIDTD TLNNQKLSQ
 451 TGSQKLHIDA QGKMDNRGRM GLQDTAPTAS NGSSNQTGNS YNASFHSST
 501 TPTTATGTGT ATVSISNITA PTFADGTIRT HGALDNSGSI IANGQTDVSA
 551 QQGLNNAGQI DIHQLNAKGS AFDNHNGTII SDAVHIQAGS LNNQNGNITT
 601 RQQLIEITDQ LDNAHGKLLS AEIADLAVSG SLNNQNGEIA TNQQLIIHDG
 651 QQSTAVIDNT NGTIQSGRDV AIQAKSLSNN GTLAADNKLD IALQDDFYVE
 701 RNIVAGNELS LSTRGSLKNS HTLQAGKRIR IKANNLDNAA QGNIQSGGTT
 751 DIGTQHNLTN RGLIDGQOTK IQAGQMNNIG TGRIYGDNIA IAATRLDNQD
 801 ENGTGAAIAA RENLNLGIGQ LNNRENSLIY SGNDMAVGGA LDTNGQATGK
 851 AQRHINAGAT IEAAGKMRIG VEKLHNTNEH LKTQLVETGR EHIVDYEAFG
 901 RHELLREGTQ HELGWSVYND ESDHLRTPDG AAHENWHKYD YEKVTQKTQV
 951 TOTAPAKIIS GNDLTIDGKE VFNTDSQIIA GGNLIVQTEK DGLHNEQTFG
 1001 EKKVFSENGK LHSYWREKHK GRDSTGHSEQ NYTLPEBITR NISLGSFAYE
 1051 SHRKALSHHA PSQGTLPQS NGISLPYTSN SFTPLPSSSL YIINPVNKG Y
 1101 LVETDPRFAN YRQWLGS DYM LDSLKLD PNN LHKRLGDGY Y EQRLINEQIA
 1151 ELTGHRRLDG YQNDEEQFKA LMDNGATAAR SMNLSVGIAL SAEQVAQLTS
 1201 DIVWLVOKEV KLPDGGTQTV LVPQVYVRVK NGDIDGKGAL LSGSNTQINV
 1251 SGSLKNSGTI AGRNALIINT DTLDNIGGRI HAQKSAVTAT QDINNIGGML
 1301 SAEQTLALLNA GNNINSQSTT ASSQNTQSS TYLDRMAGIY ITGKEKGVLA
 1351 AQAGKDINII AGQISNQSEQ GQTRLQAGRD INLDTVQTSK HQATHFDADN
 1401 HVIRGSTNEV GSSIQTKGDV TLLSGNNLNA KAAEVSSANG TLAVSAKNDI
 1451 NISAGINTTH VDDASKHTGR SGGGNKLVIT DKAQSHHETA QSSTFEGKQV
 1501 VLQAGNDANI LGSNVIDSNG TQIQAGNHVR IGTQTQSQS ETYHQTQKSG

855

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1551 LMSAGIGFTI GSKTNTQENQ SQSNEHTGST VGSLKGDTTI VAGKHYEQIG
1601 STVSSPEGNN TIYAQSIDIQ AAHNKLNST TQTYEQKGLT VAFSSPVTDL
1651 AQQAIAVAQS SKQVGQSKND RVNAMAANA GWQAYQTGKS AQNLANGTTN
1701 AKQVSISITY GEQQNRQTTQ VQANQAQASQ IQAGGKTTLI ATGAAEQSNI
1751 NIAGSDVAGK AGTILIADND ITLQSAEQSN TERGQNKSGS WNAGAAVSFG
1801 QGGWSLGVTA GGNVKGKGYGN GDSITHRSH IGDKGSQTLI QSGGDTTIKG
1851 AQVRGKGVQV NAKNLSIQSV QDRETYQSKQ QNASAQVTVG YGFSAGGDYS
1901 QSKIRADHVS VTEQSGIYAG EDGYQIKVGN HTDLKGGIIT STQSAEDKGG
1951 NRFQTATLTH SDIKNHSQYK GESFGLGASA SISGKTLGQG AQNKPNKHL
2001 TSVADKNSAS SSVGYGSDSD SQSSITKSGI NTRNIQITDE AAQIRLTGKT
2051 AAQTKADIDT NVTTDTAERH SGSLKNTFNK EAVQSELDLQ RTVSQDFSKN
2101 VQQANTEINQ HLDKLGADKE AAETAAAEAL ANGDMETAKR KAHEAQDAAA
2151 KADNWQOGKV ILNMLASGLA APTQSGAGIA AATASPAVS Y AIGQHFKDLA
2201 GQNANGKLTA SQETAHVLAH AVLGA AVAAV GDMNALAGAL SAGGSEAAAP
2251 YISKWLYGKE KGSDLTAEK ETVTATITNVL GTATGAAVGN SATDAAQGS
2301 NAQSAVENND TVEQVKFALR HPRIAIAGS VHDPGSTLE PNISTIATF
2351 QLNLFNPSEF GEGGVGNF RHVLWQATIT REFGKDIQV VGNSHESGEK
2401 INYSIRRNLS LDKADEMIDQ LNNEIGREIA LNTNRLNKE LVGLILETYK
2451 NNGFYQAERN SNGNYDVVRK RLSEKDYQNT SNILIHLDNT GAGFKIQRR
2501 KQIRAQISAR QWRR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 563 shows 79.1% identity over a 2316 aa overlap with a predicted ORF (ORF 563.ng) from *N. gonorrhoeae*:

m563/g563

```
          10      20      30      40      50
g563.pep  MNKTLYRVIFNRKRGAVVAVAETTKREGKSCADSGSGSVYVKSVSFIPTH-----SKAFC
          |||||
m563.pep  MNKTLYRVIFNRKRGAVVAVAETTKREGKSCADSDSGSAHVKSVPFGTTHAPVCRSNIFS
          10      20      30      40      50      60

          60      70      80      90     100     110
g563.pep  FSALGFSLCLALGTVNIAFADGIITDKAAPKTQQATILQTGNGIPIQVNIQTPTSAGVSVN
          |||||
m563.pep  FSLLGFSCLAVGTANIAFADGI IADKAAPKTQQATILQTGNGIPIQVNIQTPTSAGVSVN
          70      80      90     100     110     120

          120     130     140     150     160     170
g563.pep  QYAQFDVGNRGAILNNSRSNTQTQLGGWIQGNPWLTRGEARVVVNQINSSHPSQLNGYIE
          |||||
m563.pep  QYAQFDVGNRGAILNNSRSNTQTQLGGWIQGNPWLARGEARVVVNQINSSHSQMNGYIE
          130     140     150     160     170     180

          180     190     200     210     220     230
g563.pep  VGGRRAEVVIANPAGIAVNGGGFINASRATLTGQPQYQAGDFSGFKIRQGNVIAIGHGL
          |||||
m563.pep  VGGRRAEVVIANPAGIAVNGGGFINASRATLTGQPQYQAGDLSGFKIRQGNVIAIGHGL
          190     200     210     220     230     240

          240
g563.pep  DARDTDFTRIL-----
          |||||
m563.pep  DARDTDFTRILSYHSKIDAPVWGQDVRVVAGQNDVVATGNAHSPILNNAANTSNTANN
          250     260     270     280     290     300

          250     260     270     280     290
g563.pep  -----LYANKITLISTAEQAGIRNQGLFASSGNVAIDANGRLVNSGTM
          :|||
m563.pep  GTHIPLFAIDTGKLGMYANKITLISTAEQAGIRNQGLFASSGNVAIDANGRLVNSGTM
          310     320     330     340     350     360
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	300	310	320	330	340
g563.pep	AAANVQDMNNTAEHKVNIRSQAFENSGTAVSQQGTQIHSQSIQNTGKLLSAGT-----				
m563.pep	AAANAKDTDNTAEHKVNIRSQGVENSGTAVSQQGTQIHSQSIQNTGTLLSSGEILIHNSG				
	370	380	390	400	410
	420				
g563.pep	-----				
m563.pep	SLKNETSGTIEAARLAIDTDTLNNQKLSQTGSQKLHIDAQGMMDNRGRMGLQDTAPTAS				
	430	440	450	460	470
	480				
g563.pep	-----				
m563.pep	NGSSNQTGNSYNASFHSSTTTPTTATGTGTATVSISNITAPTADFADGTIRTHGALDNSGSI				
	490	500	510	520	530
	540				
g563.pep	-----				
m563.pep	IANGQTDVSAQQGLNNAQIDIHQLNAKGSFADNHNGTIISDAVHIQAGSLNNQNGNITT				
	550	560	570	580	590
	600				
g563.pep	-----EDLAVSGSLNNQNGEIATNQQLIIHDGQQSTVVIDNT				
m563.pep	ROQLEIETDQLDNAHGKLLSAEIALAVSGSLNNQNGEIATNQQLIIHDGQQSTAVIDNT				
	610	620	630	640	650
	660				
g563.pep	390	400	410	420	430
m563.pep	440				
g563.pep	NGTIQSGRDVAIQAKSLSNNGTLAADNKLDIALQDDFYVERKIVAGNELSLSTRGSLKNS				
m563.pep	NGTIQSGRDVAIQAKSLSNNGTLAADNKLDIALQDDFYVERNIVAGNELSLSTRGSLKNS				
	670	680	690	700	710
	720				
g563.pep	450	460	470	480	490
m563.pep	500				
g563.pep	HTLQAGKRIRIKANNLDNAVQGNIQSGGTTDIGTQHNLNTRGLIDGQQTQIQAGQMNNG				
m563.pep	HTLQAGKRIRIKANNLDNAAQGNIQSGGTTDIGTQHNLNTRGLIDGQQTQIQAGQMNNG				
	730	740	750	760	770
	780				
g563.pep	510	520	530	540	550
m563.pep	560				
g563.pep	TGRIYGDNIAIAATRLDNQDENGTTGAAIAARENLNGLIEQLNNRENSLIYSGNDMAVGGA				
m563.pep	TGRIYGDNIAIAATRLDNQDENGTTGAAIAARENLNGLIGQLNNRENSLIYSGNDMAVGGA				
	790	800	810	820	830
	840				
g563.pep	570	580	590	600	610
m563.pep	620				
g563.pep	LDTNDQATGKAQRIHNAGATIEAAGKMRLGVEKLHNTNEHLKTQLVETGRERIVDYEAFG				
m563.pep	LDTNGQATGKAQRIHNAGATIEAAGKMRLGVEKLHNTNEHLKTQLVETGREHIVDYEAFG				
	850	860	870	880	890
	900				
g563.pep	630	640	650	660	670
m563.pep	680				
g563.pep	RHELLREGTQHELGWVFNNSDHLRTPDGVAHENWHKYDYKVTQETQVTTGTAPAKIIA				
m563.pep	RHELLREGTQHELGWSVYNDES DHLRTPDGAHENWHKYDYKVTQKTQVTTGTAPAKIIS				
	910	920	930	940	950
	960				
	690	700	710	720	730
	740				

BNSDOCID: <WO__9957280A2_1_>

	1950	1960	1970	1980	1990	2000
g563 . pep	TASQETAHVLAHAVLGA AVAAAXGNNAPAGALGAGGSEAAAPIIGKWLYGKGDGGSINAE					
m563 . pep	TASQETAHVLAHAVLGA AVAAVGDNNALAGALSAGGSEAAAPYISKWLYGKEKGSIDLTAE					
	2210	2220	2230	2240	2250	2260

	2010	2020	2030	2040	2049
g563 . pep	EKETVSAITRMLGTAAGAAEGNSSADAVWGCFQTASDFASSFSYPINMX				
m563 . pep	EKETVTAITNVLTATGA AVGNSATDAAQGSLSNAQSAVENNDTVEQVKFALRHPRIATAI				
	2270	2280	2290	2300	2320

m563 . pep	GSVHKDPGSTLEPNISTIASTFQLNLFNSEFGGEGGVGNAFRHLVWQATITREFGKDIA					
	2330	2340	2350	2360	2370	2380

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1669>:

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m564 . seq
1   ATGAACCGCA CCCTGTACAA AGTTGTATTT AACAAACATC GAAACTGCAT
51  GATAGCCGTT GCTGAAAATG CCAAACGCGA GGGCAAAAAC ACAGCCGACA
101 CCCAAGCTGT AGGTATTTTG CCAAATGATA TTGCGGGCTT TGCGGGTTTT
151 ATCCATTCTA TCTCTGTTAT CTCATTCTCC CTTTCATTAC TGCTCGGTTT
201 TGCCCTTATC CTGACTTCTT CTTCTGCTAC TGCCCAAGGT ATCGTTGCCG
251 ACAAATCCGC ACCTGCACAG CAACAGCCTA CCATCCTGCA AACAGGTAAC
301 GGCATACCGC AAGTCAATAT TCAAACCCCT ACTTCGGCAG GGGTTTCTGT
351 TAATCAATAC GCCCAGTTTG ATGTGGGTAA TCGCGGGGCG ATTTTAAACA
401 ACAGTCGCAG CAACACCCAA ACACAGCTAG GCGGTTGGAT TCAAGGCAAT
451 CCTTGGTTGG CAAGGGGCGA AGCACGTGTG GTTGTAACC AAATCAACAG
501 CAGCCATTCT TCACAACCTGA ATGGCTATAT TGAAGTGGGC GGACGACGTG
551 CAGAAGTCGT TATTGCCAAT CCGGCAGGGA TTGCAGTCAA TGGTGGTGGT
601 TTTATCAATG CTTCCCGTGC CACTTTGACG ACAGCCCAAC CGCAATATCA
651 AGCAGGAGAC CTTAGCGGCT TTAAGATAAG GCAAGGCAAT GTTGTAATCG
701 CCGGACACGG TTTGGATGCA CGTGATACCG ATTACACACG TATTCTCAGT
751 TATCATTCCA AAATTGATGC ACCCGTATGG GGACAAGATG TTCGTGTCGT
801 CGCGGGACAA AACGATGTGG CCGCAACAGG TGATGCACAT TCGCCTATTC
851 TCAATAATGC TGCTGCCAAT ACGTCAAACA ATACAGCCAA CAACGGCACA
901 CATATCCCTT TATTTGCGAT TGATACAGGC AAATTAGGAG GTATGTATGC
951 CAACAAAATC ACCTTGATCA GTACGGTCGA GCAAGCAGGC ATTCGTAATC
1001 AAGGGCAATG GTTTGCCCTCA GCCGGCAATG TGGCAGTGAA TGCTGAGGCT
1051 AAATGGGTCA ACACGGGCAT GATTGCAGCG ACGGGAGAAA ATCATGCGGT
1101 TTCATTTCAT GCCCGCAATG TTCATAATAG CGGTACGGTT GCCTCACAGG
1151 ATGATGCCAA TATTCACAGC CAGACGCTGG ACAATTCAGG TACGGTCTTA
1201 TCCTCAGGTC GATTGACTGT TCGTAATTTA GGCCGTCTGA AAAACCAAAA
1251 CAACGGTACG ATCCAGGCTG CCCGCTTAGA TATGTCAACA GGTGGTTTGG
1301 ATAACACAGG TAATATTACT CAAACAGGTT CACAAGCATT GGATTTGGTA
1351 TCTGCCGGCA AATTCGATAA CAGTGGCAAG ATTGGTGTAA GTGACGTTCC
1401 ACAGACCGGT TTGAATCCCA ATCCATCAGT CATACCACAG ATTCCGAGTA
1451 CTGCAACAGG TTCAGGCAGC AGCACTGTCT CGGTATCTAA GCCTGGTTCA
1501 AACAATCCCG TTTCACCTAC AGCACCTGCA AAAAATACG CCGTAGGACG
1551 CATTCAAACA ACAGGAGCAT TTGACAATGC AGGATCAATT AATGCGGGTG
1601 GGCAAATTGA CATTGCCGCC CAAAACGGTT TGGGAAATTC GGGTAGTCTG
1651 AATGCGGGCTA AACTACGAGT ATCAGGCGAT TCATTTAACA ATACGGTAAA
1701 AGGCAAACTC CAGGCACACG ATCTGGCTGT TAACACTCAA ACTGCTAAAA
1751 ACAGCGGTCA CTTATTAACT CAAACCGGCA AGATTGATAA CCGTGAACGT
1801 CATAATGCCG GAGAAATTGC CGCCAACAAT CTGACACTCA TTCATTCGGG
1851 CCGCTTGAGC AATGATAAAA AAGGCAATAT TCGAGCTGCA CATTTACAGC
1901 TTGATACCGC CGGTTTACAT AATGCAGGTA ACATTCTTGC CGATAGTGGG
1951 ACCGTTACCA CCAAGAATAA TCTTCGCAAT ACAGGAAAAG TTTCTGTTGC
2001 ACGACTGAAT ACCGAAGGTC AGACTCTAGA TAATACGCGC GGACGTATAG
2051 AGGCTGAAAC GGTTAACATC CAAAGTCAGC AACTGACTAA CCAAAGCGGC
2101 CATATTACTG CTACCGAACA ACTGACTATC AATAGTCGAA ATGTAGACAA
2151 CCAAACGGGC AAATCCTAT CTGCAAAACA AGCACAATTA GCTGTTTCAG
2201 ACGGCCTATA CAACCAACAT GGTGAAATTG CCACCAACCG GCAGTTGTCT

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2251 ATTCACGATA AAAATCAAAA CACTTTGGCG TTAAACAATG CGGATGGCAC
2301 GATTCATCT GCCGGTAATG TATCGCTACA AGCCAAATCA CTCGCCAACA
2351 ATGGCACATT AACAGCCGGT AACAAACTGG ATATTGCTTT GACGGACGAT
2401 TTCGTCGTAG AGCGCGACCT CACTGCAGGC AAACAATTAA ATCTAAGCAT
2451 AAAAGGCCGT CTGAAAAATA CCCATACCCT ACAAGCAGGC CATACGCTCA
2501 AACTCAATGC CGGCAATATA GATAACCAAG TTACAGGCAA AATTATTGGT
2551 GGAGAACAAA CGGACATCAC ATCCGAACAG CATGTTGACA ACAGGGGCTT
2601 CTGGATGAAC AACATCATGC CCCACATCGG TGCAGGTCAA ACCCTGACCA
2651 ACACCGGGAC AGGCAAAATC TATGGCAACC ATATTGCCCT GGACGCGCAA
2701 ATACTGCTTA ACCGGGAAGA AACGACGGAA GGCAGTACCA AAGCGGGGGC
2751 AATAGCTGCA AGGAAACGTT TGGATATTGG AGCGAAAGAG ATTCATAACC
2801 AAGAAGGTGC CCTACTATCC AGCGAAGGTA TTTTGGCCGT AgGTAATCGA
2851 CTGGATGAAC AACATCATGC GGCAGGCATG GCCGATACCT TTGTTAATGG
2901 CAGTGCCGGT TTGGAAGTAC AAGGTGATGC ATTGATGTCC GTTCGGAATA
2951 TGCAGAATAT CAATAATCAC TTTAAACAG AGACATACTT AGCCAAAGCG
3001 GAAAAGCAAG TCCGCGACTA CACCGTACTG GGGCAAAATA CCTACTATCA
3051 GGCGGGAAAA GACGGTTTAT TCGACAATC GCAAGGACAA AAAGACCAA
3101 CTACTGCTAC GTTCCATTTA AAAAATGGTT CTCGTATTGA GGCCAAACCA
3151 TGGCATGTCC GAGACTACCA CATCGAGACT TATAAAGAAC GCATCATCGA
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3301 ACTGATGATT TAAACCAGAA AGAAATTACC AATCAAAGTA CAACAGGCAA
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3401 GATGGTACAG CGGTAGAAAA AGACAACGCC GTACTGAAAG AAACCATACT
3451 CCTTACCATG ATACCCAAT ATTTACCCAC GACTTCGACA CGCCTGTATC
3501 CGTCATCCAA CAGAATGCCG CCTCCCCTTC CTTTCAACCC GCCGCATCTG
3551 CAATCAAAT GATTGACGGA GTATCCACGG CAGCCGTCAG TGGTCAGCGC
3601 ATCCATACCG GTAATGTGGT CTCGTAAAT AACGCTACTG TTACTCTGCC
3651 TAACAGCAGC CTCTATACCA CCCATCCTGA CAATAAAGGC TGGTTGGTTG
3701 AAACCGATCC TCAATTTGCA GACTACCGCC GCTGGTTGGG CAGCGACTAC
3751 ATGTTGCAAC AACTGCAATT GGACACCAAT CATCTACACA AACGGCTTGG
3801 CGACGGCTAC TACGAACAAA AACTTGTTAA TGAACAAATC CATCAGTTAA
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3901 GCTCTGATGG ACAACGGCCT TACTGCTGCC AAAACATTCT GTCTCACCCC
3951 AGGTATCGCC TTGAGTGCAG AGCAAGTTGC CCGCTTAACT TCAGATATCG
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5301 CACTGACTAC GCCCATACCC AGGAACAAAA AGGCCTTACC GTCGCCCTCA
5351 ATGTCCCGGT TGTCACAGCT GCACAAAAT TCATACAAGC AGCCCAAAAT
5401 GTGGGCAAAA GTAAAAATAA ACGCGTTAAT GCCATGGCTG CAGCCAATGC
5451 TGCATGGCAG AGTTATCAAG CAACCAACA AATGCAACA TTTGCTCCAA
5501 GCAGCAGTGC GGGACAAGGT CAAAACAACA ATCAAAGCCC CAGTATCAGT


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5551 GTGTCCATTA CCTACGGCGA ACAGAAAAGT CGTAACGAGC AAAAAAGACA
5601 TTACACCGAA GCGGCAGCAA GTCAAATTAT CGGCAAAGGG CAAACCACAC
5651 TTGCGGCAAC AGGAAGTGGG GAGCAGTCCA ATATCAATAT TACAGGTTCC
5701 GATGTCATCG GCCATGCAGG TACTGCCCTC ATTGCCGACA ACCATATCAG
5751 ACTCCAATCT GCCAAACAGG ACGGCAGCGA GCAAAGCAAA AACAAAAGCA
5801 GTGGTTGGAA TGCAGGCGTA GCCGTCAAAA TAGGCAACGG CATCAGGTTT
5851 GGAATTACCG CCGGAGGAAA TATCGGTAAA GGTAAGAGC AAGGGGGAAG
5901 TACTACCCAC CGCCACACCC ATGTCGGCAG CACAACCGGC AAAACTACCA
5951 TCCGAAGCGG CGGGGATACC ACCCTCAAAG GTGTGCAGCT CATCGGCAAA
6001 GGCATACAGG CAGATACGCG CAACCTGCAT ATAGAAAGTG TTCAAGATAC
6051 TGAAACCTAT CAGAGCAAAC AGCAAAACGG CAATGTCCAA GTTACTGTCC
6101 GTTACGGATT CAGTGCAAGC GGCAGTTACC GCCAAAGCAA AGTCAAAGCA
6151 GACCATGCCT CCGTAACCGG GCAAAGCGGT ATTTATGCCG GAGAAGACGG
6201 CTATCAAATC AAAGTCAGAG ACAACACAGA CCTCAAGGGC GGTATCATCA
6251 CGTCTAGCCA AAGCGCAGAA GATAAGGGCA AAAACCTTTT TCAGACGGCC
6301 ACCCTTACTG CCAGCGACAT TCAAAACCAC AGCCGCTACG AAGGCAGAAG
6351 CTTCCGCATA GCGGCGAGTT TCGACCTGAA CGGCGGCTGG GACGGCACGG
6401 TTACCGACAA ACAAGGCAGG CCTACCGACA GGATAAGCCC GGCAGCCGGC
6451 TACGGCAGCG ACGGAGACAG CAAAAACAGC ACCACCCGCA GCGGCGTCAA
6501 CACCCACAAC ATACACATCA CCGACGAAGC GGGACAACCT GCCCGAACAG
6551 GCAGGACTGC AAAAGAAACC GAAGCGCGTA TCTACACCG CATCGACACC
6601 GAAACTGCGG ATCAACACTC AGGCCATCTG AAAAACAGCT TCGACAAAGA
6651 CGCGGTGCGC AAAGAGATCA ACCTGCAAAG GGAAGTAACG AAGGAGTTCC
6701 GCAGAAACGC CGCCCAAGCC GTAGCGGCCG TTGCCGACAA ACTCGGCAAT
6751 ACCCAAAGTT ACGAACGGTA TCAGGAAGCC CGAACCTGCT TGGAGGCCGA
6801 ACTGCAAAAC ACGGACAGCG AAGCCGAAAA AGCCGCCTTC CGCGCATCCC
6851 TCGGCCAAGT AAACGCCTAT CTTGCCGAAA ACCAAAGCCG CTACGACACC
6901 TGGAAAGAAG GCGGCATAGG CAGGAGCATA CTGCACGGGG CGGCAGGCGG
6951 ACTGACGACC GGCAGCCTCG GCGGCATACT GGCCGGCGGC GGCACCTCCC
7001 TTGCCGCACC GTATTTGGAC AAAGCGGCGG AAAACCTCGG TCCGGCGGGC
7051 AAAGCGGCGG TCAACGCACT GGGCGGTGCG GCCATCGGCT ATGCAACTGG
7101 TGGTAGTGGT GGTGCTGTGG TGGGTGCGAA TGATAGATTG AACATAGGC
7151 AGCTGCATCC GAAAGAAATG GCGTTGGCCG ACAAATATGC CGAAGCCCTC
7201 AAGCGCGAAG TTGAAAAACG CGAAGGCAGA AAAATCAGCA GCCAAGAAGC
7251 GGCAATGAGA ATCCGCAGGC AGATACTGCG TTGGGTGGAC AAAGGTTCCC
7301 AAGACGGCTA TACCGACCAA AGCGTCATAT CCCTTATCGG AATGAAAGGC
7351 GAAGACAAAG CCTTGGGTTA TACTTGGGAC TACCGCGACT ACGGCGCAAG
7401 AAATCCGCAA ACCTACAACG ATCCGAAGCT GTTTGAGGAA TACCGCCGAC
7451 AGGACAAACC CGAATACCGC AACCTGACCT GGCTGCACAG CGGGACGAAA
7501 GACACCAAAA TCAGGCAGGG AGAGCGGAAA AACGAAGAGT TTGCACTGAA
7551 CGTTGCCGAA GGAAGTACGA GCCTTGTCAG CCCCAATCCG AGGATAAAAG
7601 TCCCGATTCT TGCAGGCATC CGCAACCTGA AAAACATCAA GCCGACAGTT
7651 ACCGGCAGCG ATCCCTTATT GCGGGGTGCG GGAATATCC GTATCCCTGC
7701 AAACGGCAAT GTTGCGAAGG GGGACAGGAT TCCGATACG GCATTGGCTA
7751 GCAAGGGAAT CAAACATAAA GATCGTAAAG ATCAACTGGA GAAAAATAA

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This corresponds to the amino acid sequence <SEQ ID 1670; ORF 564>:

m564.pep

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1  MNRTLYKVVVF NKHRNCMIIV AENAKREGKN TADTQAVGIL PNDIAGFAGF
51  IHSISVISFS LSLLLGSALI LTSSSATAQG IVADKSAPAQ QQPTILQTGN
101 GIPQVNIQTP TSAGVSVNQY AQFDVGNRGA ILNNSRSNTQ TQLGGWIQGN
151 PWLARGEARV VVNQINSSHS SQLNGYIEVG GRRAEVVIAN PAGIAVNGGG
201 FINASRATLT TAQPQYQAGD LSGFKIRQGN VVIAGHGLDA RDTDYTRILS
251 YHSKIDAPVW QGDVRVVAGQ NDVAATGDAH SPILNNAAN TSNNTANNGT
301 HIPLFAIDTG KLGGMYANKI TLISTVEQAG IRNQGWQFAS AGNVAVNAEG
351 KLVNTGMIAA TGENHAVSLH ARNVHNSGTV ASQDDANIHS QTLDNSGTVL
401 SSGRLTVRNL GRLKNQNNGT IQAARLDMST GGLDNTGNIT QTGSQALDLV
451 SAGKFDNSGK IGVSDVPQTG LNPNPVSVIPQ IPSTATGSGS STVSVSKPGS
501 NNPVSPTAPA KNYAVGRIQT TGAFDNAGSI NAGGQIDIAA QNGLGNSGSL
551 NAAKLRVSGD SFNNTVKGKL QAHD LAVNTQ TAKNSGHLT QTGKIDNREL
601 HNAGEIAANN LTLIHSGRLS NDKKGNIRAA HLQLDTAGLH NAGNILADSG
651 TVTTKNNLRN TGKVSVARLN TEGQTLDNTR GRIEAEVNI QSQQLTNQSG
701 HITATEQLTI NSRNVDNQNG KLLSANQAQL AVSDGLYNQH GEIATNRQLS
751 IHDKNQNTLA LNNADGTIQS AGNVSLQAKS LANNGTLTAG NKLDIALTDD
801 FVVERDLTAG KQLNLSIKGR LKNTHTLQAG HTLKLNAGNI DNQVTGKIIG
851 GEQTDITSEQ HVDNRGLINS DGLTHIGAGQ TLTNTGTGKI YGNHIALDAQ

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901 ILLNREETTE GSTKAGAI AA RKRLDIGAKE IHNQEGALLS SEGIFAVGNR
951 LDEQHHAGM ADTFVNGSAG LEVQGDALMS VRNMQNINNH FKTETYLAKA
1001 EKQVRDYTEVL GQNTYYQAGK DGLFDNSQGG KDQTTATFHL KNGSRIEANQ
1051 WHVRDYHIET YKERIENRP AHITVGGDLT ASGQNLNKD SRIVVGGRII
1101 TDDLNQKEIT NQSTTGKGR T DAVGTQWDSV TKKGWYSGRK RQRRTERNHT
1151 PYHDTQLFTH DFDTPVSVIQ QNAASPSFQP AASAIKLIDG VSTA AVNGOR
1201 IHTGNVVS LN NATVTLPNSS LYTHPDNKG WLVDTPQFA DYRRWLGS DY
1251 MLQQLQLD TN HLHKRLGDGY YEQKLVNEQI HQLTGYRRLD GYRSDEEQFK
1301 ALMDNGLTAA KTFGLTPGIA LSAEQVARLT SDIVWMENQT VTLSDGSTQT
1351 VLVPKVYALA RKGDLNTSGG LISAEQVLLK LQNGNLTSNG TIAGRQAVLI
1401 QARNINSNGN IQADQIGLKA EKSINIDGGQ VQAGRLLTAQ AQNLNLNGTT
1451 QTSGNERNGN TAIDRMAGIN VVGSHTEQVD NRTSDGILSL HASNDINLNA
1501 ATVSNOVKDG TTQITAGNNL NLGTIRTEHR EAYGLDDEN HRHVRQSTEV
1551 GSSIRTONGA LLRAGNDLKI RQGELEAEEG KTVLAAGRDV TISEGRQITE
1601 LDTSVSGKSK GILSSTKTHD RYRFSHDEAV GSNIGGGKMI VAAGQDINVR
1651 GSNLISDKGI VLKAGHDIDI STAHNRYTGN EYHESKSKGV MGTGGGLGFTI
1701 GNRKTTDDTD RTNIVHTGSI IGS LNGDVT VAGNRYRQTG STVSSPEGRN
1751 VVTAKSIDVE FANNRYATDY AHTQEQKGLT VALNVFVQA AQNFIAQAQN
1801 VGKSKNKR VN AMAAANA AWQ SYQATQOMQO FAPSSSAGQG QNNNQSPSIS
1851 VSITYGEQKS RNEQKRHYTE AAASQIIGKG QTTLAATGSG EQSNINITGS
1901 DVIGHAGTAL IADNHIRLQS AKQDGSEQSK NKSSGWNAGV AVKINGIRF
1951 GITAGGNIGK GKEQGGSTTH RHTVHGSTTG KTTIRSGGDT TLKGVQLIGK
2001 GIQADTRNLH IESVQDTETY QSKQONGNVQ VTVGYGFSAS GSYRQSKVKA
2051 DHASVTGQSG IYAGEDGYQI KVRDNTDLKG GIITSSQSAE DKGKNLFQTA
2101 TLTASDIQNH SRYEGRSFGI GGSFDLNGGW DGTVTDKQGR PTDRISPAAG
2151 YGSDGDSKNS TTRSGVNTHN IHITDEAGQL ARTGRTAKET EARITYGIDT
2201 ETADQHSGLH KNSFDKDAVA KEINLQREVT KEFGRNAQA VAAVADKLGN
2251 TQSYERYQEA RTLLEAELQN TDSEA EKA AF RASLGQVNAY LAENQSR YDT
2301 WKEGGIGRSI LHGAAGGLTT GSLGGILAGG GTSLAAPYLD KAAENLG PAG
2351 KAAVNALGGA AIGYATGGSG GAVVGANVDW NNRQLHPKEM ALADKYAEAL
2401 KREVEKREGR KISSQEAAMR IRRQILRWVD KGSQDGYTDQ SVISLGMKG
2451 EDKALGYTWD YRDYGARNPQ TYNDPKLFEE YRRQDKPEYR NLTWLHSGTK
2501 DTKIROGERK NEEFALNVAE GLTSLVNP NP RIKVPILAGI RNLKNIKPTV
2551 TGSDPLLAGA GNIRIPANGN VAKGD RIPDT ALASKGIKHK DRKDQLEKK*

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Computer analysis of this amino acid sequence gave the following results:

Homology with fha

m564/fha

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ID FHAB BORPE STANDARD; PRT; 3591 AA.
AC P12255;
DT 01-OCT-1989 (REL. 12, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE FILAMENTOUS HEMAGGLUTININ. . . .

```

SCORES Init1: 190 Initn: 524 Opt: 594
 Smith-Waterman score: 866; 21.7% identity in 2427 aa overlap

```

          10      20      30      40      50      60
m564 .pep  MNRTLYKVVF NKHRCMIAVAENAKREGKNTADTQAVGILPNDIAGFAGFIHSISVISFS
          || :||::||: || : : ||: | || : : | : | : | : : ||: : :
fhab_borpe MNTNLYRLVFSHV RGM LVPVSEHCTV-G-NTFCGRTRG---QARSGARATSLSVAPNALA
          10      20      30      40      50

          70      80      90      100     110     119
m564 .pep  LSLLLG-SALILTSSSATAQGIVADKSAPAQQQPTILQTGNGIPQVNIQTPTSAGVSVNQ
          :||: :|| :||: ||: | | | :|| || :| ||| |:|: ||| | :
fhab_borpe WALMLACTGLPLVTH---AQGLV-----P-QGQTQVLQGGNKVPVVNIADPNSGGVSHNK
          60      70      80      90      100

          120     130     140     150     160     170     179
m564 .pep  YAQFDVGNRGAILNNSRSNTQTQLGGWIQGNPWLARGEARVVVNQINSSHSSQLNGYIEV
          : ||: ||| :||: ||: : : ||: | | | :| : : : : : | :| | :|
fhab_borpe FQQFNVANPGVVFNNGLTGDSVRIGGALTKNPNLTR-QASAILAEVTDTSPSRLAGTLEV
          110     120     130     140     150     160

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	180	190	200	210	220	230	239																																																					
m564 .pep	G	G	R	R	A	E	V	V	I	A	N	P	A	G	I	A	V	N	G	G	G	F	I	N	A	S	R	A	T	L	T	T	A	Q	P	Q	Y	Q	A	G	D	L	S	G	F	K	I	R	Q	G	N	V	V	I	A	G	H	G	L	D
fhab_borpe	Y	G	K	G	A	D	L	I	I	A	N	P	N	G	I	S	V	N	G	L	S	T	I	N	A	S	N	L	T	L	T	T	G	R	P	S	V	N	G	G	R	I	-	G	L	D	V	Q	Q	G	T	V	T	I	E	R	G	G	V	N
	170	180	190	200	210	220																																																						
	240	250	260	270	280	290																																																						
m564 .pep	A	R	D	T	D	Y	T	R	I	L	S	Y	H	S	K	I	D	A	P	V	---	W	G	Q	---	D	V	R	V	V	A	G	Q	N	D	V	A	A	T	G	D	A	H	S	P	I	L	N	N	A	A	A	N	T	S	N				
fhab_borpe	A	T	G	L	G	Y	F	D	V	V	A	R	L	V	K	L	Q	G	A	V	S	S	K	Q	G	K	P	L	A	D	I	A	V	V	A	G	A	N	R	Y	D	H	A	T	R	R	A	T	P	I	---	A	A	G	A	R	G			
	230	240	250	260	270	280																																																						
	300	310	320	330	340	350																																																						
m564 .pep	N	T	A	N	G	T	H	I	P	L	F	A	I	D	T	G	K	L	G	M	Y	A	N	K	I	T	L	I	S	T	V	E	Q	A	G	I	R	N	Q	G	W	F	A	S	A	G	N	V	A	V	N	A	E	G	K	L	V			
fhab_borpe	A	A	A	G	A	---	---	Y	A	I	D	G	T	A	A	G	A	M	Y	G	K	H	I	T	L	V	S	S	D	S	G	L	G	V	R	Q	L	G	S	-	L	S	S	P	S	A	I	T	V	S	S	Q	G	E	I	A				
	290	300	310	320	330																																																							
	360	370	380	390	400	410																																																						
m564 .pep	N	T	G	M	I	A	A	T	G	E	N	H	A	V	S	L	H	A	R	N	V	H	N	S	G	T	V	A	S	Q	D	D	A	N	I	H	S	Q	T	L	D	N	S	G	T	V	L	S	S	G	R	L	T	V	R	N	L	G	R	L
fhab_borpe	---	L	G	D	A	T	V	Q	R	G	P	L	S	L	K	G	A	G	V	V	S	A	G	K	L	A	S	G	G	G	A	V	---	N	V	A	G	G	G	A	V	K	I	A	---	S	A	S	S	V	G	N	L							
	340	350	360	370	380																																																							
	420	430	440	450	460	470																																																						
m564 .pep	K	N	Q	N	G	T	I	Q	A	A	R	L	D	M	S	T	G	G	L	D	N	T	G	N	I	T	Q	T	G	S	Q	A	L	D	L	V	S	A	G	K	F	D	N	S	G	K	I	G	V	S	D	V	P	Q	T	G	L	N	P	
fhab_borpe	A	V	Q	G	G	G	K	V	Q	A	T	L	L	N	A	G	---	---	G	T	L	L	V	S	G	R	Q	A	V	Q	L	G	A	A	S	R	Q	A	L	S	V	N	A	G	G	A	L	K	A	D	K	L	S	A						
	390	400	410	420	430																																																							
	480	490	500	510	520	530																																																						
m564 .pep	N	P	S	V	-	I	P	Q	I	P	S	T	A	T	G	S	G	S	T	V	S	V	S	K	P	G	S	N	N	P	V	S	P	T	A	P	A	K	N	Y	A	V	G	R	I	Q	T	T	G	A	F	D	-	N	A	G	S	I	N	
fhab_borpe	T	R	R	V	D	V	D	G	K	Q	A	V	A	L	G	S	A	S	S	N	A	L	S	V	R	A	G	G	A	---	L	K	A	G	K	L	S	A	T	G	R	L	D	V	D	G	K	Q	A	V	T	L	G	S	V	A				
	440	450	460	470	480	490																																																						
	540	550	560	570	579																																																							
m564 .pep	A	G	G	Q	I	D	I	A	A	Q	N	G	L	G	N	S	G	S	L	N	A	A	K	L	R	V	S	G	---	D	S	F	N	N	T	---	V	K	G	K	L	Q	A	H	D	L	A	V	N	T										
fhab_borpe	S	D	G	A	L	S	V	S	A	G	G	N	L	R	A	N	E	L	V	S	S	A	Q	L	E	V	R	G	Q	R	E	V	A	L	D	D	A	S	S	A	R	G	M	T	V	V	A	A	G	A	L	A	R	N	L	Q	S	K	G	
	500	510	520	530	540	550																																																						
	580	590	600	610	620	630																																																						
m564 .pep	Q	T	A	K	N	S	G	H	L	L	T	Q	T	G	K	I	D	N	R	E	L	H	---	N	A	G	E	I	A	A	N	N	L	T	L	I	H	S	G	R	L	S	N	D	K	K	G	N	I	R	A	A	H	L	Q	L	D	T	A	
fhab_borpe	A	I	G	V	Q	G	E	A	V	S	V	A	N	A	N	S	D	A	E	L	R	V	R	G	R	Q	V	D	L	H	D	L	S	A	A	R	G	A	D	I	S	G	E	G	R	V	N	I	G	R	A	R	S	D	S	D	V	K		
	560	570	580	590	600	610																																																						
	640	650	660	670	680	690																																																						
m564 .pep	G	L	H	N	A	G	N	I	L	A	D	S	G	T	V	T	T	K	N	N	L	R	N	T	G	K	V	S	V	A	R	L	N	T	E	G	Q	T	L	D	N	T	R	G	R	I	E	A	E	T	V	N	I	Q	S	Q	Q	L	T	N
fhab_borpe	-	V	S	A	H	G	A	L	S	I	D	S	M	T	A	L	G	A	I	G	V	Q	A	G	G	S	V	S	A	K	D	M	R	S	R	G	A	V	T	V	S	G	G	---	A	V	N	L	G	D	V	Q	---							
	620	630	640	650	660																																																							
	700	710	720	730	740	750																																																						
m564 .pep	Q	S	G	H	I	T	A	T	E	Q	L	T	I	N	S	R	N	V	D	N	Q	N	G	K	L	L	S	A	N	Q	A	Q	L	A	V	S	D	G	L	Y	N	Q	H	E	I	A	T	N	R	Q	L	S	I	H	D	K	N	Q	N	
fhab_borpe	S	D	G	Q	V	R	A	T	S	A	G	A	M	T	V	R	D	V	---	---	A	A	A	D	L	A	L	Q	A	G	D	A	L	Q	A	G	F	L	K	S	A	G	A	M	T	V	N	G	R	D	A	V								
	670	680	690	700	710																																																							

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760      770      780      790      800      810
m564 .pep TLALNNADGTIQSAGNVSLQAKSLANNGTLTAGNKLDIALTDDFVVERDLTAGKQL-NLS
      |  ||: ::||: ::: : | |::| :| : : : | :| |::|
fhab_borpe RL-----DGA-HAGGQLRVSSDQQAALGSLAAKGELTVSAARAATVA-EL---KSLEDNIS
      720      730      740      750      760

820      830      840      850      860      870
m564 .pep IKGRLEK-NTHTLQAGHTLKLNA-GNIDNQVTGKIIGGEQTDITSEQHVDNRGLNSDGLT
      : | : ::::: : :| | :| : : : | :| : :| :|
fhab_borpe VTGGERVSVQSVNSASRVAISAHGALD---VGKV--SAKSGIGLE---GWGAVGADSL-
      770      780      790      800      810

880      890      900      910      920      930
m564 .pep HIGAGQTLTNTGTGKIYGNHIALDAQILLNREETEGSTKAGAIARKRLDI-GAKEIHN
      | : : : :| : : : | :| : : :| :| : | :| :| : :
fhab_borpe --GSDGAISVSGRDAVRVDQARSLADISLG---AEGGATLGAVEAAGSIDVRGGSTV--
      820      830      840      850      860

940      950      960      970      980      990
m564 .pep QEGALLSSEGIFAVGNRLDEQHHAAAGMADTFVNGSAGLEVQGDALMSVRNMQNNHFKT
      ::| :: : : | : | : :| : : :| :| : :| :| : : :
fhab_borpe AANSLHANRDVRVSGK--DAVRVTAATSGGLHVSSGRQLDLGAVQA-RGALALDGGAGV
      870      880      890      900      910      920

1000     1010     1020     1030     1040     1050
m564 .pep ETYLAKAEK--QVRDYTVLGQNTYYQAGKDLFDNSQGGQKQDQTATFHLKNGSRIEANK-
      ||| :| : | :| : | : :| :| :| :| :| :| :| :|
fhab_borpe ALQSAKASGTLHVQGGHELDLGTAAVAVDV---NGTGDVRVAKLVSDAGADLQAGRS
      930      940      950      960      970

1060     1070     1080     1090     1100
m564 .pep --WHVRDYHIETYKERIENRPAHITVGGDLTASGQNLNPKDSRIVVGGRIITDDLNOKE
      : | : : : : : :| :| :| :| :| :| :| :| :|
fhab_borpe MTLGIVDTTGDLQARAQQKLELGSVKSDDGLQAAAGGALSAAAEEVAGALELS---GQGV
      980      990      1000     1010     1020     1030

1110     1120     1130     1140     1150     1160
m564 .pep ITNQSTTGKGRDVGTVQWDSVTKKGWY--SGRKRQRRTERNHTPYHDTQLFTHDFDTPV
      : : : :| |::| : : : :| :| :| :| :| :| :| :|
fhab_borpe TVDRASASRARIDSTGSGVIGALKAGAVEAASPRRARRALR-----QDFFTPG
      1040     1050     1060     1070      1080

1170     1180     1190     1200     1210     1220
m564 .pep SVI---QONAAPSFQPAASAIKLIDGVSTAANGQRIHTGNVSVLNNATVTLPNSSLYT
      ||: | |:: :| : : :| : :| : :| : :| :| :| :|
fhab_borpe SVVVRAQGNVTVGRGDEPHQGVLAQGDIMDA--KGGTLLLRNDALTENGTVTISADSAVL
      1090     1100     1110     1120     1130     1140

1230     1240     1250     1260     1270     1280
m564 .pep THPDNKGWLVETD-PQFADYRRWLGS DYMLQQLQLDTNHLHKRLGDGYEQLVNEQIHQ
      | : : : :| : :| : :| :| : :| : :| : :| :|
fhab_borpe EHSTIESKISQSVLAAKGDKGKPAVSVKVAKKLFL--NGTLRAVNDN--NETMSGRIQIDV
      1150     1160     1170     1180     1190

1290     1300     1310     1320     1330     1340
m564 .pep LTGYRRLDGYRDEEQFKALMDNGLTAAKTFGLTGP-IALSAEQVARLTSDIVWMENQTV
      : | : : :| :| : : : :| :| :| :| :| :| :|
fhab_borpe VDGRPQI----TDAVTGEARKDES VSDAALVADGGPIVVEAGELVSHAGGIGNGRNK--
      1200     1210     1220     1230     1240     1250
```

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		1350	1360	1370	1380	1390	1400
m564	.pep	T LSDGSTQTVLPKVYALARKGDLNTSGGLISAEQVLLKLQNGNLTNSGTIAGRQAVLIQ					
		: : : : : : : : : : : : : : : :					
fhab_borpe		--ENGASVTVRTT-----GNLVNKGYISAGKQGVLEV-GGALTNEFLVGS DGTQRIE					
		1260		1270	1280	1290	1300
		1410		1420	1430	1440	1450
m564	.pep	ARNINSNGNIQ-----ADQIGLKAESINIDGGQVQAGRLLTAQ----AQNINLNGTT					
		: : : : : : : : : : : : : : :					
fhab_borpe		AQRIENRGTFQSQAPAGTAGALVVKAAEAIVHDGVMATKGEMQIAGKGGGSPTVTAGAKA					
		1310	1320	1330	1340	1350	1360
		1460	1470	1480	1490	1500	
m564	.pep	QTSGNERNGNTAI-DRMAGINVV-GSHTQVDNRTSD-GILSLHASNDINLNAATVSNQV					
		: : : : : : : : : : : : : : :					
fhab_borpe		TTSANKLSVDVASWDNAGSLDIKKGGAQVTVAGRYAEHGEVSIQGDYTVSADAIALAAQV					
		1370	1380	1390	1400	1410	1420
		1510	1520	1530	1540		1550
m564	.pep	--KDGTQTITAGNNLNLGT-IRTE---HREAYGTLDENHRHVRQST-----EVGS					
		: : : : : : : : : : : : : : : : : : : : : : : :					
fhab_borpe		TQRGGAANLTSRHDTFRFSNKIRLMGPLQVNAGGPVSNTGNLKVREGVTVTAASFDNETGA					
		1430	1440	1450	1460	1470	1480
		1560	1570	1580	1590	1600	
m564	.pep	SIRTQNGALLRAGNDLKIRQGELEAEEGKTVLAAGR DV--TISEGRQITELDTS---VSG					
		: : : : : : : : : : : : : : : : : : : : : : : :					
fhab_borpe		EVMAKSATLTTSGAARN--AGKMVQVEAATIVAASVSNPGTFTAGKDITVTSRGGFDNEG					
		1490	1500	1510	1520	1530	
		1610	1620	1630	1640	1650	1660
m564	.pep	K---SKGILSSTKTHDRYRF---SHDEAV-GSNIGGGKMIVAAGQDINVRGSLISDKGI					
		: : : : : : : : : : : : : : :					
fhab_borpe		KMESNKDIVIKTEQFSNGRVLDAKHDLTVTASGQADNRGSLKAGHDFTVQAQRI--DNSG					
		1540	1550	1560	1570	1580	1590
		1670	1680	1690	1700	1710	
m564	.pep	VLKAGHDIDISTAHNRYTG-----NEYHESKKSGVMGTGGLGFTIGNRKTDDTDRTNIV					
		: : : : : : : : : : : : : : :					
fhab_borpe		TMAAGHDATLKAHLRNTGQVVAGHDIHIINSKLENTGRV--DARN DIALDVADFTN--					
		1600	1610	1620	1630	1640	1650
		1720	1730	1740	1750	1760	1770
m564	.pep	HTGSIIGSLNGDVTVAGNRYRQT----GSTVSSPEGRNTVTAKSIDVEFANNRYATDYA					
		: : : : : : : : : : : : : : :					
fhab_borpe		-TGSLYAEHDA-TLTLAQGTQRDVLVDQDHILPVAEGTLRVKAKSLTEIETGNPGSLIA					
		1660	1670	1680	1690	1700	1710
		1780	1790	1800	1810	1820	1830
m564	.pep	HTQEOKGLTVALNVPVQAAQNFIQAAQNVGKSKNKR VNAMAAANAA-WQSYQATQOMQ					
		: : : : : : : : : : : : : : :					
fhab_borpe		EVQE-----NIDNKQA----IVVGKDLTLS-SAHGNVANEANALLWAAGELTVKAQN					
		1720	1730	1740	1750		
		1840	1850	1860	1870	1880	1890
m564	.pep	FAPSSSAGQGQNNNQSPSISVSITYGEQKSRNEQKRHYTEAAASQIIGKQTTLAATGSG					
		: : : : : : : : : : : : : : : : : : :					
fhab_borpe		ITNKRAALIEAGGNARLTA AVALLNKLGRIRAGEDMHL D---APRI----ENTAKLSGEV					
		1760	1770	1780	1790	1800	1810
		1900	1910	1920	1930	1940	1950
m564	.pep	EQSNINITGSDVIGHAGTALIADNHIRLQSAKQDGSEQSKNKSSGWNAGVAVKIGNGIRF					
		: : : : : : : : : : : : : : : : : : : :					
fhab_borpe		QRKGVQDVGGGEHGRWSGIGYVNYWLRAGNGKKAGT-----IAAPWYGGDLTAEQSLIEV					
		1820	1830	1840	1850	1860	

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		1960	1970	1980	1990	2000	2010
m564	.pep	GITAGGNIGKGEQGGSTTHRHVHGSTTGKTTIRSGGDTTLKGVQLIGKGIQADTRNLH					
		:		:	: : :		: : :
fhab_borpe		GKDLYLNAGARKDE-----HRHL-----LNEGVIQAGGHGHIHG-----DVDNRSV-					
		1870	1880	1890		1900	

		2020	2030	2040	2050	2060
m564	.pep	IESVQDTETYQSKQQNGNVQVTVGYGFSASGSYRQSKVKA-----DHASVTGQSGIYAGE				
		: : :	: :	: :	:	:
fhab_borpe		VRTVSAMEYFKTPLPVSLTALDNRAGLSPATWNFQSTYELLDYLLDQNRYEYIWGLYPTY				
		1910	1920	1930	1940	1950

		2070	2080	2090	2100	2110	2120
m564	.pep	DGYQIKVRDNTDLKGGIITSSQSAEDKGNLFQTATLTASDIQNHS--RYEGRSFGIGGS					
		: : :	:	: :	:	: : :	: :
fhab_borpe		TEWSVNTLKNLDL-GYQAKPAPTAPPMPKA-----PELDLRGHTLESAEGRKI-FGEY					
		1970	1980	1990	2000	2010	

		2130	2140	2150	2160	2170
m564	.pep	FDLNGGWDGT-----VTDKQGRPTDRISPAAGYGS DGD SKNSTTRSGVNTHNIHITDEAG				
		: : :	: : :	: :	: : :	: : :
fhab_borpe		KKLQGEYEKAKMAVQAVEAYGEATRVRHDQLG-----QRYGKALGGMDAETKEVDGIIQ				
		2020	2030	2040	2050	2060

		2180	2190	2200	2210	2220	2230
m564	.pep	QLARTGRTAKETEARIYTGIDTETADQHSGLKNSFDKDAVAKEINLQREVTKEFGRNAA					
		: :	: :	: :	: :	: :	: : :
fhab_borpe		EFAADLRTVYAKQADQAT-IDAET-DKVAQRYKSQID--AVRLQAIQPGRV--LAKALS					
		2080	2090	2100	2110	2120	

		2240	2250	2260	2270	2280	2290
m564	.pep	QAVAAVADKLGNTQSYERYQEARTLLE-AELQNTDSEAEKAAFRASLGQVNAYL-----					
		: :	: :	: : :	: :	: :	: :
fhab_borpe		AALGADWRALGHSQLMQRWKDFKAGKRGAEIAFYPKQTVLAAGAGLTLSNGAIHNGENA					
		2130	2140	2150	2160	2170	2180

		2300	2310	2320	2330	2340	2350
m564	.pep	AENQSRDYTWKEGGIGRSILHGAAGGLTTGSLGGILAGGGTSLAAPYLDKAAENLGPAGK					
		: : :	: : :	: : :	: : :	: : :	: : :
fhab_borpe		AQNRGRPEGLKIGAHSA TS VSGSFDALRDVGLEKRLDIDDALAAVLVNP HIFTRIGAAQT					
		2190	2200	2210	2220	2230	2240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1671>:

```

g565.seq
1  atggacagca cattgtctaa aacgtgttgc gtttcgtgca tattgttgag
51  cgtaaccacc accattttcg cccgtcccag accggcggct tccaatactt
101 ccttcggttt cgcacgcgcg aacgacaccg gctcgctgca acttctggct
151 acctgcacgc gtgcgatgac caagtcgagc gcgaaatacg gaatacctc
201 ttggggcgaa gacgcgtccg accgtctgcc cgcccctgcc gaagccgaca
251 atcagcacat gatcagactt gctcatcgct tccaccaaca tgctgtgacg
301 atcgagcgac ttcattgtccc agcttga

```

This corresponds to the amino acid sequence <SEQ ID 1672; ORF 565.ng>:

```

g565.pep
1  MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
51  TCTRAMSKSS AKYGISSLGE DASDRLPAPA EADNQHMIRL AHRFHQHAVQ
101 IERLHVPA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1673>:

```

m565.seq
1  ATGGACAGCA CATTGTCTAA AACGTGTTGC GTTTCGTGCA TATTGTTGAG
51  CGTAACCACC ACCATTTCG CCCGTCCCAG ACCGGCGGCT TCCAATACTT
101 CCCTGCGTTT CGCATCGCCG AACGACACCG GTTCGCCC GC ACTTCTGGCA
151 ACCTGCACCC GCGCAATGTC CAAGTCGAGC GCGAAATACG GAATATCCTC
201 TTGGGCAAGG ACGCGTCCGA CCGTCTGCCC GCCCCTGCCG AAGCCGACAA

```

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```

251 TCAGCACATG GTCGGACTTG CTCATGGTTT CTACCAGCAT ACTGTGCAGA
301 TCGAGCGACT TCATGTCCCA GCTTGACTTG ACCAAACGCC CGACCAGCGC
351 ATCGCTGCCG CCAAGAGGA AGGGCGCGAT AATCATCGAC AGCAGAACCG
401 CCGCCGTCGC CGCCTGTTCC CATTCTGGCG AAACCATATC AAGCTGCCCC
451 GCAATGGCCA GCATCACGAA GCCGAAC TCG CCGCCCTGCG CGAGATACAA
501 AGCCGTTTGG AGGCTGTCGC CGACCGAATG TTTCATTTTG AAGGCAATGG
551 CAAACACAAC CAGTGCCTTC AACACCAGCA GCATTGCCAA CAGCATCAAT
601 ACCTGCCGCC AGCCGCCGAT CAATGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1674; ORF 565>:

```

m565.pep
  1 MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
 51 TCTRAMSKSS AKYGISSWAR TRPTVCPPLP KPTISTWSDL LMVSTSILCR
101 SSDFMSQLDL TKRPTSASLP PKRKGAIID SRTAAVAACS HSGETISSCP
151 AMASITKPNS PPCARYKAVL RLSPTTECFIL KAMANTTSAF NTSSSIANSIN
201 TCRQPPINA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m565/g565 100.0% identity in 67 aa overlap

```

              10      20      30      40      50      60
m565.pep      MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
g565           MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
              10      20      30      40      50      60

              70      80      90      100     110     120
m565.pep      AKYGISSWARTRPTVCPPLPKPTISTWSDLLMVSTSILCRSSDFMSQLDLTKRPTSASLP
              |||||||
g565          AKYGISSLGEDASDRLPAPAEADNQHMIRLAHRFHQHAVQIERLHVPAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1675>:

```

a565.seq
  1 ATGGACAGCA CATTGTCTAA AACGTGTTGC GTTTCGTGCA TATTGTTGAG
 51 CGTAACCACC ACCATTTTCG CCCGTCCCAG ACCGGCGGCT TCCAATACTT
101 CCTGCGTGT CCGATCGCCG AACGACACCG GTTCGCCCCG ACTTCTGGCA
151 ACCTGCACCC GCGCAATGTC CAAGTCGAGC GCGAAATACG GAATATCCTC
201 TTGGGCAAGG ACGCGTCCGA CCGTCTGCCG GCCCCTGCCG AAGCCGACAA
251 TCAGCACATG GTCGGACTTG CTCATGGTTT CTACCAGCAT ACTGTGCAGA
301 TCGAGCGACT TCATGTCCCA GCTTGACTTG ACCAAACGCC CGACCAGTGC
351 ATCGCTGCCG CCAAGAGGA AGGGCGCGAT AATCATCGAC AGCAGAACCG
401 CCGCCGTCGC CGCCTGTTCC CATTCTAGCG AAACCATATC AAGCTGCCCC
451 GCAATGGCCA GCATCACGAA GCCGAAC TCG CCGCCCTGCG CGAGATACAA
501 AGCCGTTTGG AGGCTGTCGC CGACCGAATG TTTCATTTTG AAGGCAATGG
551 CAAACACAAC CAGTGCCTTC AACACCAGCA GCATTGCCAA CAGCATCAAT
601 ACCTGCCGCC AGCCGCCGAT TAATGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1676; ORF 565.a>:

```

a565.pep
  1 MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
 51 TCTRAMSKSS AKYGISSWAR TRPTVCPPLP KPTISTWSDL LMVSTSILCR
101 SSDFMSQLDL TKRPTSASLP PKRKGAIID SRTAAVAACS HSSETISSCP
151 AMASITKPNS PPCARYKAVL RLSPTTECFIL KAMANTTSAF NTSSSIANSIN
201 TCRQPPINA*

```

m565/a565 99.5% identity in 209 aa overlap

```

              10      20      30      40      50      60
m565.pep      MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

```

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```

a565      MDSTLSKTCVSCILLSVTTTIFARPRPAASNTSLRFASPNDTGSPALLATCTRAMSKSS
           10      20      30      40      50      60
m565.pep  AKYGISSWARTRPTVCPPLPKPTISTWSDLLMVSTSLICRSSDFMSQLDLTKRPTSASLP
           70      80      90      100     110     120
a565      AKYGISSWARTRPTVCPPLPKPTISTWSDLLMVSTSLICRSSDFMSQLDLTKRPTSASLP
           70      80      90      100     110     120
m565.pep  PKRKGAIIDSRTAAVAACSHSGETISSCPAMASITKPNSPPCARYKAVLRLSPTECFIL
           130     140     150     160     170     180
a565      PKRKGAIIDSRTAAVAACSHSSETISSCPAMASITKPNSPPCARYKAVLRLSPTECFIL
           130     140     150     160     170     180
m565.pep  KAMANTTSAFNTSSSIANSINTCRQPPINAX
           190     200     210
a565      KAMANTTSAFNTSSSIANSINTCRQPPINAX
           190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1677>:

```

g566.seq..
1  atgccgtctg aacaatatct tttcagacgg cattttgtat ggggggtaac
51 ggttggtcag cccgagtagc tcctgcatat cgtacaaacc cgttttgccg
101 tttacccaaa ctgcggcgcg gacggcaccg gcggaagagg tcatgctggc
151 gccggccttg tgggtgattt ccacgcgttc gccgtcgggt gccaagaggg
201 cggtgtggtc gccgactatg tcgcctgcgc ggacggtggc aaagccgatg
251 gtggaaggat cgcgcggacc agtgtggcct tcgcggccgt aaacggcgca
301 ttgtttgagg tcgcggccga ggcgcggcgc gatgacttcg cccattcgta
351 a

```

This corresponds to the amino acid sequence <SEQ ID 1678; ORF 566.ng>:

```

g566.pep..
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFAVYPNCGA DGTGGKGHAA
51 AGFVGDFHAF AVGGEEGGVV ADYVACADGG KADGGRIART SVAFAAVNGA
101 LFEVAAERAG DDFAHSA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1679>:

```

m566.seq..
1  ATGCCGTCTG AACAAATATCT TTTCAGACGG CATTTTGTAT GGGGGTTAAC
51 GGTGTGTTTCA CCGAGTAGC TCCTGCATAT CGTACAAACC CGTTTGTCCG
101 TTGACCCAAA CTGCGGCGCG GACGGCACC GCGGCAAAGG TCATGCGGCT
151 GCTGGCCTTG TGGGTGATT CCACGCGTC GCCGTGCGTG GCGAAGAGGG
201 CGGTGTGGTC GCCGACGATG TCGCCTGCGC GGACGGTGGC AAAGCCGATG
251 GTCGACGGAT CGCGCGGACC GGTGTGGCCT TCGCGGCCGT AAACGGCGCA
301 TTGTTTGAGG TCTCTGCCGA GCGCGCCGCG GATGACTTCG CCCATGCGTA
351 A

```

This corresponds to the amino acid sequence <SEQ ID 1680; ORF 566>:

```

m566.pep..
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFAVDPNCGA DGTGGKGHAA
51 AGLVGDFHAL AVGGEEGGVV ADDVACADGG KADGRRRIART GVAFAAVNGA
101 LFEVSAERAG DDFAHSA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m566/g566 93.1% identity in 116 aa overlap

```

m566.pep  MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFAVDPNCGADGTGGKGHAAAGLVGDFHAL
           10      20      30      40      50      60
           |||||

```



```
a566.seq
1  ATGCCGCTCTG AACAAATATCT TTTCAGACGG CATTTTGTAT GGGGGTTAAC
51  GGTTGTTTCAG CCCGAGTACG TCCTGCATAT CGTACAAACC CGTTTTACCG
101 TTTACCCAAA CTGCGGCGCG GACGGCGCCG CGCGCAAAGC TCATGCGCGT
151 GCTTGCCCTTG TGGGTGATTT CCACGCGCTC GCCGTGGGTG GCGAAGAGGG
201 CCGTGTGGTC GCCGACGATG TCGCCCGCGC GGACGGTGGC AAAGCCGATG
251 GTGGACGGAT CGCGCGGGCC GGTGTGGCCT TCGCGGCCGT AAACGGCGCA
301 TTGTTTGAGG TCTCTGCCGA GCGCGCCGGC GATGACTTCG CCCATGCGTA
351 A
```

a566.pep

1	MPSEQYLFRR	HFVWGLTVVQ	PEYVLHIVQT	RFTVYPNCGA	DGAGGKGHAA
51	ACLVGDFHAL	AVGGEEGGVV	ADDVARADGG	KADGGRIARA	GVAFAAVNGA
101	LFEVSAERAG	DDFAHA*			

	10	20	30	40	50	60
m566.pep	MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFAVDPNCGADGTGGKGHAAAGLVGDFHAL					
a566	MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFTVYPNCGADGAGGKGHAAACLVGDFHAL					
	10	20	30	40	50	60
	70	80	90	100	110	
m566.pep	AVGGEEGGVVADDVACADGGKADGRRIRARTGVAFAAVNGALFEVSAERAGDDFAHAX					
a566	AVGGEEGGVVADDVARADGGKADGGRIARAGVAFAAVNGALFEVSAERAGDDFAHAX					
	70	80	90	100	110	

```
g567.seq..
  1  atgcgacgac  gggcagcggc  atcgacaagg  cgggtttgca  gtccggcggt
51  tatcaggtct  tattgggcga  tgcggacgtg  cagtcggcgg  cggtacgcag
101 caaagagggc  ggatacggcg  tgttgggtgc  gaacgcgcgc  gcttgccggc
151 cgggaatcgc  agctggtgca  ggaaatcgcc  cgggaagtgc  gtttgaaaaa
201 cgcgctcaag  gcagtgggcg  aagattacga  ctttatcctg  atcgactgtc
251 cgccttcgct  gacgctgttg  acgcttaacg  gcttggtggc  ggcgggcggc
301 gtgattgtgc  cgaatgtgtg  cgaatattac  gcgctggaag  ggatttcgga
351 tttgattcgc  accgtgcgca  aaatccgtca  gcggtgcaat  cccgatttgg
401 acatcacggg  catcgtgcgt  acgatgtacg  acagccgcag  caggctgggt
451 gccgaagtca  gcgaacagtt  gcgcagccat  ttcggggatt  tgctttttga
501 aaccgccatc  ccgcgcaata  tccgccttgc  ggaagcgccg  agccacggta
551 tgccggtgat  ggctactcac  gcgcaggcaa  aggggtccaa  ggcgatatct
601 gccttggcgg  acgaactggc  ggcgagggtg  tcggggaaat  aq
```

g567.pep

1	MRRRAASTR	RVCSPAFIRS	YWAMRTCSRR	RYAAKRADTA	CWVRTRALAG
51	AEIELVQEIA	REVLRLKNALK	AVAEDYDFIL	IDCPPSLTLL	TLNGLVAAGG
101	<u>VIVPMLCEYY</u>	ALEGISDLIA	TVRKIRQAVN	PDLDITGIVR	TMYDSRSRLV
151	AEVSEQLRSH	FGDLLFETAI	PRNIRLAEAP	SHGMPVMAYD	AQAKGAKAYL
201	ALADELAARV	SGK*			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1685>:

```
m567.seq..
1  ATGAGTGCGA  ACATCCTTGC  CATCGCCAAT  CAGAAGGGCG  GTGTGGGCAA
51  AACGACGACG  ACGGTAAATT  TGGCGGCTTC  GCTGGCATCG  CGCGGCAAAC
101 GCGTGCTGGT  GGTTCGATTG  GATCCGCAGG  GCAATGCGAC  GACGGGCAGC
151 GGCATCGACA  AGGCGGGTTT  GCAGTCCGGC  GTTTATCAGG  TCTTATTGGG
201 CGATGCGGAC  GTGCAGTCGG  CGGCGGTACG  CAGCAAAGAG  GGCGGATACG
251 CTGTGTTGGG  TGCGAACCGC  GCGCTGGCCG  GCGCGGAAAT  CGAACTGGTG
301 CAGGAAATCG  CCCGGGAAGT  GCGTTTGAAA  AACGCGCTCA  AGGCAGTGGA
351 AGAAGATTAC  GACTTTATCC  TGATCGACTG  CCCGCCTTCG  CTGACGCTGT
401 TGACGCTTAA  CGGGCTGGTG  GCGGCGGGCG  GCGTGATTGT  GCCGATGTTG
451 TGCGAATATT  ACGCGCTGGA  AGGGATTTCC  GATTTGATTG  CGACCGTGCG
501 CAAAATCCGT  CAGGCGGTCA  ATCCCGATT  GGACATCACG  GGCATCGTGC
551 GCACGATGTA  CGACAGCCGC  AGCAGGCTGG  TTGCCGAAGT  CAGCGAACAG
601 TTGCGCAGCC  ATTTCTGGGA  TTTGCTTTTT  GAAACCGTCA  TCCCGCGCAA
651 TATCCGCTT  GCGGAAGCGC  CGAGCCACGG  TATGCCGGTG  ATGGCTTACG
701 ACGCGCAGGC  AAAGGGTACC  AAGGCGTATC  TTGCCTTGGC  GGACGAGCTG
751 GCGGCGAGGG  TGTCGGGGAA  ATAG
```

This corresponds to the amino acid sequence <SEQ ID 1686; ORF 567>:

```
m567.pep..
1  MSANILAIAN  QKGGVGKTTT  TVNLAASLAS  RGKRVLVVDL  DPQGNATTGS
51  GIDKAGLQSG  VYQVLLGDAD  VQSAAVRSKE  GGYAVLGANR  ALAGAEIELV
101 QEIAREVRLK  NALKA VEEDY  DFILIDCPPS  LTLTLNGLV  AAGGVIVPML
151 CEYYALEGIS  DLIATVRKIR  QAVNPDLIT  GIVRTMYDSR  SRLVAEVSEQ
201 LRSHFGDLLF  ETVIPRNIRL  AEAPSHGMPV  MAYDAQAKGT  KAYLALADEL
251 AARVSGK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

```
m567/g567 98.2% identity in 168 aa overlap

m567.pep      60      70      80      90      100      110      119
GVYQVLLGDADVQSAAVRSKEGGYAVLGANRALAGAEIELVQEIAREVRLKNALKA VEED
g567          AFIRSYWAMRTCSRRRYAAKRADTACWVRTRALAGAEIELVQEIAREVRLKNALKA VEED
                20      30      40      50      60      70

m567.pep      120      130      140      150      160      170      179
YDFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLIT
g567          YDFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLIT
                80      90      100      110      120      130

m567.pep      180      190      200      210      220      230      239
TGIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAKG
g567          TGIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAKG
                140      150      160      170      180      190

m567.pep      240      250
TKAYLALADELAARVSGKX
g567          AKAYLALADELAARVSGKX
                200      210
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1687>:

```
a567.seq
1  ATGAGTGCGA  ACATCCTTGC  CATCGCCAAT  CAGAAGGGCG  GTGTGGGCAA
51  AACGACGACG  ACGGTAAATT  TGGCGGCTTC  GCTGGCATCG  CGCGGCAAAC
101 GCGTGCTGGT  GGTTCGATTG  GATCCGCAGG  GCAATGCGAC  GACGGGCAGC
151 GGCATCGACA  AGGCGAGTTT  GCAGTCCGGC  GTTTATCAGG  TCTTATTGGG
201 CGATGCGGAC  GTGAAATCGG  CGGCGGTACG  CAGCAAAGAG  GGCGGATACG
```

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```

251 GCGTGTGGG TCGGAACCGC GCGCTGGCCG GCGCGGAAAT CGAGCTGGTG
301 CAGGAAATCG CCCGGGAAGT GCGTTTGAAA AACGCGCTCA AGGCAGTGGC
351 GGAAGATTAC GACTTTATCC TGATCGACTG CCCGCCTTCG CTGACGCTGT
401 TGACGCTTAA CGGCTTGGTG GCGGCAGGCG GCGTGATTGT GCCGATGTTG
451 TGCGAATATT ACGCGCTGGA AGGGATTTCG GATTTGATTG CGACCGTGCG
501 CAAAATCCGT CAGGCGGTCA ATCCCGATTG GGATATCACG GGCATCGTGC
551 GTACGATGTA CGACAGCCGC AGCAGGCTAG TTGCCGAAGT CAGCGAACAG
601 TTGCGCAGCC ATTTTCGGGA TTTGCTGTTT GAAACCGTCA TCCC CGCGCAA
651 TATCCGCCTT GCGGAAGCGC CGAGCCACGG TATGCCGGTG ATGGCTTATG
701 ATGCGCAGGC AAAGGGTGCC AAGGCGTATC TTGCCTTGGC GGACGAGCTG
751 ATGGCGAGGG TGTCGGGGA ATAG

```

This corresponds to the amino acid sequence <SEQ ID 1688; ORF 567.a>:

```

a567.pep
  1 MSANILAIAN QKGGVGKTTT TVNLAASLAS RGKRVLVVDL DPQGNATTGS
 51 GIDKASLQSG VYQVLLGDAD VKSAAVRSKE GGYGVLGANR ALAGAEIELV
101 QEIAREVRLK NALKAVAEDY DFILIDCPPS LTLTLNGLV AAGGVIVPML
151 CEYYALEGIS DLIATVRKIR QAVNPDLIT GIVRTMYDSR SRLVAEVSEQ
201 LRSHFGDLLF ETVIPRNIRL AEAPSHGMPV MAYDAQAKGA KAYLALADEL
251 MARVSGK*

```

m567/a567 97.7% identity in 257 aa overlap

```

              10      20      30      40      50      60
m567.pep      MSANILAIANQKGGVGKTTTTVNLAASLASRGKRVLVVDLDPQGNATTGSGIDKASLQSG
              |||||||
a567           MSANILAIANQKGGVGKTTTTVNLAASLASRGKRVLVVDLDPQGNATTGSGIDKASLQSG
              10      20      30      40      50      60

              70      80      90     100     110     120
m567.pep      VYQVLLGDADVQSAAVRSKEGGYAVLGANRALAGAEIELVQEIAREVRLKNALKAVEEDY
              |||||:|||||:|||||
a567           VYQVLLGDADVQSAAVRSKEGGYVGLGANRALAGAEIELVQEIAREVRLKNALKAVEEDY
              70      80      90     100     110     120

              130     140     150     160     170     180
m567.pep      DFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLIT
              |||||||
a567           DFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLIT
              130     140     150     160     170     180

              190     200     210     220     230     240
m567.pep      GIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAKGT
              |||||||
a567           GIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAKGA
              190     200     210     220     230     240

              250
m567.pep      KAYLALADELAARVSGKX
              |||||||
a567           KAYLALADELMARVSGKX
              250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1689>:

```

g568.seq
  1 atgctcaggg tcagaccggt attatttgcc gtcaaggctt ccgcctcttc
 51 gataccttgc agaatctgcc gattaaagcg ttcgcggctg cccaatattt
101 tcaggcgcat attgttttcg tgcaggcggc gtacctgttt ttgcaaaaggc
151 tgtaaaaaaca gcccacacag gaacgaaact tcgtcttcgg ggcgacgccca
201 gttttcgggt gaaaaggcaa acacggtcag atattgcacg ccagtttg
251 cgcaatgctt caccatattt tccaacgcgt ccaagccgcy tttgtgtccc
301 attatacgcg ggagaaaacg ttttttcgcc caacggccgt tgccgtccat
351 aattacggcg atgtgcctcg ggatggcggt gtgttccaaa atggtctgcy

```

```
g568.pep
  1  MLRVRPVLFA VKASASSIPC RICRLKRSRL PNIFRRILFS CRRRTCFCCKA
 51  CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFITF SNASKPRLCP
101  IIRGRKRFFA QRPLPSIITA MCLGMAVCSK MVCVLLFISA FRGSAFKCLR
151  NAAP*
```

```
m568.seq
1 ATGCTCAGGG TCAGGCCGGT ATTGTTTGCC GTCAACGCTT CCGCCTCTTC
51 GATGCCCTTG AGAATCTGCC GGTGAAGCG TTCGCGGCTG CCCAATATCT
101 TCAGGCGCAT ATTGTTTCG TGCAGGCGCG GTACCTGTTT TCGCAAAGCC
151 TGTAAAAACA GCCCATCAG GAACGAACT TCGTCTTCGG GCGGCGCCA
201 GTTTTCGGTT GAAAAGGCAA ACACGGTCAG ATATTGCACA CCCAGTTTGG
251 CGCAATGCTT CACCATATTT TCCAATGCGT CCAACGCGG TTTGTGTCCC
301 ATTATGCGCG GGAGGAAACG TTTTTCGCC CAACGCCCGT TCGGCTCCAT
351 AATCACGGCG ATATGCTTGG GAATGGCGGT GTGTTCCAAA ACGGCCTGCG
401 TGCTGCTTTT CATGTCTGCC TTTGCGGTT CGGCATTCAA ATGCCGTCTG
451 AACGCCGAAC CGTGCAAGTT AAATTGCCAT CAAATCTTCT TCTTTGGCAG
501 TCAGGAGTTT GTCGGCTTCG GTAATGTATT TGTGGTCAG TTTTTGAACC
551 GCTTCTTCGC CGCGACGTGC CTCGTCTTCG GAAATTTCTT TGTCTTTGAG
601 GAGTTTTTTG ATGTGGTCGT TGGCATCGCG GCGCACGTTG CGGATAGAGA
651 CGCGGCCTTC TTCCGCTTCG CCGCGTACGA CTTTAATCAG GTCTTTGCGG
701 CGTTCCTCGG TCAGCATGGG CATCGGCACG CGGATCAGGT CGCCGACAGC
751 TGCCGGGTTT AGTCCCAAGT TTGA
```

```
m568.pep..
  1  MLRVRPVLFA  VNASASSMPC  RICRLKRSRL  PNIFRRILFS  CRRRTCFCCKA
  51  CKNSPIRNET  SSSGRRQFSV  EKANTVRYCT  PSLAQCFITF  SNASKPRLCP
101  IMRGKRFFFA  QRPLPSIITA  ICLGMVACSK  TACVLLFMSA  FRGSAFKCRL
151  NAEPCLLNCH  QIFFFGSQEF  VGFGNVFVGQ  FLNRFFAATC  LVFGNFFVFE
201  EFFDVVVVGA  AHVADRDAAF  FRFAAYDFNQ  VFAAFLGQHG  HRHADQVADS
251  CRVOSOV*
```

Homology with a predicted ORF from *N. gonorrhoeae*

BNSDOCID: <WO 9957280A2 1>

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1693>:

```
a568.seq
1  ATGCTCAGGG TCAGGCCGGT ATTGTTTGCC GTCAAGGCTT CCGCCTCTTC
51  GATGCCCTTC AGGATTGAC  GGTGAAGCG TTCGCGGCTG CCCAGTATTT
101 TCAGGCGCAT ATTGTTTCG  TGCAGGCGG GTACCTGTTT TTGCAAAGCC
151 TGTA AAAACA GCCCATCAG  GAACGAACT TCGTCTTCGG GCGGCGCCA
201 GTTTTCGGTT GAAAAGGCAA ACACGGTCAG ATATTGCACA CCCAGTTTGG
251 CGCAATGCTT CACCATATTT TCCAATGCGT CCAAACCGCG TTTGTGTCCC
301 ATTATGCGCG GGAGGAAACG TTTTTCGCC CAACGGCCGT TGCCGTCCAT
351 AATCACGGCG ATATGCTTGG GAATGGCGGT GTGTTCCAAA ACGGCTGCG
401 TGCTGCTTTT CATGTCTGCC TTTCGCGGTT CCGCATTCAA ATGCCGTCTG
451 AACCCGAAC CGTGCAGGT AAATTGCCAT CAAATCTTCT TCTTTGGCAG
501 TCAGGAGTTT GTCGGCTTCG GTAATGTATT TGTCGGTCAG TTTTGAACC
551 GCTTCTTCGC CGCGACGTGC CTCGTCTTCG GAAATTTCTT TGTCTTTGAG
601 GAGTTTTTTG ATGTGGTCGT TGGCATCGCG GCGCACGTTG CGGATGGAGA
651 CGCGGCCTTC TTCCGCTTCG CCGCGTACGA CTTTAATCAG GTCTTTGCGG
701 CGTTCCTCGG TCAGCATGGG CATCGGCACG CGGATCAGGT CGCCGACAGC
751 TGCCGGGTTC AGTCCAAGT TTGA
```

This corresponds to the amino acid sequence <SEQ ID 1694; ORF 568.a>:

```
a568.pep
1  MLRVRPVLFA VKASASSMPF RI*RLKRSRL PSIFRRILFS CRRRTCFCCKA
51  CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCTIF SNASKPRLCP
101 IMRGRKRFFA QRPLPSIITA ICLGMAVCSK TACVLLFMSA FRGSAFKCRL
151 NAEPCRLNCH QIFFFGSQEF VGFGNVFVGQ FLNRFFAATC LVFGNFFVFE
201 EFFDVVGIA AHVADGDAAF FRFAAYDFNQ VFAAFLGQHG HRHADQVADS
251 CRVQSQV*
```

m568/a568 98.1% identity in 257 aa overlap

m568.pep	10	20	30	40	50	60
a568	10	20	30	40	50	60
m568.pep	70	80	90	100	110	120
a568	70	80	90	100	110	120
m568.pep	130	140	150	160	170	180
a568	130	140	150	160	170	180
m568.pep	190	200	210	220	230	240
a568	190	200	210	220	230	240
m568.pep	250					
a568	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1695>:

```
g569.seq..
1  atgctgaaac aacgggtaat aaccgctatg tggctgctgc cgctgatgct
51  gggcatgctg ttttacgcgc cgcaatggct gtgggctgca ttttgcgggc
101 tgattgccct gaccgccttg tgggagtatg cccgatggc cggtttgtgc
```

```

151 aaaaccgaaa ccaaccatta cctcgccgca accttggttt tcggcgtagt
201 tgcctatgcg ggcggctgga tgctgcctaa ttgggtttgg tatgttggtt
251 tggcattttg gctcgccgtt atgcctttgt gggttgagatt caaatggagg
301 ctcaacggcg gttggcaggt ttatgccgtc ggctggcttt tgctcatgcc
351 gttttggttc gcgctcgat ccttggcgcc cgcacccga tga

```

This corresponds to the amino acid sequence <SEQ ID 1696; ORF 569.ng>:

g569.pep

```

1 MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALTAL WEYARMAGLC
51 KTETNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRFKWR
101 LGGGWQVYAV GWLLMPFWF ALVSLAPASR *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1697>:

m569.seq..

```

1 ATGCTGAAAC AACGGGTAAT AACCGCCATG TGGCTGCTGC CGCTGATGCT
51 GGGCATGCTG TTTTACGCGC CGCAATGGTT GTGGGCTGCA TTTTGCGGAC
101 TGATTGCCCT GATTGCCTTG TGGGAATATG CCCGTATGGG CGGTTTGTGC
151 AAAATTAAAA CCAACCATTA CCTCGCCGCA ACCTTGTTTT TCGGCGTGGT
201 TGCCTATGCG GCGCGCTGGA TGCTGCCTAA TTTGGTTTGG TATGTTGTTT
251 TGGCATTTTG GCTCGCCGTT ATGCCTTTAT GGTTGAGATT CAAATGGAGG
301 CTCACGCGCG GTTGGCAGGT TTATGCCGTC GGCTGGCTTC TGGTCATGCC
351 GTTTTGGTTC GCGCTCGTAT CCCTGCGCCC GCATCCCGAT GATGCCCTGC
401 CGCTGCTCGC CGTGATGGGT TTGGTGTGGG TTGCCGATAT TTGCGCGTAT
451 TTCAGCGGCA AGGCGTTCGG CAAACACAAA ATCGCGCCGG CAATCAGCCC
501 CGGCAAAAGC TGGGAAGGTG CAATCGGCGG CGCGGTTTGC GTGGCAGTGT
551 ACATGACCGC CGTACGAAGT GCCGGCTGGC TGGCATTCTA TACAGGCTGG
601 TTCGATACCG TGTTAATCGG TTTGGTGTCT ACCGTGTGCA GCGTATGCGG
651 CGACCTTTTG GAAAGCTGGC TCAAGCGCGC GGCAGGCATC AAAGACAGCA
701 GCAAGCTGCT GCCCGGACAC GCGCGCGTGT TCGACCGTAC CGACAGCCTG
751 ATTGCCGTTA TCAGCGTCTA TGCAGCGATG ATGTCCGTTT TAAATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1698; ORF 569>:

m569.pep..

```

1 MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALIAL WEYARMGGLC
51 KIKTNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRFKWR
101 LGGGWQVYAV GWLLVMPFWF ALVSLRPHPD DALPLLAVMG LVWVADICAY
151 FSGKAFGKHK IAPAI SPGKS WEGAIGGAVC VAVYMTAVRS AGWLAFDTGW
201 FDTVLIGLVL TVSVCGDLL ESWLKRAAGI KDSSKLLPGH GGVFDRDTSL
251 IAVISVYAAM MSVLN*

```

m569/g569 95.3% identity in 127 aa overlap

	10	20	30	40	50	60
m569.pep	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGLCKIKTNHYLAA					
g569	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALTALWEYARMAGLCKTETNHYLAA					
	10	20	30	40	50	60
m569.pep	TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLVMPFWF					
g569	TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLMPFWF					
	70	80	90	100	110	120
m569.pep	ALVSLRPHPD DALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAI SPGKS WEGAIGGAVC					
g569	ALVSLAPASRX					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1699>:

a569.seq

```

1 ATGCTGAAAC AACGGGTGAT AACCGCCATG TGGCTGCTGC CGCTGATGCT
51 GGGCATGCTG TTTTACGCGC CGCAATGGTT GTGGGCTGCA TTTTGCGGAC
101 TGATTGCCCT GATTGCCTTG TGGGAATATG CCCGTATGGG CGGTTTGTGC

```

```

151 AAAATTAAAA CCAACCATTA CCTCGCCGCA ACCTTGTTT TCGGCGTGGT
201 TGCCTATGCG GCGCGCTGGA TGCTGCCTAA TTTGGTTTGG TATGTTGTTT
251 TGGCATTTTG GCTCGCCGTT ATGCCTTTAT GGTGAGATT CAAATGGAGG
301 CTCAACGGCG GTTGGCAGGT TTATGCCGTC GGCTGGCTTC TGGTCATGCC
351 GTTTTGGTTC GCGCTCGTAT CCCTGCGCCC GCATCCCGAT GATGCCCTGC
401 CGCTGCTCGC CGTGATGGGT TTGGTGTGGG TTGCCGATAT TTGCGCGTAT
451 TTCAGCGGCA AGGCGTTCGG CAAACACAAA ATCGCACCGG CAATCAGCCC
501 CGGCAAAAGC TGGGAAGGTG CAATCGGCGG CGCGGTTTGC GTGGCCGTGT
551 ACATGACCGC CGTACGAAGT GCCGGCTGGC TGGCATTCGA TACAGGCTGG
601 TTCGATAACG TGTTAATCGG TTTGGTGTG ACCGTGTGCA GCGTATGCGG
651 CGACCTTTTG GAAAGCTGGC TCAAGCGCGC GGCAGGCATC AAAGACAGCA
701 GCAACCTGCT GCCCGGACAC GGCGGCGTGT TCGACCGCAC CGACAGCCTG
751 ATTGCCGTTA TCAGCGTCTA TGCAGCGATG ATGTCGGTTT TAAATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1700; ORF 569.a>:

```

a569.pep
1  MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALIAL WEYARMGGLC
51  KIKTNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAEFWLAV MPLWLRFKWR
101 LNGGWQVYAV GWLLVMPFWF ALVSLRPHPD DALPLLAVMG LVWVADICAY
151 FSGKAFGKHK IAPAI SPGKS WEGAIGGAVC VAVYMTAVRS AGWLAFTDGTW
201 FDTVLI GLVL TVVSVCGDLL ESWLKRAAGI KDSSNLLPGH GGVFDRDTSI
251 IAVISVYAAM MSVLN*

```

m569/a569 99.6% identity in 265 aa overlap

```

              10      20      30      40      50      60
m569.pep    MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGLCIKTNHYLAA
              |||
a569         MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGLCIKTNHYLAA
              10      20      30      40      50      60

              70      80      90      100     110     120
m569.pep    TLVFGVVAYAGGWMLPNLVWYVVLAEFWLAVMPLWLRFKWRLNNGGWQVYAVGWLLVMPFWF
              |||
a569         TLVFGVVAYAGGWMLPNLVWYVVLAEFWLAVMPLWLRFKWRLNNGGWQVYAVGWLLVMPFWF
              70      80      90      100     110     120

              130     140     150     160     170     180
m569.pep    ALVSLRPHPD DALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAI SPGKS WEGAIGGAVC
              |||
a569         ALVSLRPHPD DALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAI SPGKS WEGAIGGAVC
              130     140     150     160     170     180

              190     200     210     220     230     240
m569.pep    VAVYMTAVRSAGWLAFTDGTWFDTVLI GLVLT VVSVCGDLL ESWLKRAAGI KDSSKLLPGH
              |||
a569         VAVYMTAVRSAGWLAFTDGTWFDTVLI GLVLT VVSVCGDLL ESWLKRAAGI KDSSNLLPGH
              190     200     210     220     230     240

              250     260
m569.pep    GGVFDRDTSLIAVISVYAAMMSVLNX
              |||
a569         GGVFDRDTSLIAVISVYAAMMSVLNX
              250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1701>:

g570.seq..

```

1  atgatecgtt tgaccgcgc gtttgccgcc gccctgacgt gtttatgctg
51  caccacagcg gcgcacgcgc acaccttcca aaaaatcggc tttatcaaca
101 ccgagcgcat ctacctcgaa tccaagcagg cgcgcaacat ccaaaaaacg
151 ctggacggcg aattttccgc ccgtcaggac gaattgcaaa aactgcaacg
201 cgaaggcttg gattttgaaa ggcagctcgc cggcggcaaa cttaggacg
251 caaaaaagcg gcaagccgaa gaaaaatggc gcgggctggt cgaagcgctt
301 cgcaaaaaac aggcgcagtt tgaagaagac tacaacctcc gccgcaacga
351 agagtttgcc tccctccagc aaaacgcaa cgcgctcatc gtcaaaatcg

```

401 ccaaacagga aggttacgat gtcattttgc aggacgtgat ttacgtcaac
 451 acccaatagc acgttaccga cagcgtcatt aaagaaatga acgcccgtg
 501 a

This corresponds to the amino acid sequence <SEQ ID 1702; ORF 570.ng>:

g570.pep..

1 MTRLTRFAAA ALIGLCCTTG AHADTFQKIG FINTERIYLE SKQARNIQKT
 51 LDGEFSARQD ELQKLQREGL DLERQLAGGK LKDAKKAQAE EKWRGLVEAF
 101 RKKQAQFEED YNLRNNEEFA SLQQNANRVI VKIAKQEGYD VILQDVIYVN
 151 TQYDVTDSVI KEMNAR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1703>:

m570.seq..

1 ATGACCCGTT TGACCCGCGC GTTTGCCGCG GCTCTGATCG GTTTGTGCTG
 51 CACCGCAGGC GCGCACGCCG ACACCTTCCA AAAAATCGGC TTTATCAACA
 101 CCGAGCGCAT CTACCTCGAA TCCAAGCAGG CGCGCAAGAT TCAAAAAACG
 151 CTGGACAGCG AATTTTCCGC TCGTCAGGAC GAATTGCAAA AACTGCAACG
 201 CGAAGGTCTG GATTTGGAAA GGCAGCTTGC CGAAGGCAAA CTCAGAAACG
 251 CAAAAAAGGC GCAAGCCGAA GAAAAATGGC GCGGGCTGGT CGCAGCGTTC
 301 CGCAAAAAAC AGGCGCAGTT TGAAGAAGAC TACAACCTCC GCCGCAACGA
 351 AGAGTTTGCC TCCCTCCAGC AAAACGCCAA CCGCGTCATC GTCAAAATCG
 401 CCAAACAGGA AGGTACGAT GTCATTTTGC AGAACGTGAT TTACGTCAAC
 451 ACCCAATACG ACGTTACCGA CAGCGTCATT AAAGAAATGA ACGCCCGCTG
 501 A

This corresponds to the amino acid sequence <SEQ ID 1704; ORF 570>:

m570.pep

1 MTRLTRFAAA ALIGLCCTAG AHADTFQKIG FINTERIYLE SKQARKIQKT
 51 LDSEFSARQD ELQKLQREGL DLERQLAEGK LRNAKKAQAE EKWRGLVAAF
 101 RKKQAQFEED YNLRNNEEFA SLQQNANRVI VKIAKQEGYD VILQNVYVN
 151 TQYDVTDSVI KEMNAR*

m570/g570 94.6% identity in 166 aa overlap

	10	20	30	40	50	60
m570.pep	MTRLTRFAAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTLDSEFSARQD					
g570	MIRLTRFAAAALIGLCCTTAGAHADTFQKIGFINTERIYLESKQARNIQKTLDGEFSARQD					
	10	20	30	40	50	60
m570.pep	ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAPRKKQAQFEEDYNLRNNEEFA					
g570	ELQKLQREGLDLERQLAGGKLRDAKKAQAEKWRGLVEAFRKKQAQFEEDYNLRNNEEFA					
	70	80	90	100	110	120
	130	140	150	160		
m570.pep	SLQQNANRVIVKIAKQEGYDVILQNVYVNTQYDVTDSVIKEMNARX					
g570	SLQQNANRVIVKIAKQEGYDVILQDVIYVNTQYDVTDSVIKEMNARX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1705>:

a570.seq

1 ATGACCCGTT TGACCCGCGC GTTTGCCGCG GCTCTGATCG GTTTGTGCTG
 51 CACCGCAGGC GCGCACGCCG ACACCTTCCA AAAAATCGGC TTTATCAACA
 101 CCGAGCGCAT CTACCTCGAA TCCAAGCAGG CGCGCAAGAT TCAAAAAACG
 151 CTGGACAGCG AATTTTCCGC CCGCCAGGAC GAATTGCAAA AACTGCAACG
 201 CGAAGGTCTG GATTTGGAAA GGCAGCTTGC CGAAGGCAAA CTCAAAGACG
 251 CAAAAAAGGC GCAAGCCGAA GAAAAATGGT GCGGGCTGGT CGCAGCGTTC
 301 CGCAAAAAAC AGGCGCAGTT TGAAGAAGAC TACAACCTCC GCCGCAACGA
 351 AGAGTTTGCC TCCCTCCAGC AAAACGCCAA CCGCGTCATC GTCAAAATCG
 401 CCAAACAGGA AGGTACGAT GTCATTTTGC AGGACGTGAT TTACGTCAAC
 451 ACCCAATACG ACGTTACCGA CAGCGTCATT AAAGAAATGA ACGCCCGCTG

501 A

This corresponds to the amino acid sequence <SEQ ID 1706; ORF 570.a>:

```
a570.pep
  1  MTRLTRAFAA ALIGLCCTAG AHADTFQKIG FINTERIYLE SKQARKIQKT
 51  LDSEFSARQD ELQKLQREGL DLERQLAEGK LKDAKKAQAE EKWCGLVAAF
101  RKKQAQFEED YNLRNNEEFA SLQQNANRVI VKIAKQEGYD VILQDVIYVN
151  TQYDVTDSVI KEMNAR*
```

m570/a570 97.6% identity in 166 aa overlap

	10	20	30	40	50	60
m570.pep	MTRLTRAFAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTLDSEFSARQD					
a570	MTRLTRAFAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTLDSEFSARQD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m570.pep	ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRNNEEFA					
a570	ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRNNEEFA					
	70	80	90	100	110	120
	130	140	150	160		
m570.pep	SLQQNANRVIVKIAKQEGYDVILQNVIVNTQYDVTDSVIKEMNARX					
a570	SLQQNANRVIVKIAKQEGYDVILQNVIVNTQYDVTDSVIKEMNARX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1707>:

```
g571.seq (partial)
  1  atgcgcgttt tccgagtaaa ccgatttggt gttaccggtt tcggcgggcgg
 51  tataggttct gccgtccac acgctgcctg cgtcggcaaa cagggtcagg
101  cggacggtgc gtgcgtcttt cgcaccgggc atcgggaaga gcagctcggc
151  ggagacgttg gctttttgtg tgcgcgcgta gctgattttt tcgcgcgtatt
201  cgtcatacac ttccgggccc agcgtgccgc ttctgtagcc gcgcaccgaa
251  cccaggccgc cgccgtagaa gttttcaaag aaggggattt ctttggttct
301  gccgtagccg cccgcaatgc cgacttcgcc gccgagcatc agcgtgaagg
351  ttttgct...
```

This corresponds to the amino acid sequence <SEQ ID 1708; ORF 571.ng>:

```
g571.pep (partial)
  1  MRVFRVNRV VTFVGGGIGS AVPHAACVGK QAQADGACVF RTGHREEQLG
 51  GDVGFFVAHV ADFFAVFVIH FRAERAAVFA AHRTQAAAVE VFKEGDFFGS
101  AVAARNADFA AEHQREGFA...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1709>:

```
m571.seq
  1  ATGGGTATTG CCGGCGCCGT AAATGTTTGT AACCCCTGCCG CCGGTCGCGG
 51  AACTGCTGTT GTCGTCGTAG GTTTTGCCGT CCCACACGCT GCCTGCGTCG
101  GCAAACAGGC TCAGGCGGAC GGTGCGCGCG TCTTTCGCGC CGGGCATCGG
151  GAAGAGCAGC TCGGCGGAGA CGTTGGCTTT TTTGTTGCCG CCGTAGCTGA
201  TTTTTCGCCG GTATTTCGTA TAGACTTTCG GACCGAGCGT GCCGCTTTCG
251  TATCCGCGCA CCGAACCCAG GCCGCCGCCG TAGAAGTTT CAAAGAAGGG
301  GATTTCTTTG GTTCTGCCGT AGCCGCCCGC AATGCCGACT TCGCCGCCGA
351  GCATCAGCGT GAAGGTTTTG CTCAGGGGGA AGAACAGGT TTGTTGTGG
401  GTGGCGGAGT AGTATTGCAG TTGCTGCCA GGCAGGGCGA TTTCGGCGTT
451  CACGCCCGTC AGGTAGCCGC GCGTCGGCCA TAA
```

This corresponds to the amino acid sequence <SEQ ID 1710; ORF 571>:

```
m571.pep
  1  MGIAGAVNVL NPAAGRGTAV VVVGFAVPHA ACVGKQAQAD GARVFRAGHR
 51  EEQLGGDVGF FVAADVFFA VFVIDFRTER AAFVSAHRTQ AAAVEVFKEG
101  DFFGSAVAAR NADFAAEHQE EGFAQGEFPG LVVGGGVVLQ FAARQGDFFG
151  HARQVAARRP *
```

m571/q571 93.1% identity in 102 aa overlap

```

              10      20      30      40      50      60
m571.pep    MGIAGAVNVLPAAAGRTAVVVVGFAVPHAACVGKQAQADGARVFRAGHREEQLGGDVG
              :| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g571         MRVFRVNRFFVTVFGGGIGSAVPHAACVGKQAQADGACVFRTGHREEQLGGDVG
              10      20      30      40      50
              70      80      90      100     110     120
m571.pep    FVAAVADFFAVFVIDFRTERAAFVSAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQ
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g571         FVAAVADFFAVFVIHFRAERAAFVAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQ
              60      70      80      90      100     110
              130     140     150     160
m571.pep    EGFAQGEEPLVVGGVVLQFAARQGDGFVHARQVAARRPX
              |||
g571         EGFA
              119

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1711>:

```
a571.seq
1  ATGGGTATTG CCGGCGCCGT AAATGTTTTG AACCTGCCG CCGGTGCGGG
51  AACTGCTGTT GTCGTCGTAG GTTTTGCCGT CCCACACGT GCCTGCGTCG
101 GCAAACAGGC TCAGCGCGAG GGTGCGCGCG TCTTTCGCGC CGGCTACGCG
151 GAAGAGCAGC TCGGCGGAGA CGTTGGCTTT TTTGTTGCCG CCGTAGCTGA
201 TTTTTTCGCC GTATTCTGTC TACACTTTCG GACCGAGCGT GCCGCTTTCG
251 TATCCGCGCA CCGAACCCAG GCCGCCGCCG TAGAAGTTTT CAAAGAAGGG
301 GATTTCTTTG GTTCTGCCGT AGCCGCCCGC AATGCCGACT TCGCCGCCGA
351 GCATCAGCGT GAAGGTTTTG CTTAAGGGGA AGAACAGGT TTGGTTGTGG
401 GTGGCGGAGT AGTATTGCAG TTTGCTGCCG GGCAGGGCGA TTTCCGCGTT
451 CACGCCCGTC AGGTAGCCGC CGCTCGGCCA TAA
```

This corresponds to the amino acid sequence <SEQ ID 1712; ORF 571.a>:

```
a571.pep
1  MGIAGAVNVL NPAAGRGTAV VVVGFAVPHA ACVKGQAQAD GARVFRAGHR
51  EEQLGGDVGF FVAAVADFFA VFVIHFRTER AAFVSAHRTQ AAAVEVFKEG
101 DFFGSAVAAR NADFAAEHQE EGFA*GEEPG LVVGGGVVLQ FAAGQGDFGV
151 HAROVAARRP *
```

m571/a571 98.1% identity in 160 aa overlap

	10	20	30	40	50	60
m571.pep	MGIAGAVNVLNPAAGRGTAVVVVGFAVPHAACVGKQAQADGARVFRAGHREEQLGGDVGF					
a571	MGIAGAVNVLNPAAGRGTAVVVVGFAVPHAACVGKQAQADGARVFRAGHREEQLGGDVGF					
	10	20	30	40	50	60
m571.pep	70	80	90	100	110	120
	FVAAVADFFFAVFVIDFRTERAAAFVSAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQR					
a571	FVAAVADFFFAVFVIHFRTERAAAFVSAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQR					
	70	80	90	100	110	120
m571.pep	130	140	150	160		
	EGFAQGEEPGLVVGGGVVLQFAARQGDFGVHARQVAARRPX					
a571	EGFAXGEEPGLVVGGGVVLQFAAGQGDFGVHARQVAARRPX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1713>:

g572.seq..

```

1  atgtgcgcca tgcgtcggggc ggccggggctg ccttccgcgc tcgcagcggc
51  gcaaaaagggc aaaaccattt atctggcaaa caaagaaacg ctggtggttt
101 ccggcgcggtt gtttatggaa accgcccgcg caaacggcgc ggcagtgttg
151 cccgtcgaca gcgaacacaa cgccattttc caagttttgc cgcgcgatta
201 cacagaccgt ctgaacgaac acggcatcga ttcgattatc ctgaccgctt
251 ccggcgggccc gtttttaaca accgatttaa gcacgttcga cagcattacg
301 cccgagcagg cggtcaaaca cccaattgg cgtatggggc gcaaaatctc
351 cgtcgattca gccactatgg caaacaaggg cttggaactg attgaagcgc
401 attggtgtgt caactgtccg cccgacaaac tcgaagtcgt catccatccc
451 caatccgtga tacacagtat ggtgcgctac cgcgacggct ccgtgctggc
501 gcaactggggc aatcccgata tgcgaacgcc catcgcttat tgtttgggct
551 tgcccagagcg catcgattcg ggtgtcggca aactcgattt cggcgcatcg
601 tccgcgctga ccttccaaaa gcccgacttc ggccgcttcc cctgcctgaa
651 gttcgcttat gaaaccataa acgcaggcgg agccgcgccc tgcgtattga
701 acgcgcgcaa cgaaaccgcc gtcgcccgtt ttttgacgg acagattaag
751 tttaccgaca ttgccaaaac cgtcgcccac tgtcttgcac aagacttttc
801 aaacggcatg ggcgatatag aaggactgtt ggcgcaagat gcccggacac
851 gcgcacaagc gcgggcattt atcggcacac tgcgctga

```

This corresponds to the amino acid sequence <SEQ ID 1714; ORF 572.ng>:

g572.pep..

```

1  MCAIVGAAGL PSALAAQKG KTIYLANKET LVVSGALFME TARANGAAVL
51  PVDSEHNAIF QVLPRDYDTR LNEHGIDSII LTASGGPFLT TDLSFDSTIT
101 PEQAVKHPNW RMGRKISVDS ATMANKGLEL IEAHWLFNCP PDKLEVVIHP
151 QSVIHSVMRY RDGSVLAQLG NPD MRTPIAY CLGLPERIDS GVGKLDLFDAL
201 SALTFAQPDF GRFPCLKFAY ETINAGGAAP CVLNAANETA VAAFLDGQIK

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1715>:

m572.seq..

```

1  ATGTGCGCCA TCGTCGGGGC GGTGGGGCTG CCTTCCGCGC TCGCAGCGGC
51  GCAAAAAGGC AAAACCATT TCTGGCAAA CAAAGAAACG CTGGTGGTTT
101 CCGCGCGGTT GTTTATGGAA ACCGCCGTG CAAACGGCGC GGCAGTGCTG
151 CCGGTCGACA CGAACACAA CGCCGTTTTT CAAGTTTTGC CGCGCGATTA
201 CCGCGGCCGT CTGAACGAAC ACGGCATCGC TTCGATTATC CTGACCGCTT
251 CCGCGGGCCC GTTCTGACC GCCGATTAA ACACGTTTCA CCGCATTACG
301 CCGCCCCAAG CGGTCAAACA CCCCATTGG CGTATGGGAC GCAAAATCTC
351 CGTCGATTCC GCCACCATGA TGAACAAAGG TTTGGAGCTG ATTGAAGCGC
401 ATTGGCTGTT CAACTGTCCG CCGACAAAC TCGAAGTCGT CATCCATCCG
451 CAATCCGTGA TACACAGCAT GGTGCGCTAC CGCGACGGCT CCGTGCTGGC
501 GCAACTGGGC AATCCCGATA TGCGAACGCC CATCGCTTAT TGTTTGGGTT
551 TGCCCGAGCG CATCGATTCT GGTGTCGGCG ACCTGGATT TCGACGCATTG
601 TCCGCGCTGA CCTTCCAAA GCCCGACTTT GACCGCTTCC CCGCTGAG
651 GCTGCGCTAT GAAGCCATGA ACGCAGGCGG AGCCGCGCCC TCGGTATTGA
701 ACGCCGCCAA CGAAGCCGCC GTCGCCGCT TTTTGACGG ACAGATTAAG
751 TTTACCGACA TTGCCAAAC CGTCGCCAC TGTCTTGAC AAGACTTTTC
801 AGACGGCATA GGCATATAG GGGGCTCTT GCGCAAGAT GCCCGACAC
851 GCGACAAGC GCGAGCATT ATCGGCACAC TCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1716; ORF 572>:

m572.pep..

```

1  MCAIVGAVGL PSALAAQKG KTIYLANKET LVVSGALFME TARANGAAVL
51  PVDSEHNAVF QVLPRDYAGR LNEHGIASII LTASGGPFLT ADLNTFDRIT
101 PAQAVKHPNW RMGRKISVDS ATMANKGLEL IEAHWLFNCP PDKLEVVIHP
151 QSVIHSVMRY RDGSVLAQLG NPD MRTPIAY CLGLPERIDS GVGDLDFDAL
201 SALTFAQPDF DRFPCLRLAY EAMNAGGAAP CVLNAANEAA VAAFLDGQIK
251 FTDIKTVAH CLAQDFSDGI GDIGLLAQD ARTRAQARAF IGTLR*

```

m572/g572 92.9% identity in 295 aa overlap

```

          10      20      30      40      50      60
m572.pep  MCAIVGAVGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAAVL PVDSEHNAVF
          |||
g572       MCAIVGAAGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAAVL PVDSEHNAIF
          |||

          70      80      90     100     110     120
m572.pep  QVLPRDYAGRLNEHGIASII LTASGGPFLTADLNTFDRITPAQAVKHPNWRMGRKISVDS
          |||
g572       QVLPRDYDTRLNEHGIDSII LTASGGPFLTDLSTFDSITPEQAVKHPNWRMGRKISVDS
          |||

```

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	70	80	90	100	110	120
m572 . pep	130	140	150	160	170	180
	ATMMNKGLELIEAHWLFNCPPDKLEVVIHPQSVIHSMVRYRDGSVLAQLGNPDMRTP	IAAY				
g572	ATMANKGLELIEAHWLFNCPPDKLEVVIHPQSVIHSMVRYRDGSVLAQLGNPDMRTP	IAAY				
	130	140	150	160	170	180
m572 . pep	190	200	210	220	230	240
	CLGLPERIDSGVGDLDFDALSALTFOKPDFDRFPCLRLAYEAMNAGGAAPCVLNAANEAA					
g572	CLGLPERIDSGVGKLDLFGALSALTFOKPDFGRFPCLKFAYETINAGGAAPCVLNAANETA					
	190	200	210	220	230	240
m572 . pep	250	260	270	280	290	
	VAAFLDGQIKFTDIAKTVAHCLAQDFS	SDGIGDIGLLAQDARTRAQARAFIGTLRX				
g572	VAAFLDGQIKFTDIAKTVAHCLAQDFS	SNMGMDIEGLLAQDARTRAQARAFIGTLRX				
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1717>:

```
a572.seq
1 ATGTGCGCCA TCGTCGGGGC GGTGGGGCTG CCTTCCGCGC TCGCAGCGGC
51 GCAAAAAAGG AAAACCATTT ATCTGGCGAA CAAAGAGACG CTGGTGGTTT
101 CCGGCGCGTT GTTTATGGAA ACCGCCGTG CAAACGGCGC GGCAGTGCTG
151 CCCGTCGACA GCGAACACAA CGCCGTTTTT CAAGTTTTGC CGCGCGATTA
201 CACAGGTCGC CTGAACGAAC ACGGCATCGC TTCGATTATC CTGACCGCTT
251 CCGGCGGCCC GTTCTGACC GCCCAATTTA ACACGTTCGA CAGCATTACG
301 CCCGACCAAG CGGTCAACAA CCCCATTGG CGTATGGGAC GCAAATCTC
351 CGTCGATTCC GCCACCATGA TGAACAAAGG TTTGGAGCTG ATTGAAGCGC
401 ATTGGCTGTT CAACTGTCCG CCCGACAAAC TCGAAGTCGT CATCCATCCG
451 CAATCTGTGA TACACAGCAT GGTGCGCTAC CGCGACGGCT CCGTGTGGGC
501 GCAACTGGGC AATCCCGATA TCGAACCGCC TATCGATTAT TGTTTGGGTT
551 TGCCCGAGCG CATCGATTCC GGTGTCGGCG ACCTGGAATT GACGCATTG
601 TCCGCGCTGA CCTTCCAAA GCCCGACTTT ACCGCTTCC CCTGCCTGAA
651 GCTCGCCTAT GAAGCCATGA ACGCAGGCGG AGCCGCGCCC TCGTATTGA
701 ACGCCGCCAA CGAAGCCGCC GTCGCCGCCT TTTTGGACGG ACAGATTAAG
751 TTTACCGACA TTGCCAAAAC CGTCGCCCAT TGTCTTTTAC AAGACTTTTC
801 AGACGCGATA GGCACATAG GGGGCTCTTT GCGCGAAGAT GCCCGGACAC
851 GCGCACAAAG CGGGGCATTT ATCGGCACAC TCGCGTGA
```

This corresponds to the amino acid sequence <SEQ ID 1718; ORF 572.a>:

a572.pep

1	MCAIVGAVGL	PSALAAQKG	KTIYLANKET	LVVSGALFME	TARANGAAVL
51	PVDSEHNAVF	QVLPRDYTGR	LNEHGIASII	LTASGGPFLT	ADLNTFDSIT
101	PDQAVKHPNW	RMGRKISVDS	ATMMNKGLEL	IEAHWLFNCP	PDKLEVVIHP
151	QSVIHSVMRY	RDGSVLAQLG	NPDMRTPIAY	CLGLPERIDS	GVGDFLDFDAL
201	SALTFOKPDF	DRFSPCLKLY	EAMNAGGAAP	CVLNAANEAA	VAAFLDGGQIK
251	FTDIAKTVAH	CLKSQDFSDGI	GDIGGLLAQD	ARTRAQARAF	IGTLR*

m572/a572 98.3% identity in 295 aa overlap

	10	20	30	40	50	60
m572.pep	MCAIVGAVGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAAVLVPDSEHNAVF					
a572	MCAIVGAVGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAAVLVPDSEHNAVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m572.pep	QVLPRDYAGRLNEHGSIILTASGGPFLTADLNTFDRITPAQAVKHPNWRMGRKISVDS					
a572	QVLPRDYTGRLNEHGSIILTASGGPFLTADLNTFDSITPDQAVKHPNWRMGRKISVDS					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m572.pep	ATMMNKGLELIEAHWLFNCPDPKLEVVIHPQSVIHSMVRYRDGSLAQLGNPDMRTPIAY					
a572	ATMMNKGLELIEAHWLFNCPDPKLEVVIHPQSVIHSMVRYRDGSLAQLGNPDMRTPIAY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m572.pep	CLGLPERIDSGVGDLDFDALSALTFQKPDFDRFPCLRLAYEAMNAGGAAPCVLNAANEAA					
a572	CLGLPERIDSGVGDLDFDALSALTFQKPDFDRFPCLRLAYEAMNAGGAAPCVLNAANEAA					
	190	200	210	220	230	240
	250	260	270	280	290	
m572.pep	VAAFLDGQIKFTDIAKTVAHCLAQDFSDGIGDIGLLAQDARTRAQARAFIGTLRX					
a572	VAAFLDGQIKFTDIAKTVAHCLSQDFSDGIGDIGLLAQDARTRAQARAFIGTLRX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1719>:

g573.seq..

```

1  atgccctgtt tgtgccgcct taatcgcaat atcggcagtt tccaaatcac
51  gaatctcacc gaccataatg atgtccgggt cctgacgcag gaaagacttc
101 aaagcagcgg caaaagtcag accctgctta tcattgacgt taacctgatt
151 gatgcccgcc aggttaatct cggcagggtc ttccgccgtt gcaatattta
201 ccgactccgt attcaaaata ttcaaacagg tatagagcga caccgtctta
251 cccgaacccg tcggaccggt taccagcacc atcccgtaag gacggtgaat
301 cgcttccaac aacaattttt tctggaacgg ctcaaaacgg agctggtcga
351 tgttcaaaga cgcggcatcg gaattcaaaa tccgcatcac gaccttttcg
401 ccaaacagcg tcggcaatgt gctgacacgg aaatcgacag gcttgccgcc
451 cttttgaaag gtcagctgca tcctaccgtc ctgcggtatc cgtttttcgg
501 aaatgtccaa acgcgacatt accttaatcc ggaagcaag ctgccccctt
551 accgcaatgg gcggctgaac caccctcgcg agctgcccgt ccacacggaa
601 acggatacgc gcatttgtgt cgtaaaactc gaaatggatg tcggatgccc
651 cgctacgcaa ggcacccgac aaagttttat ggataaacct cggaaacaggg
701 cgtctctctc cctcctcgtc gtcgatatac aggggtgtggc ttctctcttc
751 ctcttgcccc tccccaaagt cctgaagcag cgatgtcgaa cgcgaacca
801 cccaatcgag caaacccgcc aactgggtcat cctcgacaat gaccaactca
851 accgcaatcc ctgcggcaga aaccgttttc tgaatttgcg gcactctgggt
901 cggatcgcaa accgcaaaaa atactttgtc gccccacggc aaaaccggca
951 cacagtggaa ctccaccatc tgctcctcgg tcaacacccc catcagcacc
1001 ctgtggcgcg gataatgacg caaatcaaga atcgaataac tgaacaccct
1051 cgcaatcaat gccgcaagcg acttgggcga aatgacacgg tctga

```

This corresponds to the amino acid sequence <SEQ ID 1720; ORF 573.ng>:

g573.pep..

```

1  MPCLCLRLNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ TLLIIDVNLI
51  DARQVNLGRV FRRCNIYRLR IQNIQTGIER HRLTRTRRTG YQHPVVRTVN
101 RFQQQFFLER LKTELVDVQR RGIGIQNPHH DLFAKQRRQC ADTEIDRLAA
151 LLKGQLHPTV LRYPPFGNVQ TRHYLNPGSK LPPYRNGRLN HLAELPVHTE
201 TDTRIVFVKL EMDVGCPATQ GIRQSFMDKP RNRAVFCLLV VDIQGVAFLE
251 LLPLPKLLKQ RCRTTRHPIE QTRQLVILDN DQLNRNFCGR NREFNLRLHLG
301 RIGNRKKYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1721>:

m573.seq..

```

1  ATGCCCTGTT TGTGCCGCCT TAATCGCAAT ATCGGCAGTT TCCAAATCAC
51  GAATCTCACC GACCATAATG ATGTCCGGGT CCTGACGCAG GAAAGACTTC
101 AAAGCAGCGG CAAAAGTCAG GCCCTGCTTA TCATTGACGT TAACCTGATT
151 GATGCCCGGC AGGTTAATCT CGGCAGGGTC TTCCGCCGTT GCAATATTTA
201 CCGACTCCGT ATTCAAAATA TTCAAACAGG TATAGAGCGA CACCGTCTTA
251 CCCGAACCCG TCGGACCGGT TACCAGCACC ATCCCGTAGG GACGGTGAAT
301 CGCTACCAAC aCaw_TTTT TCTGAAACGG CTCAAACCG AGCTGGTCGA
351 TGTTCAAAGA CGCGGCATCG GAATTCAAAA TCCGCATCAC GACCTTTTCG
401 CCAAACAGCG TCGGCAATGT GCTGACACGG AAATCGACAG GCTTGCCGCC
451 CTTTGTAAAG GTCAGCTGCA TCCTGCCGTC CTGCGGTATC CGTTTTTCGG
501 AAATGTCCAA ACGCGACATT ACCTTAATCC GTGAAGCAAG CTGCCCCCTT

```

```
551 ACCGCAATGG GCGGCTGAAC CACCTCGCGG AGCTGCCCGT CCACACGGAA
601 ACCGATACGG GCATTGTGTT CGTAAACTC GAAATGGATG TCCGATGCCC
651 CGCTGCGCAA GGCATCCGAC AAAGTCTTAT GGATAAACCT CGGAACAGGG
701 CCGTCTTCTG CCTCCTCGTT GTCGATATAC AGGGTGTGGC TTTCTCTTTC
751 CTCCTGCCCC TCCCCAAGCT CCTGAAGCAG CGATGTCGAA CGCGAACCCA
801 CCCAATCGAG CAAACCCGCC AACTGGTCAT CCTCGACAAT GACCAACTCA
851 ACCTCAATCC CTGCGGCAGA AACGGTTTTC TGAATTGCG GCATCTGTGT
901 CGGATCGGAA ACCGCAAAAA ATACTTTGTC GCCCCGACGG AAAACCGGCA
951 CACAGTGGAA CTCCACCATC TGCTCCTCCG TCAACACCCC CATCAGCACC
1001 CTGTGGCGCG GATAATGACG CAAATCAAGA ATCGAATAAC TGAACACCCT
1051 CGCAATCAAT GCCGCAAGCG ACTTGGGCGA AATGACACCG TCTGA
```

This corresponds to the amino acid sequence <SEQ ID 1722; ORF 573>:

m573.pep..

```
1 MPCLCRLNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ ALLIIDVNLI
51 DARQVNLGRV FRRCNLYRLR IQNIQTGIER HRLTRTRRTG YQHHPVGTVN
101 RYQHXFFLKR LKTELVDVQR RGIGIQNPHH DLFAKQRRQC ADTEIDRLAA
151 LLKGQLHPAV LRYPFPGNVQ TRHYLNP*SK LPPYRNGRLN HLAELPVHTE
201 TDTGIVFVKL EMDVRCPAAG GIRQSLMDKP RNRAVFCLLV VDIQGVAFLE
251 LLPLPKLLKQ RCRTRTHPIE QTRQLVILDN DQLNLNPGCR NGFLNLRHLC
301 RIGNRKKYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*
```

m573/g573 95.9% identity in 364 aa overlap

	10	20	30	40	50	60
m573.pep	MPCLCRLNRNIGSFQITNLT	DHNDVRVLTQERLQSSGKSQ	ALLIIDVNLI	DARQVNLGRV		
g573	MPCLCRLNRNIGSFQITNLT	DHNDVRVLTQERLQSSGKSQ	LLIIDVNLI	DARQVNLGRV		
	10	20	30	40	50	60
	70	80	90	100	110	120
m573.pep	FRRCNLYRLRIQNIQTGIER	HRLTRTRRTGYQHHPVGT	VNRYQHXFFLKR	LKTELVDVQR		
g573	FRRCNLYRLRIQNIQTGIER	HRLTRTRRTGYQHHPV	RTVNRFFQQFFLER	LKTELVDVQR		
	70	80	90	100	110	120
	130	140	150	160	170	180
m573.pep	RGIGIQNPHHDLFAKQRRQC	ADTEIDRLAALLKGQLHP	AVLRYPFPGNVQ	TRHYLNPXSK		
g573	RGIGIQNPHHDLFAKQRRQC	ADTEIDRLAALLKGQLH	PTVLRYPFPGNVQ	TRHYLNPGSK		
	130	140	150	160	170	180
	190	200	210	220	230	240
m573.pep	LPPYRNGRLNHLAELPVHT	ETDTGIVFVKLEMDVRC	PAAQGIRQSLMDKPR	NRRAVFCLLV		
g573	LPPYRNGRLNHLAELPVHT	ETDTRIVFVKLEMDVGC	PATQGIQSFMDKPR	NRRAVFCLLV		
	190	200	210	220	230	240
	250	260	270	280	290	300
m573.pep	VDIQGVAFLELLPLPKLLK	QRCRTRTHPIEQTRQLV	ILDNDQLNLNPGCR	NGFLNLRHLC		
g573	VDIQGVAFLELLPLPKLLK	QRCRTRTHPIEQTRQLV	ILDNDQLNRNPGCR	NRFNLRHLG		
	250	260	270	280	290	300
	310	320	330	340	350	360
m573.pep	RIGNRKKYFVAPTENRHTV	ELHLLLRQHPHQHPVAR	IMTQIKNRITEHP	RNQCRKRLGR		
g573	RIGNRKKYFVAPTENRHTV	ELHLLLRQHPHQHPVAR	IMTQIKNRITEHP	RNQCRKRLGR		
	310	320	330	340	350	360
m573.pep	NDTVX					
g573	NDTVX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1723>:

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a573.seq

```

1   ATGCCCTGTT TGTGCCGCCT TAATCGCAAT ATCGGCAGTT TCCAAATCAC
51  GAATCTCACC GACCATAATG ATGTCCGGGT CCTGACGCAG GAAAGACTTC
101 AAAGCAGCGG CAAAAGTCAG ACCCTGCTTA TCATTGACGT TAACCTGATT
151 GATGCCCGGC AGGTTAATCT CGGCAGGGTC TTCCGCCGTT GCAATATTTA
201 CCGACTCCGT ATTCAAAATA TTCAAACAGG TATAGAGCGA CACCGTCTTA
251 CCCGAACCCG TCGGACCGGT TACCAGCACC ATCCCCTAGG GACGGTGAAT
301 CGCTTCCAAC AACAATTTT TCTGAAACGG CTCAAACCG AGCTGGTCTGA
351 TGTTCAAAGA CGCGGCATCG GAATTCAAAA TCCGCATCAC GACCTTTTCG
401 CCAAACAGCG TCGGCAATGT GCTGACACGG AAATCGACAG GCTTGCCGCC
451 CTTTTGAAAG GTCAGCTGCA TCCTGCCGTC CTGCGGTATC CGTTTTTCGG
501 AAATGTCCAA ACGCGACATT ACCTTAATCC GGGAAGCAAG CTGCCCCCTT
551 ACCGCAATGG GCGGCTGAAC CACCTCGCGG AGCTGCCCCT CCACACGGAA
601 ACGGATACGG GCATTGTGTT CGTAAACTC GAAATGGATG TCCGATGCCC
651 CGCTGCGCAA GGCATCCGAC AAAGTCTTAT GGATAAACCT CGGAACAGGG
701 CCGTCTTCTG CCTCCTCGTT GTCGATATAC AGGGTGTGGC TTTCTCTTC
751 CTCCTGCCCC TCCCCAAGCT CCTGAAGCAG CGATGTCGAA CGCGAACCCA
801 CCCAATCGAG CAAACCCGCC AACTGGTCAT CCTCGACAAT GACCAACTCA
851 ACCTCAATCC CTGCGGCAGA AACGGTTTTT TGAATTTGCG GCATCTGTGT
901 CGGATCGGAA ACCGCAAAA ATACTTTGTC GCCCCGACGG AAAACCGGCA
951 CACAGTGGAA CTCCACCATC TGCTCCTCCG TCAACACCCC CATCAGCACC
1001 CTGTGGCGCG GATAATGACG CAAATCAAGA ATCGAATAAC TGAACACCCT
1051 CGCAATCAAT GCCGCAAGCG ACTTGGGCGA AATGACACCG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1724; ORF 573.a>:

a573.pep

```

1   MPCLCRLNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ TLLIIDVNLI
51  DARQVNLGRV FRRNCNIYRLR IQNIQTGIER HRLTRTRRTG YQHHPVGTVN
101 RFQQQFFLKR LKTELVDVQR RGIGIQNPHH DLFQKRRQC ADTEIDRLAA
151 LLKGQLHPAV LRYPPFGNVQ TRHYLNPGSK LPPYRNGRLN HLAELPVHTE
201 TDTGIVFVKL EMDVRCPAAG GIRQSLMDKP RNRAVFCLLV VDIQGVAFLE
251 LLPLPKLLKQ RCRTRTHPIE QTRQLVILDN DQLNLNPGCR NGFLNLRHLC
301 RIGNRKKYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*

```

m573/a573 98.6% identity in 364 aa overlap

	10	20	30	40	50	60
m573.pep	MPCLCRLNRNIGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ ALLIIDVNLI DARQVNLGRV					
a573	MPCLCRLNRNIGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ TLLIIDVNLI DARQVNLGRV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m573.pep	FRRNCNIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTNVNRYQHXXFLKRLKTELVDVQR					
a573	FRRNCNIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTNVNRFQQQFFLKRLKTELVDVQR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m573.pep	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFGNVQTRHYLNXPXSK					
a573	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFGNVQTRHYLNPGSK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m573.pep	LPPYRNGRLNHLAELPVHTE TDTGIVFVKLEMDVRCPAAGGIRQSLMDKPRNRAVFCLLV					
a573	LPPYRNGRLNHLAELPVHTE TDTGIVFVKLEMDVRCPAAGGIRQSLMDKPRNRAVFCLLV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m573.pep	VDIQGVAFLELLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
a573	VDIQGVAFLELLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
	250	260	270	280	290	300

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	310	320	330	340	350	360
m573.pep	RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
a573	RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
	310	320	330	340	350	360
m573.pep	NDTVX					
a573	NDTVX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1725>:

g574.seq

```

1  atgctgccga atctgccaaa cagccttaag aaagccgata tggacaacga
51  attgtggatt atcctgctgc cgattatcct tttgcccgtc ttcttcacga
101 tgggctgggt tgcgcgccgc gtggatatga aaaccgtatt gaagcaggca
151 aaaagcatcc cttcgggatt ttataaaagc ctggacgctt tggtcgaccg
201 caacagcggg cgcgcgccaa gggagtggc ggaagtcgtc gacggccggc
251 cgcaatcgta tgatttgaac cttaccctcg gcaaaactta ccgtcagcgc
301 ggcgaaaacg acaaagccat caacatacac cggaacaatgc tcgattctcc
351 cgatccgtgc cgcgaaaagc gcgcgcgcgt cctgtttgaa ttggcgcaaa
401 actaccaaag cgcggtttg gtcgatcgtg ccgaacagat ttttttgggg
451 ctgcaagacg gtgaaatggc gcgtgaagcc agacagcacc tgctcaatat
501 ctaccagcag gacagggatt gggaaaaagc ggttgaaacc gcccaacttc
551 ttagtcacga cgaacagaca tatcagtttg agattgcaca gttttattgc
601 gaacttgccc aagccgcgct gttcaagtcc aatttcgatg ccgcgcgttt
651 caatgtcggc aaggcactcg aagccaacaa aaaatgcacc cgcgccaaca
701 tgattttggg cgacattgaa caccgacaag gcaatttccc tgccgcgcgtc
751 gaagcctatg ccgccatcga gcagcaaaac catgcatact tgagcatggt
801 cggcgagaag ctttacgaag cctatgccgc gcagggaaaa cctgaagaag
851 gcttgaaacc tctgacagga tatatgcaga cgtttcccca acttgacctg
901 atcaatgtcg tgtacgagaa atccctgctg cttaaggggc agaaagaagc
951 cgcgcaaaac ccgctcgagc ttgtccgcgc caagccgcac cttaacggcg
1001 tgtaccgcct gctcggtttg aaactcagcg atttggatcc ggcttggaaa
1051 gccgatgccg acatgatgctg ttcggttatc ggacggcagc tccagcgcag
1101 cgtgatgtac cgttgccgca actgccactt caaatcccaa gtctttttct
1151 ggcactgtcc cgcctgcaac aaatggcaga cgtttacgcc gaataaaatc
1201 gaagtttaa

```

This corresponds to the amino acid sequence <SEQ ID 1726; ORF 574.ng>:

g574.pep..

```

1  MLPNLPNSLK KADMDNELWI ILLPIILLPV FFTMGWFAAR VDMKTVLKQA
51  KSIPSGFYKS LDALVDRNSG RAARELAEV DGRPQSYDLN LTLGKLYRQR
101 GENDKAINIH RTMLDSPDTV GEKRARVLF LAQNYQSAGL VDRAEQIFLG
151 LQDGEAREAR RQHLLNIYQQ DRDWEKAVET AQLLSHDEQT YQFEIAQFYC
201 ELAQALFKS NFDAARFNVG KALEANKKCT RANMILGDI HRQGNFPAAV
251 EAYAAIEQQN HAYLSMVGEK LYEAYAAQ GK PEEGLNRLTG YMQTFPELDL
301 INVVEKSL LKGEKEAAQT AVELVRRKPD LNGVYRLLGL KLSDLDPFAWK
351 ADADMMRSVI GRQLQRSVMY RCRNCHFKSQ VFFWHCPACN KWQTFPNKI
401 EV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1727>:

m574.seq..

```

1  ATGCGCCCGA ATCTACCAA CAGCCTTAAG AAAGCCGATA TGGACAACGA
51  ATTGTGGATT ATCTGCTGCG CGATTATCCT TTTGCCCGTC TTCTTCGCGA
101 TGGGCTGGTT TGCCGCCCGC GTGGATATGA AAACCGTATT GAAGCAGGCA
151 AAAAGCATCC CTTGCGGATT TTATAAAAGC TTGGACGCTT TGGTCGACCG
201 CAACAGCGGG CGCGCGGCAA GGGAGTTGGC GGAAGTCGTC GACGGCCGGC
251 CGCAATCGTA TGATTGAAC CTCACCCTCG GCAAACTTTA CCGCCAGCTC
301 GCGGAAAACG ACAAAGCCAT CAACATACAC CGGACAATGC TCGATTCTCC
351 CGATACGGTC GCGGAAAAGC GCGCGCGCGT CCTGTTTGAA TTGGCGCAAA
401 ACTACCAAAG TGCGGGGTTG GTCGATCGTG CCGAACAGAT TTTTGTGGGG
451 CTGCAAGACG GTAAATGGC GCGTGAAGCC AGACAGCACC TGCTCAATAT
501 CTACCAACAG GACAGGGATT GGGAAAAAGC GGTGAAACC GCCCGGCTGC
551 TCAGCCATGA CGATCAGACC TATCAGTTTG AAATCGCCCA GTTTTATTGC
601 GAACCTGCCC AAGCGCGCTG GTTCAAGTCC AATTCGATG TCGCGCGTTT

```


m574.pap..

1	MRPNLPNSLK	KADMDNELWI	ILLPIILLPV	FFAMGWFAAR	VDMKTVLKQA
51	KSIPSGFYKS	LDALVDRNSG	RAARELAEVU	DGRPQSYDLN	L7LGLKLYRQR
101	GENDKAINIH	RTMLSDPDTV	GKEARVLFE	LAQNYQSAGL	VDRAEQIFLG
151	LQDQGMARE	QRHLLNIYQQ	DRDWEKAVTE	ARLLSHDDQT	YQFEIAFPYC
201	EALQAALFKS	NFDVARFNVG	KALEANKKCT	RANMILGDIE	HRQGNFPAAV
251	EAYAAIEQQN	HAYLSMVGEK	LYEAYAAQKG	PEEGLNRLTG	YMQTFPELDL
301	INVVYEKSL	LKCEKEAAQT	AVELVRRKPD	LNGVYRLLEL	KLSDMNPAAK
351	ADADMRRSVI	GRQLQRSVMY	RCRNCHFKSQ	VFFWHCPACN	KWQTFTPNKI
401	EV*				

m573/g573 97.8% identity in 402 aa overlap

Date		Time		Place		Remarks	
1911	10/10	10:00	10:15	10:30	10:45	11:00	11:15
1911	10/11	10:00	10:15	10:30	10:45	11:00	11:15
1911	10/12	10:00	10:15	10:30	10:45	11:00	11:15
1911	10/13	10:00	10:15	10:30	10:45	11:00	11:15
1911	10/14	10:00	10:15	10:30	10:45	11:00	11:15
1911	10/15	10:00	10:15	10:30	10:45	11:00	11:15
1911	10/16	10:00	10:15	10:30	10:45	11:00	11:15
1911	10/17	10:00	10:15	10:30	10:45	11:00	11:15
1911	10/18	10:00	10:15	10:30	10:45	11:00	11:15
1911	10/19	10:00	10:15	10:30	10:45	11:00	11:15
1911	10/20	10:00	10:15	10:30	10:45	11:00	11:15
1911	10/21	10:00	10:15	10:30	10:45	11:00	11:15
1911	10/22	10:00	10:15	10:30	10:45	11:00	11:15
1911	10/23	10:00	10:15	10:30	10:45	11:00	11:15
1911	10/24	10:00	10:15	10:30	10:45	11:00	11:15
1911	10/25	10:00	10:15	10:30	10:45	11:00	11:15
1911	10/26	10:00	10:15	10:30	10:45	11:00	11:15
1911	10/27	10:00	10:15	10:30	10:45	11:00	11:15
1911	10/28	10:00	10:15	10:30	10:45	11:00	11:15
1911	10/29	10:00	10:15	10:30	10:45	11:00	11:15
1911	10/30	10:00	10:15	10:30	10:45	11:00	11:15
1911	10/31	10:00	10:15	10:30	10:45	11:00	11:15

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1729>:

```
a574.seq
1  ATGCGCCCGA ATCTGCCAAA CAGCCTTGAG AAAGCCGATA TGGACAATGA
51  ATTGTGGATT ATCCTGCTGC CGATTATCCT TTTGCCCGTT TTCTTCGCGA
101 TGGGCTGGTT TGCCGCCCGC GTGGATATGA AGACTGTATT AAAGCAGGCA
151 AAAAGCATAC CGTCGGGATT TTATAAAAGT CTGGATGCCT TGGTTGACCG
201 CAACAGCGGG CGCGCGGCAA GGGAGTTGGC GGAAGTCGTC GACGCGCGGC
251 CGCAATCGTA TGATTTGAAC CTCACCCTCG GCAAACTTTA CCGCCAGCGT
301 GGCAGAAAACG ACAAAGCCAT CAATATGCAC CAAACATTGC TTGACTCTCC
351 CGATACAACC GGAGCCAAGC GCGCGCGCGT CCTGTTTGAA TTGGCGCAAA
401 ACTACCAAAG TGCGGGGTTG GTCGATCGTG CCGAACAGAT TTTTGGGG
451 CTGCAAGACG GTGAAATGGC GCGTGAAGCC AGACAGCACC TGCTCAATAT
501 CTACCAACAG GACAGGGATT GGGAAAAAGC GGTGAAACC GCCGGCTGTC
551 TCAGCCATGA CGATCAGACC TATCAGTTTG AAATCGCCCA GTTTTATTGC
601 GAAGCTGCCC AAGCCGCGCT GTTCAAGTCC AATTCGATG CCGCGCGTTT
651 CAATGTCGGC AAGGCACTCG AAGCCAACAA AAAATGCACC CGCGCCAACA
701 TGATTTGGG CGACATCGAA CACCGACAAG GCAATTTCCC TGCCGCCGTC
751 GAAGCTATG CCGCCATCGA GCAGCAAAAC CATGCATACT TGAGTATGGT
801 CGGCGAGAAG CTTTACGAAG CCTATGCCGC GCAGGGAAAA CCTGAAGAAG
851 GCTTGAACCG TCTGACAGGA TATATGCAGA CGTTTCCCGA ACTTGACCTG
901 ATCAATGTCG TGTACGAGAA ATCCCTGCTG CTTAAGTGCG AGAAAGAAGC
951 CGCGCAAACC GCCGTCGAGC TTGTCCGCCG CAAGCCCGAC CTCAACGGCG
1001 TGTACGCCT GCTTGGTTTG AAATCAGCG ATTTGGATCC GGCTTGGAAA
1051 GCCGATGCCG ATATGATGCG TTCGGTTATC GGACGGCAGC TACAGCGCAG
1101 CGTGATGTAC CGGTGCCGAA ACTGCCACTT CAAATCACAA GTCTTTTCT
1151 GGCATTGTCC TGCCTGCAAC AAATGGCAGA CGTTTACGCC AAACAAAATC
1201 GAAGTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1730; ORF 574.a>:

```
a574.pep
1  MRPNLPNSLE KADMDNELWI ILLPIILLPV FFAMGWFAAR VDMKTVLKQA
51  KSIPSGFYKS LDALVDRNSG RAARELAEVV DGRPQSYDLN LTLGKLYRQR
101 GENDKAINMH QTLSDSPDTT GAKRARVLFE LAQNYQSAGL VDRAEQIFLG
151 LQDGEMAREA RQHLLNIYQQ DRDWEKAVET ARLLSHDDQT YQFEIAQFYC
201 ELAQAAALFKS NFDAARFNVG KALEANKKCT RANMILGDIE HROGNFPAAV
251 EAYAAIEQQN HAYLSMVGEK LYEAYAAQ GK PEEGLNRLTG YMQTFPELDL
301 INVVYEKSL LKCEKEAAQT AVELVRRKPD LNGVYRLLGL KLSDLDPAWK
351 ADADMRSVI GRQLQRSVMY RCRNCHFKSQ VFFWHCPACN KWQTFTPNKI
401 EV*

m574/a574 97.5% identity in 402 aa overlap

10 20 30 40 50 60
m574.pep MRPNLPNSLKKADMDNELWIIILLPIILLPVFFAMGWFAARVDMKTVLKQAKSIPSGFYKS
a574 MRPNLPNSLEKADMDNELWIIILLPIILLPVFFAMGWFAARVDMKTVLKQAKSIPSGFYKS
10 20 30 40 50 60

70 80 90 100 110 120
m574.pep LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGKLYRQRGENDKAINIHRTMLDSPDTV
a574 LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGKLYRQRGENDKAINMHQTLSDSPDTT
70 80 90 100 110 120

130 140 150 160 170 180
m574.pep GEKRARVLFELAQNYQSAGLVDRAEQIFLGLQDGKMAAREARQHLLNIYQQDRDWEKAVET
a574 GAKRARVLFELAQNYQSAGLVDRAEQIFLGLQDGEMAREARQHLLNIYQQDRDWEKAVET
130 140 150 160 170 180

190 200 210 220 230 240
m574.pep ARLLSHDDQTYQFEIAQFYCYCELAQAALFKSNFDFVARFNVGKALEANKKCTRANMILGDIE
a574 ARLLSHDDQTYQFEIAQFYCYCELAQAALFKSNFDAARFNVGKALEANKKCTRANMILGDIE
```

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	190	200	210	220	230	240
	250	260	270	280	290	300
m574.pep	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQGPKEEGLNRLTGVMQTFPELDL					
a574	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQGPKEEGLNRLTGVMQTFPELDL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m574.pep	INVVYEKSLLLKCEKEAAQTAVELVRRKPDNLNGVYRLLGLKLSDMNPAWKADADMMSVI					
a574	INVVYEKSLLLKCEKEAAQTAVELVRRKPDNLNGVYRLLGLKLSDDLPAWKADADMMSVI					
	310	320	330	340	350	360
	370	380	390	400		
m574.pep	GRQLQRSVMYRCRNCHFKSQVFFWHCPACNKWQTFTPNKIEVX					
a574	GRQLQRSVMYRCRNCHFKSQVFFWHCPACNKWQTFTPNKIEVX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1731>:

```

g575.seq (partial)
1  ..atgccgtgcc tccgccggca agcagcaagg tgtacgaacc gccgaacaga
51  ccgtcaaaaca gtccgcttct ggttctctct tccgcagaaa cctgttcgac
101 aggttcggca acgggttcgg cgcaacttc actggtgtt tccgcaacag
151 gtccggaac ggtgttaccg gtctcgtcgg tcggcggtgc gatggcagaa
201 gcggcggtt cttggggggg cggattcggc agcgggttcc gatgcggcag
251 tatttgcagc ggttacaggc ccgggttggc gttctgtcgc cgaagccgga
301 gtttcggaca ctgcgggtt gggttcgggt cgaacggccg gttttccgc
351 ttttgcttcg ggccgggcaa cttttgcttc aggtttttca accggttttt
401 cgacaggttt ctctatcggc ttctccacag ttgcctgtt ggacggttca
451 gacggcatgg atgcagtttc ggctttgggt ttccgccgtt gcggtttggg
501 ttgttccgct ttgatttttt tgggtgctgc cgctttgatc ctgttcagat
551 tcggaatgtg a*

```

This corresponds to the amino acid sequence <SEQ ID 1732; ORF 575.ng>:

```

g575.pep (partial)
1  ..MPCLRRQAAR CTNRRTDRQT VRFRLLRQK PVRQVRQVR RQLHWLFPPQ
51  VRKRCYRFR SACRWQKRRL LGGADSAAVS DAAVFAAGTG PGWRSVAEAG
101 VSDTAGLGS RTAGFSAFAS GAATFASGFS TGFSTGFSIG FSTVACL DGS
151 DGMDAVSALG FAVCGLGCSA LIFLGAAL LFRFGM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1733>:

```

m575.seq..
1  ATGTTTCGG GCGAGGAAG CTCAGGAAG CCTGCCAGTC CGGAGGGTGA
51  GGCAGGTTTT GCGGAAGCTG TTTCTTCTGT GCCGATATGG TTGTTGAGG
101 GCAGGTTGTC GGAGAAATCG GTATCGACGG TTTCCGGTTT GTTTTCGGCA
151 GTTTGGGCGA CAGATTCCGG TTCGGGCGTG TCGATGACGA TTTCGACAGG
201 GTTGACGGG TTGAAGGTCT CGGGCTCGTA CACGCTGTCT GTGGATTCTA
251 TGGCGTTCCA ATCGGCATCC GCGCGTTTTT GGGTTTCTTC ATCCTGCGTA
301 AGTGCGCCGG ATAAATGCC GTTTTGC GCTGCCAGGC TGTCGAAATC
351 CAAGTCGATG CGGTTGGAAG GCGTATCGGT TTCGACATCG AACGTTGTT
401 TTGCCGATAA CTCTTCTTCA GATTCCCAT CTAAGCAAG TGTGTCGTT
451 ACATCGTTTT TCGGAGCGGG TTCGGGCGTT GCCGGAGTTT CCACTTCGGC
501 AAAGGTGATT TCTATGCCGT CGTCTGCCGC GTCGTCAAGG TCAGGCTCTT
551 CCTCAGGGAC GGATTCTTCG GTACGGCGCG CGCGTTTGA TTGGGCAAGG
601 CGCAAAGCA GCAGCAGGGC GATTAATGCC GCGCTCCGC CGGCAAGCAG
651 CAAGGTGTAT GAACGCCGA ACAGACCGTC AAACAGTCC GTTTCGGTTT
701 CTCTTTCGGC AGAAACCTGT TCGACAGGTT CGGAAACGGC GTTACCGGTT
751 TCGTCGGTCG GCGTGTCTGAT GGCAGAAGCG GCGGCTTCTT GGGGGCGGGA
801 TTCGGCAGCG GTTTCGATG CGGCAGTATT TGCAGCGGGT ACAGGTTTCG
851 TTCGAACGGC CGGTTTTTCC GCTTTTGCTT CGGGCGCGGC AACTTTGCT
901 TCAGGTTTTT CAACCGGTTT CTCTACCGTT GCCTGTTTGG ACGGTTTCGA
951 CGGCATGGAT GCGGTTTCGG CTTTGGGTTT CGCCGTTTGC GTTTGGGTT
1001 GTTCCGCTTT GATCCTGTTC AGATTCCGAA TGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1734; ORF 575>:

m575.pep
 1 MVSGEAEFRK PASPEGEAGF AEAUSSVPIW LFEGRLSEKS VSTVSGLFSA
 51 VWATDSGSGV SMTISTGLYG LKVSYSYTLS VDSMAFQSAS ARFWVSSSCV
 101 SAPDKMPFCA AARLSKSKSM RLEGVSVSTS NVCFADNSSS DSPSKASVSF
 151 TSFFGAGSGV AGVSTSAKVI SMPSSAASSR SGSSSGTDSS VRRARLDWAR
 201 RKSSSRAINA APPPASSKVY EPPNRPNSP LSVSSSAETC STGSETALPV
 251 SSVGVMAEA AASWGADSA VSDAAVFAAG TSGRTAGFS AFASGAATFA
 301 SGFSTGFSTV ACLDGS DGM DAVSALGFAVC GLGCSALILF RFGM*

m575/g575 70.2% identity in 114 aa overlap

	240	250	260	270	280
m575.pep	SSAETCSTGSETALPVSSVGVMAEAAA	SWGADSAVSDAAVFAAGTG	-----		
g575	LHWLFPPQVRKRCYRFRRSACRWQKRRL	LGGADSAVSDAAVFAAGTGP	GWRSVAEAGVS		
	50	60	70	80	90 100

	290	300	309	310	320
m575.pep	-----SGRTAGFSAFASGAATFASGFSTGFST	-----	VACLDGSDGMDAVSALGFA		
g575	DTAGLGSRTAGFSAFASGAATFASGFSTGFSTGFSIGFSTVACLDGSDGMDAVSALGFA				
	110	120	130	140	150 160

	330	340
m575.pep	VCGLGCSALI-----LFRFGMX	
g575	VCGLGCSALIFLGAAALILFRFGMX	
	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1735>:

a575.seq
 1 ATGGTTTTCGG GCGAGGAAGC CTTCAGGAAG CCTGCCAGTC CGGAGGGTGA
 51 GGCAGGTTTT GCGGAAGCTG TTTCTTCTGT GCCGATATGG TTGTTTGAGG
 101 GCAGGTTGTC GGAGAAATCG GTATCGACGG TTTCCGGTTT GTTTTCGGCA
 151 GTTTGGGCGA CAGATTCCGG TTCGGGCGTG TCGATGACGA TTTCGACAGG
 201 GTTGTACGGG TTGAAGGTCT CGGGCTCGTA CACGCTGTCT GTGGATTCTGA
 251 TGGCGTTCCA ATCGGCATCC GCGCGTTTTT GGGTTTCTTC ATCCTGCGTA
 301 AGTGCGCCGG ATAAAATGCC GTTTTGCGCG GCTGCCAGGC TGTGCAAATC
 351 CAAGTCGATG CGGTTGGAAG GCGTATCGGT TTCGACATCG AACGTTTGTT
 401 TTGCCGACAA CTCTTCTTCA GATCCCCAT CTAAGGCAAG TGTGTCGTTT
 451 ACATCGTTTT TCGGAGCGGG TTCGGGCGTT GCCGAGTTT CCACTTCGGC
 501 AAAGGTGATT TCTATGCCGT CGTCTGCCGC GTCGTCAAGG TCAGGCTCTT
 551 CCTCAGGGAC GGATTCTTCG GTACGGCGCG CGCGTTTGA TTGGGCAAGG
 601 CGCAAAAGCA GCAGCAGGGC GATCAATGCC GCGCCTCCGC CGGCAAGCAG
 651 CAAGGTGTAC GAACCGCCGA ACAGTCCGCT TTCGGTTTCT TCTTCGGCAG
 701 AAACCTGTTC GACAGGTTTC GAAACGCGT TACCGGTTTC GTCGGTCGGC
 751 GTGTCGATGG CAGAAGCGGC GGCTTCTTGG GGGGCGGATT CGGCAGCGGT
 801 TTCCGATGCG GCAGTATTTG CAGCGGGTAC AGGTTCTGGG CGAACGCGCG
 851 GTTTTTCCGC TTTTGCTTCG GCGCGGCAA CTTTTGCTTC AGGTTTTTCA
 901 ACCGGTTTCT CTACCGTTGC CTGTTTGGAC GGTTCGGACG GCATGGATGC
 951 GGTTCGGCT TTGGGTTTCG CCGTTTGC GG TTTGGGTTGT TCCGCTTTGA
 1001 TCCTGTTCAG ATTCGGAATG TGA

This corresponds to the amino acid sequence <SEQ ID 1736; ORF 575.a>:

a575.pep
 1 MVSGEAEFRK PASPEGEAGF AEAUSSVPIW LFEGRLSEKS VSTVSGLFSA
 51 VWATDSGSGV SMTISTGLYG LKVSYSYTLS VDSMAFQSAS ARFWVSSSCV
 101 SAPDKMPFCA AARLSKSKSM RLEGVSVSTS NVCFADNSSS DSPSKASVSF
 151 TSFFGAGSGV AGVSTSAKVI SMPSSAASSR SGSSSGTDSS VRRARLDWAR
 201 RKSSSRAINA APPPASSKVY EPPNSPLSVS SSAETCSTGS ETALPVSSVG
 251 VSMAEAAASW GADSAAVSDA AVFAAGTGS RTAGSAFAS GAATFASGFS
 301 TGFSTVACLD GSDGMDAVSA LGFAVCGLGC SALILFRFGM *

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m575/a575 98.8% identity in 344 aa overlap

m575.pep	10	20	30	40	50	60
	MVSGEEAFRK	PASPEGEAGFAE	AVSSVPIWLF	EGRLSEKSVST	VSGLFS	SAVWATDSGSGV
a575	10	20	30	40	50	60
	MVSGEEAFRK	PASPEGEAGFAE	AVSSVPIWLF	EGRLSEKSVST	VSGLFS	SAVWATDSGSGV
m575.pep	70	80	90	100	110	120
	SMTISTGLY	GLKVSGSYT	LSVDSMAFQ	SASARFWV	SSSCVSA	PDKMPFCAAARLSKSKSM
a575	70	80	90	100	110	120
	SMTISTGLY	GLKVSGSYT	LSVDSMAFQ	SASARFWV	SSSCVSA	PDKMPFCAAARLSKSKSM
m575.pep	130	140	150	160	170	180
	RLEGVSVST	SNVCFADN	SSSDSPSKAS	VSFTSFFG	AGSGVAGV	STSAKVISMPSAASSR
a575	130	140	150	160	170	180
	RLEGVSVST	SNVCFADN	SSSDSPSKAS	VSFTSFFG	AGSGVAGV	STSAKVISMPSAASSR
m575.pep	190	200	210	220	230	240
	SGSSSGTD	SSVRRARLD	WARRKSSSR	AINAAPP	PASSKVYE	PPNRPNSPLSVSSSAETC
a575	190	200	210	220	230	240
	SGSSSGTD	SSVRRARLD	WARRKSSSR	AINAAPP	PASSKVYE	PPN----SPLSVSSSAETC
m575.pep	250	260	270	280	290	300
	STGSETAL	PVSSVGVS	MAEAAASW	GADSAAV	SDAAVFA	AGTGSGRTAGFSAFASGAATFA
a575	240	250	260	270	280	290
	STGSETAL	PVSSVGVS	MAEAAASW	GADSAAV	SDAAVFA	AGTGSGRTAGFSAFASGAATFA
m575.pep	310	320	330	340		
	SGFSTGFST	VACLDGSD	GMDAVS	ALGFAV	CGLGCS	ALILFRFGMX
a575	300	310	320	330	340	
	SGFSTGFST	VACLDGSD	GMDAVS	ALGFAV	CGLGCS	ALILFRFGMX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1737>:

g576.seq.. (partial)

```

1 ..atgggcgtgg acatcgagacg ctccctgaaa caaatgaagg aacaggggcgc
51 ggaaatcgat ttgaaagtct ttaccgatgc catgcaggca gtgtatgacg
101 gcaaagaaat caaaatgacc gaagagcagg cccagggaagt gatgatgaaa
151 ttcttgacag agcagcaggc taaagccgta gaaaaacaca aggcggatgc
201 gaaggccaac aaagaaaaag gcgaagcctt cctgaaggaa aatgccgccc
251 aagacggcgt gaagaccact gcttccgggtc tgcagtacaa aatcaccaaa
301 cagggtgaag gcaaacagcc gacaaaagac gacatcgta ccgtggaata
351 cgaaggccgc ctgattgacg gtaccgtatt cgacagcagc aaagccaacg
401 gcggcccggc caccttcctt ttgagccaag tgattccggg ttggaccgaa
451 ggcgtacggc ttctgaaaga aggcggcgaa gccacgttct acatcccgtc
501 caaccttgcc taccgcgaac aggggtgcggg cgaaaaaatc ggtccgaacg
551 ccactttggt atttgacgtg aaactgggtc aaatcggcgc acccgaaac
601 gcgcccgcga agcagccgga tcaagtcgac atcaaaaaag taaattaa

```

This corresponds to the amino acid sequence <SEQ ID 1738; ORF 576.ng>:

g576.pep.. (partial)

```

1 ..MGVDIGRSLK QMKEQGA EID LKVFTDAMQA VYDGKEIKMT EEQAQEVMMK
51 FLQEQQAKAV EKHKADAKAN KEKGEAFLKE NAEEDGVKTT ASGLQYKITK
101 QGEGKQPTKD DIVTVEYEGR LIDGTVFDDSS KANGGPATFP LSQVIPGWTE
151 GVRLLKEGGE ATFYIPSNLA YREQGAGEKI GPNATLVFDV KLVKIGAPEN
201 APAKQPDQVD IKKVN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1739>:

m576.seq.. (partial)

```

1 ..ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA

```

```

51   GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
101  CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC CGAAGAGCAG
151  GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
201  AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
251  TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCGGGC
301  CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
351  CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
401  TCGACAGCAG CAAAGCCAAC GCGGCCCCG TCACCTTCCC TTTGAGCCAA
451  GTGATTCGGG GTTGACCGA AGCGTACAG CTCTGAAAG AAGGCGGCGA
501  AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
551  GCGACAAAAT CGGTCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
601  AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
651  CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1740; ORF 576>:

m576.pep.. (partial)

```

1   ..MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
51  AQEVMKFLO EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVRTTASG
101 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
151 VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVDVKLV
201 KIGAPENAPA KQPAQVDIKK VN*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m576/g576 97.2% identity in 215 aa overlap

	10	20	30	40	50	60
m576.pep	MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ AQEVMKFLO					
g576	MGVDIGRSLKQMK EQGAEIDLKV FTDAMQAVYD GKEIKMTEEQ AQEVMKFLO					
	10	20	30	40	50	
	70	80	90	100	110	120
m576.pep	EQQAKAVEKHKADAKANKEKGEAFLENAAKDGVRTTASGLQYKITKQEGGKQPTKDDIV					
g576	EQQAKAVEKHKADAKANKEKGEAFLENAAEDGVKTTASGLQYKITKQEGGKQPTKDDIV					
	60	70	80	90	100	110
	130	140	150	160	170	180
m576.pep	TVEYEGRLIDGTVFDSSKANGGPVTFPLSQVIPGWTEGVQLLKEGGEATFYIPSNLAYRE					
g576	TVEYEGRLIDGTVFDSSKANGGPATFPLSQVIPGWTEGVRLLEKGEATFYIPSNLAYRE					
	120	130	140	150	160	170
	190	200	210	220		
m576.pep	QGAGDKIGPNATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
g576	QGAGEKIGPNATLVFDVKLVKIGAPENAPAKQPDQVDIKKVN					
	180	190	200	210		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1741>:

a576.seq

```

1   ATGAACACCA TTTTCAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTTCCGCC TGCGGCAAAA AAGAAGCCGC CCCC GCATCT GCATCCGAAC
101 CTGCGCCGCG TTCTCCGCG CAGGGCGACA CCTCTCGAT CGGCAGCAGC
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCGGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GCGGCCCCG TCACCTTCCC TTTGAGCCAA

```

```

601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGACAAAAT CGGCCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1742; ORF 576.a>:

```

a576.pep
1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

m576/a576 99.5% identity in 222 aa overlap

m576.pep
10 20 30
MQQASYAMGV DIGRSLKQMK EQGAEIDLKV
|||||
a576 CGKKEAAPAS ASEPAASSA QGDTSSIGST MQQASYAMGV DIGRSLKQMK EQGAEIDLKV
30 40 50 60 70 80

m576.pep
40 50 60 70 80 90
FTEAMQAVYD GKEIKMTEEQ AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA
|||||
a576 FTEAMQAVYD GKEIKMTEEQ AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA
90 100 110 120 130 140

m576.pep
100 110 120 130 140 150
KDGVKTTASGL QYKITQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
|||||
a576 KDGVKTTASGL QYKITQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
150 160 170 180 190 200

m576.pep
160 170 180 190 200 210
VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV KIGAPENAPA
|||||
a576 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV KIGAPENAPA
210 220 230 240 250 260

m576.pep
220
KQPAQVDIKK VN
|||||
a576 KQPAQVDIKK VN
270

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1743>:

```

g576-1.seq
1  ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTTCCGCC TCGCGCAAAA AAGAAGCCGC CCCCAGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTGCCGCG CAGGGCGACA CCTCTTCAAT CGGCAGCAGC
151 ATGCAGCAGG CAAGCTATGC AATGGGCGTG GACATCGGAC GCTCCCTGAA
201 ACAAATGAAG GAACAGGGCG CGGAAATCGA TTGAAAGTC TTACCGATG
251 CCATGCAGGC AGTGATGAC GGCAAAGAAA TCAAATGAC CGAAGAGCAG
301 GCCCAGGAAG TGATGATGAA ATTCCTGCAG GAGCAGCAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGATG CGAAGGCCAA CAAAGAAAAA GGCGAAGCCT
401 TCCTGAAGGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGCT
451 CTGCAGTACA AAATACCAA ACAGGGTGAA GGCAAACAGC CGACAAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACCGTAT
551 TCGACAGCAG CAAAGCCAAC GCGCGCCCGG CCACCTTCCC TTGAGCCAA
601 GTGATTCCGG GTTGGACCGA AGGCGTACGG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGAAAAAAT CGGTCCGAAC GCCACTTTGG TATTTGACGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG ATCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1744; ORF 576-1.ng>:

g576-1.pep

```

1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASAA QGDTSSIGST
51  MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTDAMQAVYD GKEIKMTEEQ
101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITQGE GKOPTKDDIV TVEYEGRLID GTVFDSSKAN GGPATFPLSQ
201 VIPGWTEGVR LLKEGGEATF YIPSNLAYRE QGAGEKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPDQVDIKK VN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1745>:

m576-1.seq

```

1  ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTTCCGCC TCGGGCAAAA AAGAAGCCGC CCCC GCATCT GCATCCGAAC
101 CTGCCCGCGC TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCAGC
151 ATGCAGCAGC CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
601 GTGATTCCGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGCGGCGA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGACAAAAT CGGTCCGAAC GCCACTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1746; ORF 576-1>:

m576-1.pep

```

1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITQGE GKOPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

```

g576-1/m576-1 97.8% identity in 272 aa overlap

	10	20	30	40	50	60
g576-1.pep	MNTIFKISAL TLSAALALSACGKKEAAPASASEPAASAAQGDTSSIGSTMQQASYAMGV					
m576-1	MNTIFKISAL TLSAALALSACGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
	10	20	30	40	50	60
g576-1.pep	70	80	90	100	110	120
	DIGRSLKQMK EQGAEIDLKV FTDAMQAVYD GKEIKMTEEQ AQEVMMKFLQ EQQAKAVEKH					
m576-1	DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ AQEVMMKFLQ EQQAKAVEKH					
	70	80	90	100	110	120
g576-1.pep	130	140	150	160	170	180
	KADAKANKEK GEAFLENAA KDGVKTTASGLQYKITQGE GKOPTKDDIV TVEYEGRLID					
m576-1	KADAKANKEK GEAFLENAA KDGVKTTASGLQYKITQGE GKOPTKDDIV TVEYEGRLID					
	130	140	150	160	170	180
g576-1.pep	190	200	210	220	230	240
	GTVFDSSKAN GGPATFPLSQ VIPGWTEGVRLLEKGEATFYIPSNLAYREQGAGEKIGPN					
m576-1	GTVFDSSKAN GGPVTFPLSQ VIPGWTEGVQLLEKGEATFYIPSNLAYREQGAGDKIGPN					
	190	200	210	220	230	240
g576-1.pep	250	260	270			
	ATLVFDVKLV KIGAPENAPAKQPDQVDIKK VN*					
m576-1	ATLVFDVKLV KIGAPENAPAKQPAQVDIKK VN*					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1747>:

a576-1.seq


```

1  ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCGG CCGCTTTGGC
51  ACTTTCCGCC TGCGGCAAAA AAGAAGCCGC CCCCAGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCACG
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCTTCAG GAACAACAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAG ACAGGGCGAA GGCAAACAGC CGACCAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCAG
701 GCGCAAAAAT CGGCCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1748; ORF 576-1.a>:

a576-1.pep

```

1  MNTIFKISAL TLSAALALS CGKKEAAPAS ASEPAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

```

a576-1/m576-1 99.6% identity in 272 aa overlap

	10	20	30	40	50	60
a576-1.pep	MNTIFKISALTLSAALALSACGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
m576-1	MNTIFKISALTLSAALALSACGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
	10	20	30	40	50	60
	70	80	90	100	110	120
a576-1.pep	DIGRSLKQMKEQGAEIDLKVFTTEAMQAVYDGKEIKMTEEQAEVMMKFLQEQQAKAVEKH					
m576-1	DIGRSLKQMKEQGAEIDLKVFTTEAMQAVYDGKEIKMTEEQAEVMMKFLQEQQAKAVEKH					
	70	80	90	100	110	120
	130	140	150	160	170	180
a576-1.pep	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITQGEKGKPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITQGEKGKPTKDDIVTVEYEGRLID					
	130	140	150	160	170	180
	190	200	210	220	230	240
a576-1.pep	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
m576-1	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
	190	200	210	220	230	240
	250	260	270			
a576-1.pep	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
m576-1	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
	250	260	270			

Expression of ORF 576

The primer described in Table 1 for ORF 576 was used to locate and clone ORF 576. ORF 576 was cloned in pET and pGex vectors and expressed in E.coli as above described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 3A shows the results of affinity purification and Figure 3B shows the expression in E.coli. Purified His-fusion protein was used to immunize mice, whose sera were used for ELISA (positive result), FACS analysis (Figure 3C), western blot (Figure 3D). These experiments confirm that ORF 576 is a surface-exposed protein and that it is a useful immunogen. The

hydrophilicity plots, antigenic index, and amphipatic regions of ORF 576 are provided in Figure 7. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 576 and the amino acid sequence encoded thereby is provided in Example 1.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1749>:

```
g577.seq..
  1 atggaaagga gcggtgtatt tggtaaaatt gtcggcaatc gcatactccg
 51 tatgccgtcc gaacacgctg ccgcattcta tccgaaaccg tgcaaatcgt
101 ttaaactaac gcaatcttgg ttcagagtgc gaagctgtcc gtgcggcggt
151 tttattttacg gagcaaacat gaaacttatc tataccgtca tcaaaatcat
201 tatcctgctg ctcttctctg tgcttgccgt cattaatatg gatgccgtta
251 ccttttccta tcttcggggg cagagtgtca atctgccgct gattgtcgta
301 ttgttcggcg cgtttgctgt cggcatcgtg ttcggaatgt ttgccctgtt
351 cgggcggtg ctgtccttgc gcggcgaaaa cagccgctg cgtgcggaag
401 tgaagaaaag tgcgcgcttg agcggacaga aattgactgc accgccgata
451 caaatgctg ccgaatctgc caaacagcct taa
```

This corresponds to the amino acid sequence <SEQ ID 1750; ORF 577.ng>:

```
g577.pep
  1 MERSGVFGKI VGNRILRMPS EHAAAFYPKP CKSFKLQSW FRVRSCPCGV
 51 FIYGANMKLI YTVIKIIILL LFLLLAVINM DAVTFSYLPQ QSVNPLIVV
101 LFGAFVVGIV FGMFALFGRL LSLRGENSRL RAEVKKSARL SGQKLTAPPI
151 QNAESAQKP *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1751>:

```
m577.seq..
  1 ATGGAAAGGA ACGGTGTATT TGGTAAATTT GTCGGCAATC GCATACTCCG
 51 TATGTCGTCC GAACACGCTG CCGCATCCTA TCCGAAACCG TGCAAATCGT
101 TTAACTAGC GCAATCTTGG TTCAGAGTGC GAAGCTGTCT GGGCGGCGTT
151 TTTATTACG GAGCAAACAT GAAACTTATC TATACCGTCA TCAAAATCAT
201 TATCCTGCTG CTCTTCCTGC TGCTTGCCGT CATTAATACG GATGCCGTTA
251 CCTTTTCCTA CTGCGCGGGG CAAAATTCG ATTTGCCGCT GATTGTCGTA
301 TTGTTCCGCG CATTTGTAGT CCGTATTATT TTTGGAATGT TTGCCTTGTT
351 CGGACGGTTG TTGTCGTTAC GTGGCGAGAA CGGCAGGTTG CGTGCCGAAG
401 TAAAGAAAAA TGCGCGTTTG ACGGGGAAGG AGCTGACCGC ACCACCGGCG
451 CAAATGCGC CCGAATCTAC CAAACAGCCT TAA
```

This corresponds to the amino acid sequence <SEQ ID 1752; ORF 577>:

```
m577.pep..
  1 MERNGVFGKI VGNRILRMSS EHAAASYPKP CKSFKLAQSW FRVRSCLGCV
 51 FIYGANMKLI YTVIKIIILL LFLLLAVINT DAVTFSYLPQ QKFDLPLIVV
101 LFGAFVVGII FGMFALFGRL LSLRGENGRL RAEVKKNARL TGKELTAPPA
151 QNAPESTKQP *
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m577/g577 88.1% identity in 160 aa overlap

```

      10      20      30      40      50      60
m577.pep  MERNGVFGKIVGNRILRMSSEHAAASYPKPCKSFKLAQSWFRVRSCLGCVFIYGANMKLI
          |||:|||||
g577      MERSGVFGKIVGNRILRMPSEHAAAFYPKPCKSFKLQSWFRVRSCPCGVFIYGANMKLI
          |||:|||||
      10      20      30      40      50      60

      70      80      90     100     110     120
m577.pep  YTVIKIIILLLFLLLAVINTDAVTFSYLPQKFDLPLIVVLFGAFVVGIIIFGMFALFGRL
```

895

```

g577      |||||:|||||:|||||:|||||:|||||:
          YTVIKIIILLFLLLAVINMDAVTFSYLPGQSVNLPLIVVLFGAFVVGIVFGMFALFGRL
          70      80      90      100     110     120

          130      140      150      160
m577.pep  LSLRGENGRRLRAEVKKNARLTGKELTAPPAQNAPESTKQPX
          |||||:|||||:|||||:|||||:|||||:
g577      LSLRGENSRLRAEVKKSARLSGQKLTAPPIQNAESAQKQFX
          130      140      150      160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1753>:

```

a577.seq
1  ATGGAAAGGA ACGGTGTATT TGGTAAAATT GTCGGCAATC GCATACTCCG
51 TATGTCGTCC GAACACGCTG CCGCATCCTA TCCGAAACCG TGCAAATCGT
101 TTAAACTAGC GCAATCTTGG TTCAGAGTGC GAAGCTGTCC GGGCGGCGTT
151 TTTATTTACG GAGCAAACAT GAAACTTATC TATACCGTCA TCAAAATCAT
201 TATCCTGCTG CTCTCCTGCG TGCTTGCTGT CATTAAATACG GATGCCGTTA
251 CCTTTTCCTA CCTGCCGGGG CAAAATTCG ATTTGCCGCT GATTGTCTGT
301 TTGTTTCGGC CGTTTGTCTG CGGCATCGTG TTCGGAATGT TTGCCTTGTT
351 CGGACGGTTG TTGTCGTTAC GTGGCGAGAA CGGCAGGTTG CGTGCCGAAG
401 TAAAGAAAAA TGC GCGTTT AC GGGGAAGG AGCTGACCGC ACCACCGGCG
451 CAAAATGCGC CCGAATCTGC CAAACAGCCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1754; ORF 577.a>:

```

a577.pep
1  MERNGVFGKI VGNRILRMSS EHAAASYPKP CKSFKLAQSW FRVRSCPGGV
51 FIYGANMKLI YTVIKIIILL LFLLLAVINT DAVTFSYLPG QKFDLPLIVV
101 LFGAFVVGIV FGMFALFGRL LSLRGENGRL RAEVKKARLT TGKELTAPPA
151 QNAPESAKQP *

```

m577/a577 98.1% identity in 160 aa overlap

```

          10      20      30      40      50      60
m577.pep  MERNGVFGKIVGNRILRMSSEHAAASYPKPCKSFKLAQSWFRVRSCPGGVFIYGANMKLI
          |||||:|||||:|||||:|||||:|||||:
a577      MERNGVFGKIVGNRILRMSSEHAAASYPKPCKSFKLAQSWFRVRSCPGGVFIYGANMKLI
          10      20      30      40      50      60

          70      80      90      100     110     120
m577.pep  YTVIKIIILLFLLLAVINTDAVTFSYLPGQKFDLPLIVVLFGAFVVGIIFGMFALFGRL
          |||||:|||||:|||||:|||||:|||||:
a577      YTVIKIIILLFLLLAVINTDAVTFSYLPGQKFDLPLIVVLFGAFVVGIVFGMFALFGRL
          70      80      90      100     110     120

          130      140      150      160
m577.pep  LSLRGENGRRLRAEVKKNARLTGKELTAPPAQNAPESTKQPX
          |||||:|||||:|||||:|||||:|||||:
a577      LSLRGENGRRLRAEVKKNARLTGKELTAPPAQNAPESTKQPX
          130      140      150      160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1755>:

```

g578.seq
1  atgggaaagc tcgacatcgg gatattgttt gccgatttct tcaaagattt
51 cgcgccacag ttcggtggtt tccaaaacgt tggctttgcc tacggagcag
101 acttttttgc tgcgtttttg ggcggattgg aaggccacgt gggcgatgcg
151 gcggtattcg ctttcgctgt atttcattgt gttgtagcct tcgtgttcgc
201 cgtttttccaa aacacggatg ccgcgcggtt cgccgaaata aatatcgccg
251 gtaagttcgc gcacaatcaa aatatccaaa ccggcaacga tttcaggctt
301 gagcgtggag gcgttggcta a

```

This corresponds to the amino acid sequence <SEQ ID 1756; ORF 578.ng>:

```

g578.pep
1  MGKLDIGILF ADFFKDFAPQ FGGFQNVGFA YGADFFAAFL GGLEGHVGD
51 ADFAFAVFGH VVAFVFAVFQ NTDAARFAEI NIAGKFAHNQ NIQTGNDFRL

```

101 ERGGVG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1757>:

m578.seq..

```

1  ATGGGAAAGC TCGACATCAG GGTACTCTTT GCCGATTCTT TCAAAGATTT
51  CGCGCCACAA TTCGGTGGTT TCCAAAACGT TGGCTTTGCC TACGGAACAG
101 ACTTTTTTGC TGCCTTTTTC GCGGATTGG  AAGGCAACAT GGGCAATACG
151 GCGGATTTCG CTTTCGCTGT ATTTTCATGGT GTTGTAGCCT TCGCGTTCGC
201 CGTTTTCCAG AACGCGGATG CCGCGCGGTT CGCCGAAATA GATGTCGCCG
251 GTGAGTTCGC GCACAATCAA AATATCCAAA CCGGCAACGA TTTCAGGCTT

```

This corresponds to the amino acid sequence <SEQ ID 1758; ORF 578>:

m578.pep..

```

1  MGKLDIRVLF ADFFKDFAPQ FGGFQNVGFA YGTDFFAAFL GGLEGNMGNT
51  ADFAFAVFHG VVAFAFAVFQ NADAARFAEI DVAGEFAHNQ NIQTGNDFRL
101 QRGGVG*

```

m578/g578 87.7% identity in 106 aa overlap

	10	20	30	40	50	60
m578.pep	MGKLDIRVLFADFFKDFAPQFGGFQNVGFAYGTDFFAAFLGGLEGNMGNTADFAFAVFHG					
	: : :					
g578	MGKLDIGILFADFFKDFAPQFGGFQNVGFAYGADFFAAFLGGLEGHVGDADFAFAVFHG					
	10	20	30	40	50	60
	70	80	90	100		
m578.pep	VVAFAFAVFQ NADAARFAEIDVAGEFAHNQNIQTGNDFRLQRGGVGX					
	: : : :					
g578	VVAFAFAVFQNTDAARFAEINIAGKFAHNQNIQTGNDFRLERGGVGX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1759>:

a578.seq

```

1  ATGGGAAAGC TCGACATCAG GGTATTCTTT GCCGATTCTT TCAAAGATTT
51  CGCGCCACAA TTCGGTGGTT TCCAAAACGT TGGCTTTGCC TACGGAGCAG
101 ACTTTTTTGC TGCCTTTTTC GCGGATTGG  AAGGCGACGT GGGCAATACG
151 GCGGATTTCG CTTTCGCTGT ATTTTCATGGT GTTGTAGCCT TCGCGTTCGC
201 CGTTTTCCAG AACACGGATG CCGCGCGGTT CGCCGAAATA AATATCGCCG
251 GTGAGTTCGC GCACAATCAA AATATCCAAA CCCGCAACGA TTTCAGACTT
301 GAGCGTGGAG GCGTTGGCTA G

```

This corresponds to the amino acid sequence <SEQ ID 1760; ORF 578.a>:

a578.pep

```

1  MGKLDIRVFF ADFFKDFAPQ FGGFQNVGFA YGADFFAAFL GGLEGDVGNT
51  ADEFAFAVFHG VVAFAFAVFQ NTDAARFAEI NIAGEFAHNQ NIQTRNDFRL
101 ERGGVG*

```

m578/a578 91.5% identity in 106 aa overlap

	10	20	30	40	50	60
m578.pep	MGKLDIRVLFADFFKDFAPQFGGFQNVGFAYGTDFFAAFLGGLEGNMGNTADFAFAVFHG					
	: : :					
a578	MGKLDIRVFFADFFKDFAPQFGGFQNVGFAYGADFFAAFLGGLEGDVGNTADFAFAVFHG					
	10	20	30	40	50	60
	70	80	90	100		
m578.pep	VVAFAFAVFQ NADAARFAEIDVAGEFAHNQNIQTGNDFRLQRGGVGX					
	: : : :					
a578	VVAFAFAVFQNTDAARFAEINIAGEFAHNQNIQTRNDFRLERGGVGX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1761>:

g579.seq..

```

1  ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT

```

```

51  TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101 CATTGGGACG GTTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 GGCGCGGGTT TGGCGGTGGC GTTGTCCCTA AAAGACCAGC TGTCCAATTT
201 TGCCGCCGGC GCGCTGATTA TCCTGTTCCG CCCGTTCAAA GTCGGCGACT
251 TTATCCGTGT CGGCGGTTTT GAAGGATATG TCCGGGAAAT CAAAATGGTG
301 CAGACTTCTT TGCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351 CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCAGCCTG CCGCTTTGCC
401 GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATT TAAAGTGGCG
451 AAAGAGGCGG TGTGAAAGC CGCCGCCGAA CACCCCTTGA GCGTTCAAAA
501 CGAAGAGCGG CAGCCCGCCG CCTACATCAC CGCCTTGGGC GACAATGCCA
551 TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG
601 CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651 CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1762; ORF 579.ng>:

```

g579.pep..
1  MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51  GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTS LRRTDNE EVVLPNSVVM GNSIVNRSSL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAAE HPLSVQNEER QPAAAYITALG DNAIEITLWA WANEADRWTL
201 QCDLNEQVVE NLRKVNINIP FPQRDIHIIN S*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1763>:

```

m579.seq..
1  ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT
51  TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101 CATTGGGACG GTTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 GGCGCGGGTT TGGCGGTGGC GTTGTCCCTG AAAGACCAGC TGTCCAATTT
201 TGCCGCCGGC GCACTGATTA TCCTGTTCCG CCCGTTCAAA GTCGGCGATT
251 TTATCCGCGT CGGCGGTTTT GAAGGATATG TCCGAGAGAT TAAAATGGTG
301 CAGACTTCTT TGCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351 CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCACACTG CCGCTGTGCC
401 GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATT TAAAGTGGCG
451 AAAGAGGCGG TGTGAAAGC CGCCGTCGAA CACCCCTTGA GCGTTCAAAA
501 CGAAGAGCGG CAGGCTGCCG CCTACATCAC CGCCTTGGGC GACAATGCCA
551 TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG
601 CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651 CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1764; ORF 579>:

```

m579.pep..
1  MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51  GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTS LRRTDNE EVVLPNSVVM GNSIVNRSSL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAVE HPLSVQNEER QAAAYITALG DNAIEITLWA WANEADRWTL
201 QCDLNEQVVE NLRKVNINIP FPQRDIHIIN S*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

```

m579/g579 98.7% identity in 231 aa overlap

      10      20      30      40      50      60
m579.pep  MRAAMTRAQVDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSL
          |||
g579      MRAAMTRAQVDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSL
          |||

      70      80      90     100     110     120
m579.pep  KDQLSNFAAGALIIILFRPFKVGDFIRVGGFEGYVREIKMVQTS LRRTDNEEVVLPNSVVM
          |||
g579      KDQLSNFAAGALIIILFRPFKVGDFIRVGGFEGYVREIKMVQTS LRRTDNEEVVLPNSVVM
          |||

```

898

	130	140	150	160	170	180
m579.pep.	GNSIVNRSTLPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG					
g579	GNSIVNRSSLPLCRAQVIVGVVDYNCDLKVAKEAVLKAAAEHPLSVQNEERQPAAYITALG					
	130	140	150	160	170	180
	190	200	210	220	230	
m579.pep	DNAIEITLWAWANEADRWTLQCDLNEQVVENLRKVNINIPFPQORDIHIINSX					
g579	DNAIEITLWAWANEADRWTLQCDLNEQVVENLRKVNINIPFPQORDIHIINSX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1765>:

```

a579.seq
1   ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT
51  TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101 CATTGGGCAG ATTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 GGCGCGGGTT TGGCGGTGGC GTTGTCCTTG AAAGACCAGC TGTCCAATTT
201 TGCCGCCGGC GCGCTGATTA TCCTGTTCCG CCCGTTCAA A GTCGGCGATT
251 TTATCCGCGT CGGCGGTTTT GAAGGATATG TCCGAGAGAT TAAATGGTG
301 CAGACTTCTT TGGCGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351 CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCACACTG CCGCTGTGCC
401 GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATTT GAAAGTGGCG
451 AAAGAGGCGG TGTTGAAAGC CGCCGTCGAA CACCCCTTGA GCGTTCAAAA
501 CGAAGAGCGG CAGGCCGCCG CCTACATCAC CGCCTGGGC GACAATGCCA
551 TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG
601 CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651 CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1766; ORF 579.a>:

```

a579.pep
1   MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51  GAGLAVALSI KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSRLRTDNE EVVLPNSVVM GNSIVNRSTL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAVE HPLSVQNEER QAAAYITALG DNAIEITLWA WANEADRWTL
201 QCDLNEQVVE NLRKVNINIP FPQORDIHIIN S*

m579/a579    100.0% identity in 231 aa overlap

          10      20      30      40      50      60
m579.pep    MRAAMTRAQVDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSI
a579         MRAAMTRAQVDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSI
          10      20      30      40      50      60

          70      80      90     100     110     120
m579.pep    KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVM
a579         KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVM
          70      80      90     100     110     120

          130     140     150     160     170     180
m579.pep    GNSIVNRSTLPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG
a579         GNSIVNRSTLPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG
          130     140     150     160     170     180

          190     200     210     220     230
m579.pep    DNAIEITLWAWANEADRWTLQCDLNEQVVENLRKVNINIPFPQORDIHIINSX
a579         DNAIEITLWAWANEADRWTLQCDLNEQVVENLRKVNINIPFPQORDIHIINSX
          190     200     210     220     230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1767>:
g579-1.seq